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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 716.653 Seconds

(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-5

Perfect score: 30

Sequence: 1 CTGACGAGACCCCACTTTCGGCGTGCAG 30

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New: *
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq: *
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	73.3	23	1	PCT-US03-04088-522 Sequence 522, App
C 2	19	63.3	21	1	PCT-US03-04088-540 Sequence 540, App
C 3	19	63.3	21	1	PCT-US03-04088-544 Sequence 544, App
C 4	19	63.3	21	1	PCT-US03-04088-548 Sequence 548, App
C 5	19	63.3	21	1	PCT-US03-04088-552 Sequence 552, App
C 6	19	63.3	21	1	PCT-US03-04088-556 Sequence 556, App
C 7	19	63.3	21	1	PCT-US03-04088-560 Sequence 560, App
C 8	18	60.0	19	1	PCT-US03-04088-23 Sequence 23, App
C 9	18	60.0	19	1	PCT-US03-04088-287 Sequence 287, App
C 10	17	56.7	50	9	US-10-325-899-7470 Sequence 7470, App
C 11	16	56.0	25	12	US-60-427-808-503841 Sequence 503841, App
C 12	16	53.3	25	12	US-60-427-808-699316 Sequence 699316, App
C 13	16	53.3	21	1	PCT-US03-04088-588 Sequence 588, App
C 14	16	53.3	23	1	PCT-US03-04088-530 Sequence 530, App
C 15	16	53.3	25	12	US-60-427-836-550603 Sequence 550603, App
C 16	15	52.7	43	10	US-10-299-054A-7701 Sequence 7701, App
C 17	15	52.0	25	7	US-09-954-445A-16215 Sequence 16215, A
C 18	15	52.0	25	7	US-09-954-445A-16228 Sequence 16228, A
C 19	15	52.0	25	9	US-10-355-577-992959 Sequence 992959, App
C 20	15	52.0	25	12	US-60-427-808-239563 Sequence 239563, App

C 21	15.6	52.0	25	12	US-60-427-808-374528 Sequence 374528, A
C 22	15.4	51.3	25	9	US-10-355-577-809390 Sequence 809390, A
C 23	15.4	51.3	25	12	US-60-427-808-47221 Sequence 47221, A
C 24	15.4	51.3	25	12	US-60-427-808-546626 Sequence 546626, A
C 25	15.2	50.7	25	9	US-10-355-577-207601 Sequence 207601, A
C 26	15.2	50.7	25	12	US-60-427-808-503840 Sequence 503840, A
C 27	15.2	50.7	47	9	US-10-349-143-3806 Sequence 3806, App
C 28	15	50.0	25	9	US-10-355-577-592670 Sequence 592670, A
C 29	15	50.0	25	12	US-60-427-808-54953 Sequence 54953, A
C 30	15	50.0	25	12	US-60-427-808-54954 Sequence 54954, A
C 31	15	50.0	25	12	US-60-427-808-699317 Sequence 699317, A
C 32	15	50.0	25	12	US-60-427-808-776553 Sequence 776553, A
C 33	14.8	49.3	20	10	US-10-289-762-5017 Sequence 5017, App
C 34	14.8	49.3	25	12	US-60-427-808-449334 Sequence 449334, A
C 35	14.8	49.3	25	12	US-60-427-836-142384 Sequence 142384, A
C 36	14.8	49.3	25	12	US-60-427-836-603511 Sequence 603511, A
C 37	14.6	48.7	31	6	US-09-890-648-6 Sequence 6, App
C 38	14.6	48.7	25	7	US-09-953-570-67312 Sequence 67312, A
C 39	14.6	48.7	25	7	US-09-954-445A-73491 Sequence 73491, A
C 40	14.6	48.7	25	9	US-10-355-577-29370 Sequence 29370, A
C 41	14.6	48.7	25	9	US-10-355-577-850409 Sequence 850409, A
C 42	14.6	48.7	25	9	US-10-355-577-870013 Sequence 870013, A
C 43	14.6	48.7	25	12	US-60-427-808-239182 Sequence 239182, A
C 44	14.6	48.7	25	12	US-60-427-808-764602 Sequence 764602, A
C 45	14.6	48.7	25	12	US-60-427-836-316468 Sequence 316468, A

ALIGNMENTS

RESULT 1
PCT-US03-04088-522/c
Sequence 522, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Beiselman, Leonard
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396, 600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358, 580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363, 124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386, 782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406, 784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408, 378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409, 293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440, 129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 522
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sRNA sense
PCT-US03-04088-522

Query Match 73.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CTGACAGAGCCCACTCTTCG 22
Db      22 CTGACAGAGCCCACTCTTCG 1

RESULT 2
PCT-US03-04088-540/c
Sequence 540, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Mcswigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 540
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (20)..(21)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGACAGAGCCCACTCTTC 20
Db      19 TGACAGAGCCCACTCTTC 1

RESULT 3
PCT-US03-04088-544
Sequence 544, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Mcswigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)

Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TGACAGAGCCCACTCTTC 20
Db      1 TGACAGAGCCCACTCTTC 19

RESULT 4
PCT-US03-04088-548/c
Sequence 548, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Mcswigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 548
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
NAME/KEY: misc_feature
LOCATION: (1)..(1)
```



```
OTHER INFORMATION: 5'-3 attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3 attached terminal deoxyabasic moiety
PCT-US03-04088-548
```

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Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      2 TGACGAGCCCAACTCTTC 20
Db      19 TGACGAGCCCAACTCTTC 1
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RESULT 5

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PCT-US03-04088-552
Sequence 552, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patentin version 3.2
SEQ ID NO 552
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
```

```
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-552
```

```
Query Match      63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
QY      2 TGACGAGCCCAACTCTTC 20
Db      1 UGACGAGCCCAACUCUUC 19
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RESULT 6

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PCT-US03-04088-556/C
Sequence 556, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patentin version 3.2
SEQ ID NO 556
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(6)
OTHER INFORMATION: 2'-deoxy
```

```

NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(8)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(15)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(18)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (19)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (21)..(21)
OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
PCT-US03-04088-556

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Query Match          63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      2 TGACAGAGCCCACTCTTC 20
        |||||
Db      19 TGACAGAGCCCACTCTTC 1

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RESULT 7
PCT-US03-04088-560
Sequence 560, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PCT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129

```

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PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patentin version 3.2
SEQ ID NO 560
LENGTH: 21
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2)..(3)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)..(4)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (5)..(8)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)..(11)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (12)..(13)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14)..(19)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n stands for thymidine
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-internucleotide linkage
PCT-US03-04088-560

```

```

Query Match          63.3%; Score 19; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 TGACAGAGCCCACTCTTC 20
        :|||:|:|:|:|:|:|:|:|
Db      1 UGACAGAGCCCACTCTTC 19

```

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RESULT 8
PCT-US03-04088-23/C
Sequence 23, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PCT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20

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PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-23

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACAGAGCCCACTCT 18
DB 18 CTGACAGAGCCCACTCT 1

RESULT 9

PCT-US03-04088-287
Sequence 287, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
TITLE OF INVENTION: Expression Using Short Interfering RNA (siNA)
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 287
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
PCT-US03-04088-287

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;

Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGACAGAGCCCACTCT 18
DB 2 CTGACAGAGCCCACTCT 19

RESULT 10

US-10-325-899-7470/c
Sequence 7470, Application US/10325899
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Ly, Ngoc
APPLICANT: Woodward, Robert
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
TITLE OF INVENTION: REJECTION
FILE REFERENCE: 506612000122
CURRENT APPLICATION NUMBER: US/10/325,899
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 10/131,831
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 9966
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7470
LENGTH: 50
TYPE: DNA
ORGANISM: Human adenovirus type 2
US-10-325-899-7470

Query Match 56.7%; Score 17; DB 9; Length 50;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 AGAGCCCACTCTGCGGTGGCAG 30
DB 31 AGAGCCCACTCAAGCGGTGGCAG 7

RESULT 11

US-60-427-808-503841
Sequence 503841, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 503841
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-503841

Query Match 56.0%; Score 16.8; DB 12; Length 25;
Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TGACAGAGCCCACTCTTGG 21
DB 6 TGACAGAGCCCAAGTCTCG 25

RESULT 12

US-60-427-808-699316
Sequence 699316, Application US/60427808
GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 699316
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-699316

Query Match      55.3%; Score 16.6; DB 12; Length 25;
Best Local Similarity 82.6%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      7 GAGCCCACTCTTCGCGTGCGCA 29
        |||||
DB      3 GAGCCCACTCTTCAGGCGCA 25

RESULT 13
PCT-US03-04088-588/c
; Sequence 588, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 588
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-588

Query Match      53.3%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTCTTCGCGGTGGCGAG 30
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DB      21 CTCTTCGCGGTGGCGAG 6

RESULT 14
PCT-US03-04088-530/c
; Sequence 530, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 530
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-530

Query Match      53.3%; Score 16; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 CTCTTCGCGGTGGCGAG 30
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DB      23 CTCTTCGCGGTGGCGAG 8

RESULT 15
US-60-427-836-550603/c
; Sequence 550603, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 550603
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-60-427-836-550603

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Best Local Similarity 79.2%; Pred. No. 3.7e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

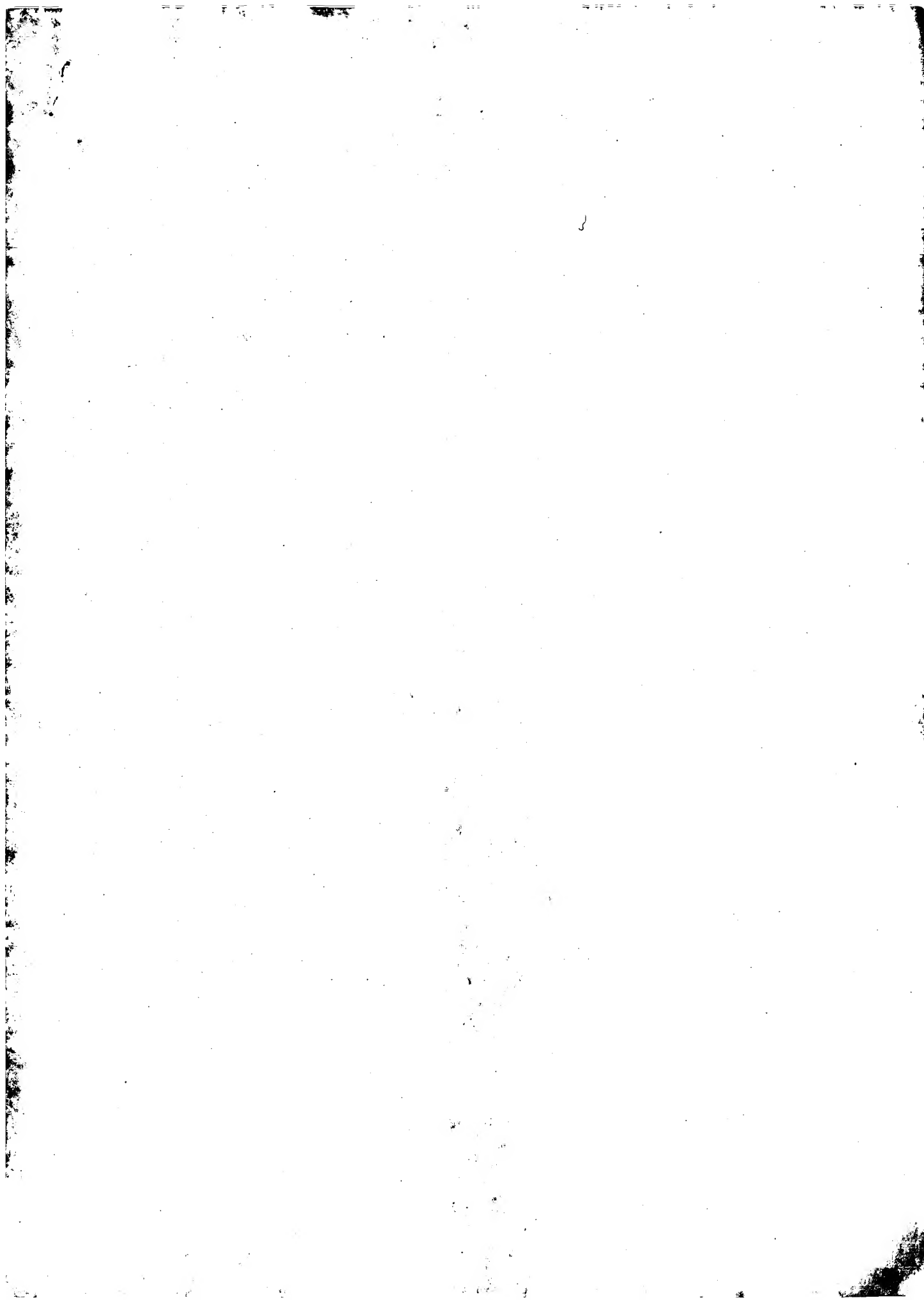
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Fri Jun 27 07:42:47 2003

us-08-770-564a-5.rnpn

Page 7



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 139.554 Seconds
(without alignments)
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Title: US-08-770-564A-4

Perfect score: 12
Sequence: 1 CGTTCCTCTTCC 12

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 45 summaries

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Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	6	AR063828
2	12	100.0	20	6	A84604
3	12	100.0	20	6	AR063827
4	12	100.0	20	6	AR079894
5	12	100.0	30	6	AR063826
6	11	91.7	20	6	A84597
7	11	91.7	20	6	AR079898
8	11	91.7	20	6	I21035
9	11	91.7	20	6	I21062
10	11	91.7	42	6	AX166899
11	10	83.3	14	6	AR036791
12	10	83.3	15	6	A35610
13	10	83.3	15	6	AR192969
14	10	83.3	16	6	AX073744
15	10	83.3	16	6	AX073745
16	10	83.3	17	6	AR101699
17	10	83.3	17	6	AR187031
18	10	83.3	17	6	AR187032
19	10	83.3	17	6	AR187033
20	10	83.3	17	6	AR187034
21	10	83.3	17	6	AX263508
22	10	83.3	17	6	AX263509
23	10	83.3	18	6	AX012429
24	10	83.3	18	6	BD001109
25	10	83.3	18	6	BD001538
26	10	83.3	18	6	E51022
27	10	83.3	19	6	AX128976
28	10	83.3	19	6	AX128977
29	10	83.3	19	6	AX128978
30	10	83.3	19	6	AX128979
31	10	83.3	19	6	AX128980
32	10	83.3	20	4	BOVINE30
33	10	83.3	20	6	AR067594
34	10	83.3	20	6	AR126656
35	10	83.3	20	6	AR160506
36	10	83.3	20	6	AX037348
37	10	83.3	20	6	AX037349
38	10	83.3	20	6	AX037350
39	10	83.3	20	6	AX037351
40	10	83.3	20	6	AX148960
41	10	83.3	20	6	AX298384
42	10	83.3	20	6	E40060
43	10	83.3	20	6	E40064
44	10	83.3	20	6	E40868
45	10	83.3	20	6	E40872

ALIGNMENTS

RESULT 1
AR063828 LOCUS 12 bp DNA
DEFINITION Sequence 4 from patent US 5846723.
ACCESSION AR063828
VERSION AR063828.1 GI:5993136
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLES Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 4 08-DEC-1998;
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 9.1e+03;
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OY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
RESULT 2
A84604 A84604 20 bp DNA linear PAT 21-JAN-2000
LOCUS Sequence 14 from Patent WO9845450.
DEFINITION A84604.
ACCESSION A84604.
VERSION A84604.1 GI:6733517
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 14 15-OCT-1998;
GERON CORP (US)
FEATURES Location/Qualifiers
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/db_xref="taxon:32644"
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Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
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A8063827 A8063827 20 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5846723.
DEFINITION A8063827
ACCESSION A8063827
VERSION A8063827.1 GI:5993135
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Method for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 3 08-DEC-1998;
FEATURES Location/Qualifiers
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OY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12

RESULT 4
A8079894 A8079894 20 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 7 from patent US 5966506.
DEFINITION A8079894
ACCESSION A8079894
VERSION A8079894.1 GI:10006647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Weinrich,S.L., Ackinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,
Pruzan,R.A. and Kealey,J.T.
TITLE Purified telomerase
JOURNAL Patent: US 5966506-A 7 19-OCT-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
RESULT 5
A8063826 A8063826 30 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 2 from patent US 5846723.
DEFINITION A8063826
ACCESSION A8063826
VERSION A8063826.1 GI:5993134
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Method for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 2 08-DEC-1998;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 8e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
RESULT 6
A84597 A84597 20 bp DNA linear PAT 21-JAN-2000
LOCUS Sequence 7 from Patent WO9845450.
DEFINITION A84597
ACCESSION A84597
VERSION A84597.1 GI:6733513
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Ackinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE

JOURNAL Patent: WO 9845450-A 7 15-OCT-1998;
 FEATURES GERON CORP (US)
 source location/Qualifiers
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QY 2 GTTCCTCTTCC 12
 Db 2 GTTCCTCTTCC 12

RESULT 7
 LOCUS AR079898 20 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 14 from patent US 5968506.
 ACCESSION AR079898
 VERSION AR079898.1 GI:10006651
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Weinrich,S.L., Atkinson,B.M. III, Lichtsteiner,S.P., Vassero,A.P.,
 Puzan,R.A., and Kealey,J.T.
 TITLE Purified telomerase
 JOURNAL Patent: US 5968506-A 14 19-OCT-1999;
 FEATURES location/Qualifiers
 source 1. .20
 /organism="unknown"

BASE COUNT 0 a 8 c 4 g 7 t 1 others
 ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
 Db 2 GTTCCTCTTCC 12

RESULT 8
 LOCUS 121035 20 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 6 from patent US 5518880.
 ACCESSION 121035
 VERSION 121035.1 GI:1601389
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Leonard,W.J., Noguchi,M. and McBride,O.Wesley,
 TITLE Methods for diagnosis of XSCID and kits thereof
 JOURNAL Patent: US 5518880-A 6 21-MAY-1996;
 FEATURES location/Qualifiers
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BASE COUNT 8 a 1 c 9 g 2 t
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Query Match 91.7%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
 Db 18 GTTCCTCTTCC 8

RESULT 9
 LOCUS 121062 20 bp DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 33 from patent US 5518880.
 ACCESSION 121062
 VERSION 121062.1 GI:1601416
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Leonard,W.J., Noguchi,M. and McBride,O.Wesley,
 TITLE Methods for diagnosis of XSCID and kits thereof
 JOURNAL Patent: US 5518880-A 33 21-MAY-1996;
 FEATURES location/Qualifiers
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 /organism="unknown"

BASE COUNT 2 a 9 c 1 g 8 t
 ORIGIN

Query Match 91.7%; Score 11; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
 Db 3 GTTCCTCTTCC 13

RESULT 10
 LOCUS AX166899 42 bp DNA linear PAT 03-JUL-2001
 DEFINITION Sequence 12 from Patent WO0141811.
 ACCESSION AX166899
 VERSION AX166899.1 GI:14596492
 KEYWORDS
 SOURCE Synthetic construct.
 ORGANISM Synthetic construct.
 REFERENCE 1 (bases 1 to 42)
 AUTHORS Horton,J.K., Smith,J.A., Teeear,M.L., Kendall,J.M. and Michael,N.P.
 TITLE Carrier peptide and method for delivery of molecules into cells
 JOURNAL Patent: WO 0141811-A 12 14-JUN-2001;
 FEATURES location/Qualifiers
 source 1. .42
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 /db_xref="taxon:32630"
 /note="synthetic oligomer"

BASE COUNT 3 a 13 c 9 g 17 t
 ORIGIN

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QY 2 GTTCCTCTTCC 12
 Db 13 GTTCCTCTTCC 23

RESULT 11
 LOCUS AR036791 14 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 33 from patent US 5800984.
 ACCESSION AR036791

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VERSION      AR036791.1  GI:5954647
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Vary,C.P.H.
TITLE        Nucleic acid sequence detection by triple helix formation at primer
              site in amplification reactions
JOURNAL      Patent: US 5800984-A 33 01-SEP-1998;
FEATURES
  source     1..14 /organism="unknown"
BASE COUNT   7 a      0 c      7 g      0 t
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           3 TTCTCTTCC 12
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Db           12 TTCTCTTCC 3

RESULT 12
A35610
LOCUS        A35610          15 bp      DNA          linear    PAT 02-DEC-1996
DEFINITION   Synthetic human IFN-alpha 2 gene oligo.
ACCESSION    A35610
VERSION      A35610.1  GI:1926992
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Camble,R. and Edge,M.D.
TITLE        Analogous interferon polypeptides, process for their preparation
              and pharmaceutical compositions containing them
JOURNAL      Patent: EP 0194006-A 55 10-SEP-1986;
              IMPERIAL CHEMICAL INDUSTRIES PLC
              Location/Qualifiers
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           1 CGTTCTCTT 10
             |||||
Db           4 CGTTCTCTT 13

RESULT 13
AR192869
LOCUS        AR192869          15 bp      DNA          linear    PAT 20-APR-2002
DEFINITION   Sequence 8457 from patent US 6346398.
ACCESSION    AR192869
VERSION      AR192869.1  GI:20238934
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Payco,P., McSwiggen,J., Stinchcomb,D. and Rocabedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 8457 12-FEB-2002;
              Location/Qualifiers
FEATURES

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Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           2 GTTCTCTTC 11
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Db           5 GTTCTCTTC 14

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LOCUS        AX073744          16 bp      DNA          linear    PAT 06-FEB-2001
DEFINITION   Sequence 4 from Patent WO0104290.
ACCESSION    AX073744
VERSION      AX073744.1  GI:12710156
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Jin,Y.X. and Liu,J.S.
TITLE        Triplex-forming oligonucleotides and their use in therapy
JOURNAL      Patent: WO 0104290-A 4 18-JAN-2001;
              Shanghai Institute of Biochemistry Chinese Academy of Sciences (CN)
              Location/Qualifiers
FEATURES
  source     1..16 /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Single stranded TFO-P"
BASE COUNT   8 a      0 c      8 g      0 t
ORIGIN
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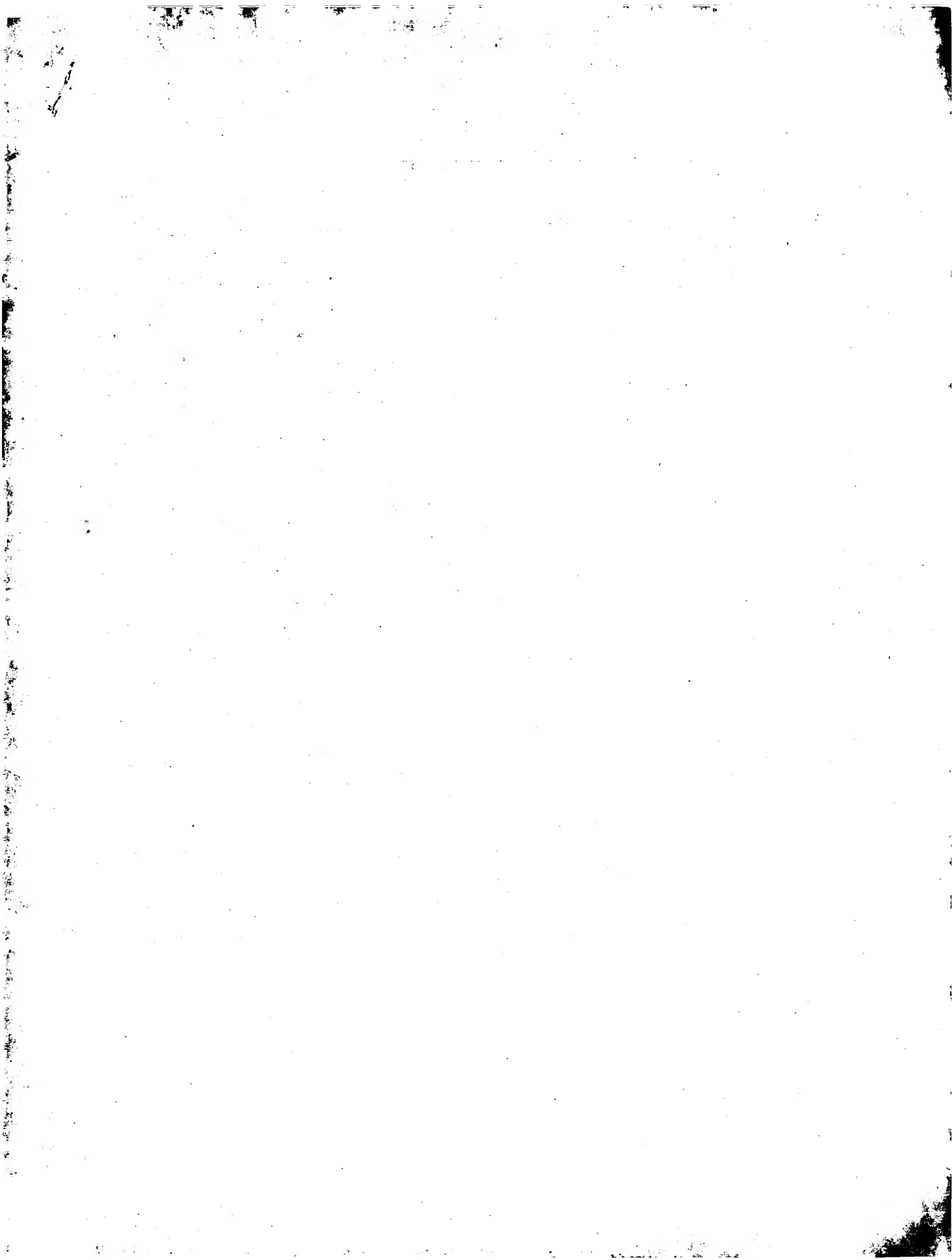
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RESULT 15
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LOCUS        AX073745          16 bp      DNA          linear    PAT 06-FEB-2001
DEFINITION   Sequence 5 from Patent WO0104290.
ACCESSION    AX073745
VERSION      AX073745.1  GI:12710157
KEYWORDS
SOURCE       synthetic construct.
ORGANISM     synthetic construct.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Jin,Y.X. and Liu,J.S.
TITLE        Triplex-forming oligonucleotides and their use in therapy
JOURNAL      Patent: WO 0104290-A 5 18-JAN-2001;
              Shanghai Institute of Biochemistry Chinese Academy of Sciences (CN)
              Location/Qualifiers
FEATURES
  source     1..16 /organism="synthetic construct"
              /db_xref="taxon:32630"
              /note="Single stranded TFO1"
BASE COUNT   8 a      0 c      8 g      0 t
ORIGIN
Query Match  83.3%; Score 10; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TTCTCTTCC 12
|||
Db 15 TTCTCTTCC 6

Search completed: June 23, 2003, 06:34:13
Job time : 141.015 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 79.745 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-4

Perfect score: 12

Sequence: 1 CGTTCCTCTTCC 12

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq.101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	12	100.0	12	19	AAV41171
2	12	100.0	20	19	AAV71226
3	12	100.0	20	19	AAV41170
4	12	100.0	20	20	AAZ23632
5	12	100.0	20	20	AAZ23636
6	12	100.0	20	22	AA509477
7	12	100.0	20	22	AA509480
8	12	100.0	30	19	AAV41169
9	11	91.7	20	15	AAQ71941

Result No.	Score	Query Match	Length	ID	Description
10	11	91.7	20	15	AAQ71914
11	11	91.7	20	21	AAA07908
12	11	91.7	20	21	AAA11686
13	11	91.7	21	21	AAZ89497
14	11	91.7	21	22	AAH62356
15	11	91.7	22	24	ABL43752
16	11	91.7	27	20	AAZ23809
17	11	91.7	40	17	AAZ70784
18	11	91.7	40	17	AAZ70788
19	11	91.7	40	17	AAZ70789
20	10	83.3	12	23	AB117903
21	10	83.3	12	23	AB145722
22	10	83.3	14	13	AAQ26598
23	10	83.3	15	18	AAZ75707
24	10	83.3	16	22	AAZ5892
25	10	83.3	16	22	AAZ5893
26	10	83.3	17	18	AAZ69769
27	10	83.3	17	18	AAZ69770
28	10	83.3	17	18	AAZ69771
29	10	83.3	17	18	AAZ69772
30	10	83.3	17	19	AAZ20569
31	10	83.3	17	19	AAZ20570
32	10	83.3	17	20	AAZ80263
33	10	83.3	17	22	ABA78053
34	10	83.3	17	22	ABA78054
35	10	83.3	18	14	AAQ52877
36	10	83.3	18	21	AAZ30195
37	10	83.3	18	24	AAH89411
38	10	83.3	19	21	AAH82608
39	10	83.3	19	21	AAH82609
40	10	83.3	19	21	AAH82610
41	10	83.3	19	21	AAH82611
42	10	83.3	19	21	AAH82612
43	10	83.3	19	22	AAH57770
44	10	83.3	19	22	AAH57771
45	10	83.3	19	22	AAH57772

ALIGNMENTS

RESULT 1
AAV41171 standard; DNA; 12 Bp.
ID AAV41171
XX
AC AAV41171;
XX
DT 08-OCT-1998. (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 14d.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F,
XX
DR WPI; 1998-377670/32.

```

XX New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX Sequence 12 BP; 0 A; 6 C; 1 G; 5 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 19; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CGTTCCTCTCC 12
DB 1 CGTTCCTCTCC 12
XX
XX RESULT 2
XX AAV71226
XX ID AAV71226 standard; DNA; 20 BP.
XX
XX AC AAV71226;
XX
XX DT 15-FEB-1999 (first entry)
XX
XX DE Antisense oligonucleotide 14ab for human telomerase RNA component.
XX
XX KW Human; telomerase RNA component; anticancer therapy; purification;
XX assay; vaccine; cancer; antisense oligonucleotide; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1
XX /note= "blotting/related"
XX
XX W09845450-A1.
XX
XX PD 15-OCT-1998.
XX
XX PF 04-APR-1997; 97WO-US06012.
XX
XX PR 04-APR-1997; 97WO-US06012.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Atkinson EM, Kealey JT, Lichtreiner SP, Pruzan RA,
XX Vaaseer AP, Weinrich SL,

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```

XX DR WPI; 1998-594485/50.
XX
XX PT Purification of telomerase on affinity material - useful for, e.g.
XX diagnosis and treatment of cancer
XX
XX PS Claim 6; Page 61; 76pp; English.
XX
XX The present sequence represents an antisense oligonucleotide
CC directed against the human telomerase RNA component gene sequences.
CC The oligonucleotide can be used as an affinity agent in the methods of
CC the invention, which are used to purify human telomerase. The methods
CC involve the use of several sequential steps, including the use of two
CC matrices that bind molecules bearing negative charges, a matrix that
CC binds molecules bearing positive charges, an affinity purification step
CC and a size separation. Telomerase is a particular target of anticancer
CC therapies, and is useful in assays for characterizing (pre)cancerous
CC cells. Telomerase can also be used to screen for specific modulators,
CC for biochemical analysis of its activity, and in preparation of
CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
CC are used in vaccines, and for treating over expression of telomerase,
CC particularly in cancer.
XX
XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;
XX
XX Query Match 100.0%; Score 12; DB 19; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CGTTCCTCTCC 12
DB 1 CGTTCCTCTCC 12
XX
XX RESULT 3
XX AAV41170
XX ID AAV41170 standard; DNA; 20 BP.
XX
XX AC AAV41170;
XX
XX DT 08-OCT-1998 (first entry)
XX
XX DE RNA component of human telomerase (hTR) antisense oligo 14ab.
XX
XX KW RNA component; human telomerase; antisense oligonucleotide; infection;
XX neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
XX contraception; sterilisation; immunosuppression; therapeutic; hTR;
XX immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN W09828442-A1.
XX
XX PD 02-JUL-1998.
XX
XX PF 19-DEC-1997; 97WO-US23619.
XX
XX PR 20-DEC-1996; 96US-0770565.
XX
XX PR 20-DEC-1996; 96US-0770564.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F,
XX WPI; 1998-377670/32.
XX
XX DR New polynucleotide(s) anti:sense to human telomerase - used for
XX detecting or inhibiting human telomerase, e.g. for treating cancers,
XX contraception, immuno-suppression or treating infection
XX
XX PS Claim 11; Page 65; 80pp; English.
XX

```

CC Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridize to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridize to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
 |||||
 Db 1 CGTTCCTCTTCC 12

RESULT 4

AAZ23632 standard; DNA; 20 BP.

XX AAZ23632;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide 14ab.

KM Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

PN US5968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 Vasserot AP;

DR WPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases
 associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 45-46; 34pp; English.

XX This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from
 CC adenovirus-transformed kidney cell line. The composition is useful for

CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. AAZ23626-223637 represent oligonucleotides used
 CC in the isolation of human clone 28-1 which contains a fragment of the
 CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
 |||||
 Db 1 CGTTCCTCTTCC 12

RESULT 5

AAZ23636 standard; DNA; 20 BP.

XX AAZ23636;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide oligo 14ab.

KM Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

PN US5968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 Vasserot AP;

DR WPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases
 associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 49-50; 34pp; English.

XX This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from
 CC adenovirus-transformed kidney cell line. The composition is useful for
 CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. AAZ23626-223637 represent oligonucleotides used
 CC in the isolation of human clone 28-1 which contains a fragment of the
 CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
 Db 1 CGTTCCTCTCC 12

RESULT 6

AAS09477
 ID AAS09477 standard; DNA; 20 BP.

XX AAS09477;
 XX

DT 24-OCT-2001 (first entry)

XX Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

XX Human; Telomerase; vaccine; antibody; cancer; EP2H;
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

XX Homo sapiens.

XX US6261556-B1.

XX 17-JUL-2001.

XX 18-OCT-1999; 99US-0420056.

XX 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;
 PI Kealey JT;

XX WPI: 2001-450477/48.

XX

PT Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations

XX

PS Disclosure; Column 2; 29pp; English.

XX

CC The sequence represents an antisense oligonucleotide used in
 CC the purification of human telomerase. The invention relates
 CC to a purified human telomerase core enzyme protein comprising

CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular

CC weight of 200-2000 Kilo Daltons (kDa). The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as

CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the

CC presence of proteins in a sample, such as cell or tissue. Identification
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.

CC Telomerase and/or telomerase associated proteins are also useful for
 CC screening compounds to identify agents that alter the association of

CC telomerase-associated proteins, such as nucleolin or EP2H with
 CC telomerase.

XX

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

XX

Query Match 100.0%; Score 12; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
 Db 1 CGTTCCTCTCC 12

RESULT 7
 AAS09480
 ID AAS09480 standard; DNA; 20 BP.
 XX AAS09480;
 XX

DT 24-OCT-2001 (first entry)

XX Antisense oligonucleotide for human telomerase, Oligo 14ab #2.

XX Human; Telomerase; vaccine; antibody; cancer; EP2H;
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

XX Homo sapiens.

XX US6261556-B1.

XX 17-JUL-2001.

XX 18-OCT-1999; 99US-0420056.

XX 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;
 PI Kealey JT;

XX WPI: 2001-450477/48.

XX

PT Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations

XX

PS Disclosure; Column 18; 29pp; English.

XX

CC The sequence represents a biotinylated antisense oligonucleotide
 CC used in the purification of human telomerase. The invention
 CC relates to a purified human telomerase core enzyme protein comprising

CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular

CC weight of 200-2000 Kilo Daltons (kDa). The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as

CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the

CC presence of proteins in a sample, such as cell or tissue. Identification
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.

CC Telomerase and/or telomerase associated proteins are also useful for
 CC screening compounds to identify agents that alter the association of

CC telomerase-associated proteins, such as nucleolin or EP2H with
 CC telomerase.

XX

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

XX

Query Match 100.0%; Score 12; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
 Db 1 CGTTCCTCTCC 12


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RESULT 8
AAV41169
ID AAV41169 standard; DNA; 30 BP.
XX
XX
AC AAV41169;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 14.
XX
XX
KM RNA component; human telomerase; antisense oligonucleotide; infection;
KM neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KM contraception; sterilisation; immunosuppression; therapeutic; hTR;
KM immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PF 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F;
XX
XX
DR WPI; 1998-377670/32.
XX
XX
PT New polynucleotide(s) anti:sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX
PS Claim 11; Page 65; 80pp; English.
XX
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX
SQ Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;
XX
XX
Query Match 100.0%; Score 12; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CGTTCCTCTTCC 12
1 |||||
1 CGTTCCTCTTCC 12
XX
Db 1 CGTTCCTCTTCC 12
XX
RESULT 9

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```

AAQ71941
ID AAQ71941 standard; DNA; 20 BP.
XX
XX
AC AAQ71941;
XX
XX
DT 03-MAY-1995 (first entry)
XX
XX
DE Human IL-2R gamma gene exon 3 Nsease primer.
XX
XX
KM IL2-R gamma gene; X-linked severe combined immunodeficiency;
KM XSCID; Interleukin; ss.
XX
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "Biotin covalently bound to cytosine"
XX
XX
PN WO9420641-A.
XX
PD 15-SEP-1994.
XX
XX
PF 10-MAR-1994; 94WO-US02891.
XX
PR 12-MAR-1993; 93US-0031143.
PR 14-SEP-1993; 93US-0121435.
XX
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX
PI Leonard WJ, McBride WO, Noguchi M;
XX
XX
DR WPI; 1994-303046/37.
XX
XX
PT Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
PT comprises detecting mutated IL-2R gamma gene, also vectors and
PT transgenic animals containing the mutated gene
XX
XX
XX
PS Claim 12; Page 88; 98pp; English.
XX
XX
CC AAQ71911 to AAQ71975 are primers for the human IL-2R gamma gene, these
CC were used to amplify DNA from mutated and normal IL-2R gamma genes.
CC The mutated gene DNA was obtained either from female carriers or
CC male sufferers of X-linked severe combined immunodeficiency (XSCID).
CC The amplified DNA from normal and affected individuals was then
CC compared using a variety of methods including northern blotting and
CC dot and slot hybridisation. From this a claimed method for the
CC diagnosis of XSCID carriers and sufferers was developed.
XX
XX
SQ Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 other;
XX
XX
Query Match 91.7%; Score 11; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 2 GTTCCCTCTTCC 12
2 |||||
2 GTTCCCTCTTCC 13
XX
Db 3 GTTCCCTCTTCC 13
XX
RESULT 10
AAQ71914/C
ID AAQ71914 standard; DNA; 20 BP.
XX
XX
AC AAQ71914;
XX
XX
DT 03-MAY-1995 (first entry)
XX
XX
DE Human IL-2R gamma gene intron 2 antisense primer.
XX
XX
KM IL2-R gamma gene; X-linked severe combined immunodeficiency;
KM XSCID; Interleukin; ss.
XX
XX

```

XX Homo sapiens.
OS
XX
XX
PN MO9420641-A.
XX
XX
PD 15-SEP-1994.
XX
XX
PE 10-MAR-1994; 94MO-US02891.
XX
XX 12-MAR-1993; 93US-0031143.
PR 14-SEP-1993; 93US-0121435.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
PI Leonard WJ, McBride WO, Noguchi M;
XX
XX
XX WPI; 1994-303046/37.
DR
XX
XX
PT Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
XX
XX
PT comprises detecting mutated IL-2R gamma gene, also vectors and
XX
XX
PT transgenic animals containing the mutated gene
XX
XX
PS Claim 12; Page 87; 98pp; English.
XX
XX
CC AAO071911 to AAO071975 are primers for the human IL-2R gamma gene, these
XX
XX
CC were used to amplify DNA from mutated and normal IL-2R gamma genes.
XX
XX
CC The mutated gene DNA was obtained either from female carriers
XX
XX
CC male sufferers of X-linked severe combined immunodeficiency (XSCID).
XX
XX
CC The amplified DNA from normal and affected individuals was then
XX
XX
CC compared using a variety of methods including northern blotting and
XX
XX
CC dot and slot hybridisation. From this a claimed method for the
XX
XX
CC diagnosis of XSCID carriers and sufferers was developed.
XX
XX
XX Sequence 20 BP; 8 A; 1 C; 9 G; 2 T; 0 other;

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Query Match      91.7%  Score 11;  DB 15;  length 20;
Best Local Similarity 100.0%  Pred. No. 4.6e+03;
Matches 11, Conservative 0, Mismatches 0, Indels 0, Gaps 0
QY      2 GTTCTCTTTC 12
        |||||
Db       18 GTTCTCTTTC 8

```

ID	AAA07908	standard; DNA; 20 BP.
XX	AAA07908;	
AC	AAA07908;	
DT	07-JUL-2000	(first entry)
XX		
DE	He-UNC-53/2 specific RT-PCR forward primer.	
XX		
KW	UNC-53; Caenorhabditis elegans; microtubule; neural regeneration;	
KW	anticancer; anti-neurodegeneration; antifibrotic; anti-adhesive; human;	
XX	antisclerotic; antineoplastic; anti-arthritis; autoimmune disease;	
XX	RT-PCR; primer; 88.	
OS	Homo sapiens.	
XX		
FN	W09963080-A1.	
XX		
PD	09-DEC-1999.	
XX		
PF	02-JUN-1999;	99MO-EP03848.
XX		
PR	03-JUN-1998;	98GB-0011962.
XX		
PA	(JANC) JANSSEN PHARM NV.	
PI	Luyten WHML, De Raeymaeker MC, Geyssen JUGH, Bogaert THOE,	
RT	Maerten LJS, Verhaesselt P, Van De Craen M,	

XX WPI; 2000-116370/10.
XX
XX Novel proteins and nucleic acids e.g. for treating neurodegeneration -
PT
XX
XX Disclosure; Fig 6b; 146pp; English.
XX
XX

CC The invasion provides vertebrate (human) protein homologue of a UNC-53
CC protein of *Caenorhabditis elegans*. The UNC-53 binds to microtubules or
CC their plus ends. The UNC-53 sequences are used to promote neural
CC regeneration, revascularization and wound healing, also for treating
CC neurodegenerative disease, acute traumatic injury, fibrotic disease and
CC autoimmune diseases (e.g., rheumatoid arthritis and sclerosis). The
CC UNC-53 polynucleotides can be used for recombinant production of the
CC proteins, as a source of probes for detecting allelic variants and
CC polymorphisms, for sequencing genomic DNA and for detecting UNC-53
CC expression; and as source of therapeutic antisense sequences. Cells that
CC express the protein are used to identify regulators of cell shape,
CC growth, motility and migration. They can also be used to identify
CC proteins that are involved in signal transduction pathways also involving
CC UNC-53, and to identify compounds that alter attachment of UNC-53 to
CC microtubules. A target gene coupled to a UNC-53 encoding sequence may be
CC used to deliver the target gene to a cellular microtubule or its plus
CC ends. Sequences ABA47502..911 represent primers specific for Hs-UNC-53/2,
CC used in RT-PCR studies of Hs-UNC-53/2 expression.

XX Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 other;

```

Query Match:          91.7%; Score 11; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTTCTCTCTTCC 12
    |||||
Db 8 GTTCTCTTCC 18

```

RESULT 12
AA11686
ID AA11686 standard; DNA; 21 BP.
XX
XX AA11686;
AC
XX
DT 14-JUL-2000 (first entry)
XX
GB Human GABA-B receptor PCR primer GB16as (he) .

KW GABA receptor; GABA-B receptor; neuroprotective; metabotropic receptor
 KW human disease marker; gene therapy; central nervous system; epilepsy;
 KW stroke; psychological disease; stress; manic depression; schizophrenia;
 KW mrigaine; FCR primer; ss.
 XX
 OS Homo sapiens;
 XX
 PN WO200015786-A1.
 XX
 PD 23-MAR-2000.
 XX
 PF 11-SEP-1999; 99WO-BP06742.
 XX
 PR 14-SEP-1998; 98DE-1041941.
 XX
 PR 04-DEC-1998; 98DE-1056066.
 XX
 PA (BADI) BASF-LYNX BIOSCIENCE AG.
 XX
 PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K,
 XX
 DR WPI, 2000-283281/24.
 XX
 PT A novel metabotropic receptor complex from the central nervous system,
 XX related coding sequences and methods of identifying binding substances,
 PT ligands and interactions with other proteins -
 XX

PS Example 5; Page 27; 66pp; German.
 XX
 CC This invention describes a novel protein heteromer, containing at least
 CC a GABA-B receptor protein and at least a protein (A) or a sequence which
 CC has a substitution, inversion, insertion or deletion of one or more amino
 CC acid residues and which retains the biological activity of the protein
 CC heteromer and which has neuroprotective activity. The encoding nucleic
 CC acid (1), the construct, (A) or the protein heteromer are useful for
 CC identifying proteins (or nucleic acids encoding such proteins) that show
 CC specific binding affinity to (A) or the protein heteromer. The two-hybrid
 CC system or biochemical methods can be used to identify interaction domains
 CC of metabotropic receptors and use for pharmacotherapeutic intervention.
 CC Structural information from the protein or protein complex is useful for
 CC identifying and manufacture of substances which have specific binding
 CC activity to the protein or protein complex. The protein heteromer and
 CC (A), or fragments of these are useful as antigens to generate specific
 CC mono- or polyclonal antibodies. (1) is useful for identifying and for
 CC isolating homologous sequences, as a marker for human disease and for
 CC gene therapy. The methods can be used to identify substances, which bind
 CC to (A) or (1) and that cause inhibition or activation of functional
 CC effects of the GABAergic signal messages in neurons of the central
 CC nervous system. The method can also identify substances that inhibit or
 CC amplify interactions of (A) with other metabotropic receptors or
 CC interaction of ligands with the protein heteromer or (A) or interactions
 CC of (A) with G-proteins or other signal transduction molecules. The
 CC analysis of the interactions of (A) and GABA-B receptors is important
 CC for identifying potential active substances against diseases such as
 CC epilepsy, stroke and psychological diseases such as stress, manic
 CC depression, schizophrenia, migraine and others. This sequence
 CC represents a PCR primer used in the method of the invention.
 SQ Sequence 21 BP; 1 A; 9 C; 2 G; 9 T; 0 other;
 XX
 SQ
 Query Match 91.7%; Score 11; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTTCCTCTTC 11
 Db 11 CGTTCCTCTTC 21
 RESULT 13
 AA289497
 ID AA289497 standard; DNA; 21 BP.
 XX
 AC AA289497;
 XX
 DT 22-JUN-2000 (first entry)
 XX
 DE Human GABA-B receptor cDNA PCR primer GBlas(hs).
 XX
 KW GABA-B receptor; neuroprotectant; gene therapy; central nervous system;
 KW metabotropic receptor; signal transduction; epilepsy; stroke; migraine;
 KW psychological disease; stress; manic depression; schizophrenia; human;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19841941-A1.
 XX
 PD 16-MAR-2000.
 XX
 PF 14-SEP-1998; 98DE-1041941.
 XX
 PR 14-SEP-1998; 98DE-1041941.
 XX
 PA (BADI) BASF-LYX BIOSCIENCE AG.
 XX
 PI Kornau H, Eisenhardt G, Kuner R, Hirschfeld K;
 DR WPI, 2000-257875/23.
 XX

PT A novel metabotropic receptor complex from the central nervous system,
 PT related coding sequences and methods of identifying binding substances,
 PT ligands and interactions with other proteins -
 XX
 PS Example 5; Page 11; 32pp; German.
 XX
 CC This invention describes a novel protein heteromer, containing at least
 CC a GABA-B receptor protein and at least a protein (A) or its derivative
 CC which retains the biological activity of the protein heteromer. The
 CC protein of the invention has neuroprotective activity and can be used
 CC for gene therapy. (A) or the protein heteromer are useful for identifying
 CC proteins (or nucleic acids encoding such proteins) that show specific
 CC binding affinity to (A) or the protein heteromer. The two-hybrid system
 CC or biochemical methods can be used to identify interaction domains of
 CC metabotropic receptors and use for pharmacotherapeutic intervention.
 CC Structural information from the protein or protein complex is useful for
 CC identifying and manufacture of substances which have specific binding
 CC activity to the protein or protein complex. The protein heteromer and (A)
 CC or fragments of these are useful as antigens to generate specific mono-
 CC or polyclonal antibodies. The encoding nucleic acid (1) is useful for
 CC identifying and isolating homologous sequences, as a marker for human
 CC disease and for gene therapy. The methods can be used to identify
 CC substances, which bind to (A) or (1) and that cause inhibition or
 CC activation of functional effects of the GABAergic signal messages in
 CC neurons of the central nervous system. The method can also identify
 CC substances that inhibit or amplify interactions of (A) with other
 CC metabotropic receptors or interaction of ligands with the protein
 CC heteromer or (A) or interactions of (A) with G-proteins or other signal
 CC transduction molecules. The analysis of the interactions of (A) and
 CC GABA-B receptors is important for identifying potential active substances
 CC against diseases such as epilepsy, stroke and psychological diseases such
 CC as stress, manic depression, schizophrenia, migraine and others. This
 CC sequence represents a PCR primer used in the amplification of the human
 CC GABA-B receptor described in the method of the invention.
 SQ Sequence 21 BP; 1 A; 9 C; 2 G; 9 T; 0 other;
 XX
 SQ
 Query Match 91.7%; Score 11; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTTCCTCTTC 11
 Db 11 CGTTCCTCTTC 21
 RESULT 14
 AAH62356
 ID AAH62356 standard; DNA; 21 BP.
 XX
 AC AAH62356;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE RBBP2 polymorphism containing DNA fragment #257.
 XX
 KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
 KW heart disease; paternally testing; forensic science; ds.
 XX
 OS Homo sapiens.
 XX
 PN Key Location/Qualifiers
 FT Variation replace(11,G)
 FT FT /tag= a
 FT FT /standard_name= "single nucleotide polymorphism"
 PN WO200138576-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US31639.
 XX
 PR 24-NOV-1999; 99US-016733A.
 XX

XX (WHEED) WHITEHEAD INST BIOMEDICAL RES.
 XX Cargill M, Ireland JS, Lander ES;
 XX WPI; 2001-367705/38.
 XX
 XX New nucleic acid segments of the human genome, particularly from genes
 PT including polymorphic sites, for phenotype correlation, forensics,
 XX paternity testing, medicine and genetic analysis
 XX
 PS Claim 1; Page 50; 80pp; English.
 XX
 CC DNA sequences AAH62100 - AAH6268 represent segments of human genes which
 CC contain single nucleotide polymorphisms (SNPs). A method is included in
 CC the invention for analysing a nucleic acid sample, which consists of
 CC determining the base occupying any one of the polymorphic sites given in
 CC the SNP containing sequences. The nucleotide sequences can be used in the
 CC diagnosis or monitoring of diseases, such as cancer, inflammation, heart
 CC diseases, diseases of the cardiovascular system, and infection by
 CC microorganisms. The oligonucleotides are also useful in the manufacture
 CC of a medicament for the treatment or prophylaxis of the diseases, and as
 CC a pharmaceutical. SNP containing oligonucleotides are useful in
 CC applications such as phenotype correlation, forensics, paternity testing,
 CC medicine and genetic analysis.
 XX
 SQ Sequence 21 BP; 3 A; 7 C; 3 G; 8 T; 0 other;
 Query Match 91.7%; Score 11; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGTCTCTCTCC 12
 DB 8 GTTCTCTCTCC 18
 RESULT 15
 ABL43752/c
 ID ABL43752 standard; DNA; 22 BP.
 XX
 AC ABL43752;
 XX
 DT 11-APR-2002 (first entry)
 XX
 DE Human chromosome 1p36-35 PCR primer SEQ ID NO:796.
 XX
 KW Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis;
 XX genome; PCR primer; ss.
 OS Homo sapiens.
 XX
 PN JP2001321190-A.
 XX
 PD 20-NOV-2001.
 XX
 PF 12-MAR-2001; 2001JP-0068285.
 XX
 PR 10-MAR-2000; 2000JP-0066716.
 XX
 PA (RIKA) RIKAGAKU KENKYUSHO.
 XX (GENO-) GENOTEX YG.
 XX
 DR WPI; 2002-144136/19.
 XX
 PT Arraying genome clones
 XX
 PS Claim 4; Page 20; 528pp; Japanese.
 XX
 CC The present invention describes a method of arraying genome clones. The
 CC method comprises: (a) clones of the genomic libraries contained in
 CC multitwell plates numbered for discrimination are mixed in each of the
 CC multitwell plates; (b) a primer designed based on the chromosome marker

CC sequence is added to the mixture to carry out an amplification reaction;
 CC (c) a signal corresponding to the marker is detected from the resultant
 CC amplified product to specify the discrimination Nos. of the multitwell
 CC plates containing the clones having said marker sequence; (d) the order
 CC of the markers is changed so that the same discrimination Nos. succeed to
 CC the maximum in the specified discrimination Nos. to array the multitwell
 CC plates; (e) the clones in the multitwell plates of the specified
 CC discrimination Nos. are mixed respectively in each well of longitudinal
 CC and lateral directions; (f) the mixed clones are cultured and the
 CC resultant cultures are amplified by using the above primer; (g) signals
 CC are detected from the amplified products; and (h) the clones in the multitwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention.
 XX
 SQ Sequence 22 BP; 7 A; 4 C; 6 G; 5 T; 0 other;
 Query Match 91.7%; Score 11; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGTCTCTCTTC 11
 DB 13 CGTCTCTCTTC 3
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 Job time : 80.0527 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 18.7888 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-4
Perfect score: 12
Sequence: 1 CATTCTCTTCC 12

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	12	100.0	20	2	US-08-770-565-3
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4	12	100.0	30	2	US-08-770-565-2
5	12	100.0	20	1	US-08-031-143B-6
6	11	91.7	20	1	US-08-031-143B-33
7	11	91.7	20	2	US-08-833-377-14
8	11	91.7	20	5	PCT-US94-02891-6
9	11	91.7	20	5	PCT-US94-02891-33
10	11	91.7	14	1	US-08-294-424-33
11	10	83.3	15	4	US-08-584-040-8457
12	10	83.3	17	4	US-08-988-706-54
13	10	83.3	17	4	US-08-584-040-2519
14	10	83.3	17	4	US-08-584-040-2520
15	10	83.3	17	4	US-08-584-040-2521
16	10	83.3	17	4	US-08-584-040-2522
17	10	83.3	18	4	US-09-306-595C-30
18	10	83.3	20	2	US-08-534-479-1
19	10	83.3	20	4	US-09-490-692-85
20	10	83.3	20	4	US-09-458-377-30
21	10	83.3	20	4	US-09-203-895-5
22	10	83.3	21	4	US-08-949-344C-18
23	10	83.3	22	1	US-07-820-412-8
24	10	83.3	22	1	US-08-488-144-4
25	10	83.3	22	1	US-08-611-155B-1
26	10	83.3	22	1	US-08-611-155B-2
27	10	83.3	22	1	US-08-611-155B-3

C 28	10	83.3	22	1	US-08-611-155B-4	Sequence 4, Appl1
C 29	10	83.3	22	1	US-08-611-155B-5	Sequence 5, Appl1
C 30	10	83.3	22	1	US-08-611-155B-6	Sequence 6, Appl1
C 31	10	83.3	22	2	US-08-916-120A-1	Sequence 1, Appl1
C 32	10	83.3	22	2	US-08-916-120A-2	Sequence 2, Appl1
C 33	10	83.3	22	2	US-08-916-120A-3	Sequence 3, Appl1
C 34	10	83.3	22	2	US-08-916-120A-4	Sequence 4, Appl1
C 35	10	83.3	22	2	US-08-916-120A-5	Sequence 5, Appl1
C 36	10	83.3	22	2	US-08-916-120A-6	Sequence 6, Appl1
C 37	10	83.3	24	5	PCT-US94-09851-66	Sequence 66, Appl1
C 38	10	83.3	26	2	US-08-646-367-27	Sequence 27, Appl1
C 39	10	83.3	28	3	US-08-884-324-17	Sequence 17, Appl1
C 40	10	83.3	28	3	US-08-884-324-19	Sequence 19, Appl1
C 41	10	83.3	30	1	US-08-210-880B-4	Sequence 4, Appl1
C 42	10	83.3	30	1	US-08-485-692-19	Sequence 19, Appl1
C 43	10	83.3	30	1	US-08-485-692-20	Sequence 20, Appl1
C 44	10	83.3	30	1	US-08-419-519-19	Sequence 19, Appl1
C 45	10	83.3	30	1		

ALIGNMENTS

RESULT 1
US-08-770-565-4
; Sequence 4, Application US/08770565
; Patent No. 5846723

GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-4

Query Match 100.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCTCTTCC 12

Db 1 CGTTCCTCTCC 12

RESULT 2
US-08-770-565-3
Sequence 3, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald L.
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-3

Query Match 100.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12

RESULT 3
US-08-833-377-7
Sequence 7, Application US/0883377
Patent No. 586506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vasserot, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "Oligo 14ab"
US-08-833-377-7

Query Match 100.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12

RESULT 4
US-08-770-565-2
Sequence 2, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald L.
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565

FILED DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2

Query Match 100.0%; Score 12; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCTTCC 12
DB 1 GGTCTCTTCC 12

RESULT 5
US-08-031-143B-6/C
Sequence 6, Application US/08031143B
Patent No. 551880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2

Query Match 100.0%; Score 12; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCTTCC 12
DB 1 GGTCTCTTCC 12

RESULT 5
US-08-031-143B-6/C
Sequence 6, Application US/08031143B
Patent No. 551880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2

Query Match 100.0%; Score 12; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCTCTTCC 12
DB 1 GGTCTCTTCC 12

INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-6
Query Match 91.7%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12
DB 18 GTTCTCTTCC 8

RESULT 6
US-08-031-143B-33
Sequence 33, Application US/08031143B
Patent No. 551880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2

Query Match 91.7%; Score 11; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12
DB 3 GTTCTCTTCC 13

RESULT 7
US-08-833-377-14
Sequence 14, Application US/08833377

Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinlich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassercot, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod base= OTHER
FEATURE: OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "biotinylated Oligo 14ab"
US-08-833-377-14
Query Match: 91.7%; Score 11; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 GTTCTCTTCC 12
Db 2 GTTCTCTTCC 12
RESULT 8
PCT-US94-02891-6/c
Sequence 6, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: XSCID
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FETLER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-6
Query Match: 91.7%; Score 11; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 GTTCTCTTCC 12
Db 18 GTTCTCTTCC 8
RESULT 9
PCT-US94-02891-33
Sequence 33, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,133
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILNER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-33

Query Match 91.7%; Score 11; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
DB 3 GTTCCTCTTCC 13

RESULT 10
US-08-294-424-33/c
Sequence 33, Application US/08294424
Patent No. 5800984
GENERAL INFORMATION:
APPLICANT: VARY, Calvin
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE DETECTION BY
TITLE OF INVENTION: TRIPLE HELIX FORMATION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,424
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/000,922
FILING DATE: 16 JAN 1993
APPLICATION NUMBER: US/07/629,601B
FILING DATE: 17-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00088-037001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-424-33

Query Match 83.3%; Score 10; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTCCTCTTCC 12
DB 12 TTTCCTCTTCC 3

RESULT 11
US-08-584-040-8457
Sequence 8457, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 8457:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-8457

Query Match 83.3%; Score 10; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTTC 11
|:|:|:|:|:
Db 5 GUUCCUUCUC 14

RESULT 12

US-08-988-706-54/c
Sequence 54, Application US/08988706
Patent No. 6083698

GENERAL INFORMATION:

APPLICANT: OLSEN, Sheri J.
APPLICANT: ANGELLY, Tracy S.
APPLICANT: LAWRENCE, Tammy
APPLICANT: LESCALLET, Jennifer L.
APPLICANT: MURPHY, Patricia D.
APPLICANT: ALLEN, Antoinette P.
APPLICANT: THRUER, Denise B.
APPLICANT: WHITE, Marga B.
APPLICANT: ZENG, Bin
APPLICANT: SADZEWICZ, Lisa K.
TITLE OF INVENTION: CANCER SUSCEPTIBILITY MUTATIONS OF BRCA1
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oncomed, Inc.
STREET: 205 Perry Parkway
CITY: Galtherburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,706
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: TARCA, John E.
REGISTRATION NUMBER: 33,638
REFERENCE/DOCKET NUMBER: PA-0108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-208-1888
TELEFAX: 301-926-6125
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "PROBE"
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
STRAIN: BRCA1
US-08-988-706-54

Query Match 83.3%; Score 10; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTT 10
|:|:|:|:|:
Db 10 CGTTCCTCTT 1

RESULT 13

US-08-584-040-2519
Sequence 2519, Application US/08584040
Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Pavco, Pamela
APPLICANT: MCSWIGEN, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2519:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-2519

Query Match 83.3%; Score 10; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCTCTTC 11
|:|:|:|:|:
Db 7 GUUCCUUCUC 16

RESULT 14

US-08-584-040-2520
Sequence 2520, Application US/08584040

```
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2520:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-2520

Query Match      83.3%; Score 10; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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QY      2 GTTCTCTTC 11
      |::||::|
Db      6 GUUCCUCUC 15
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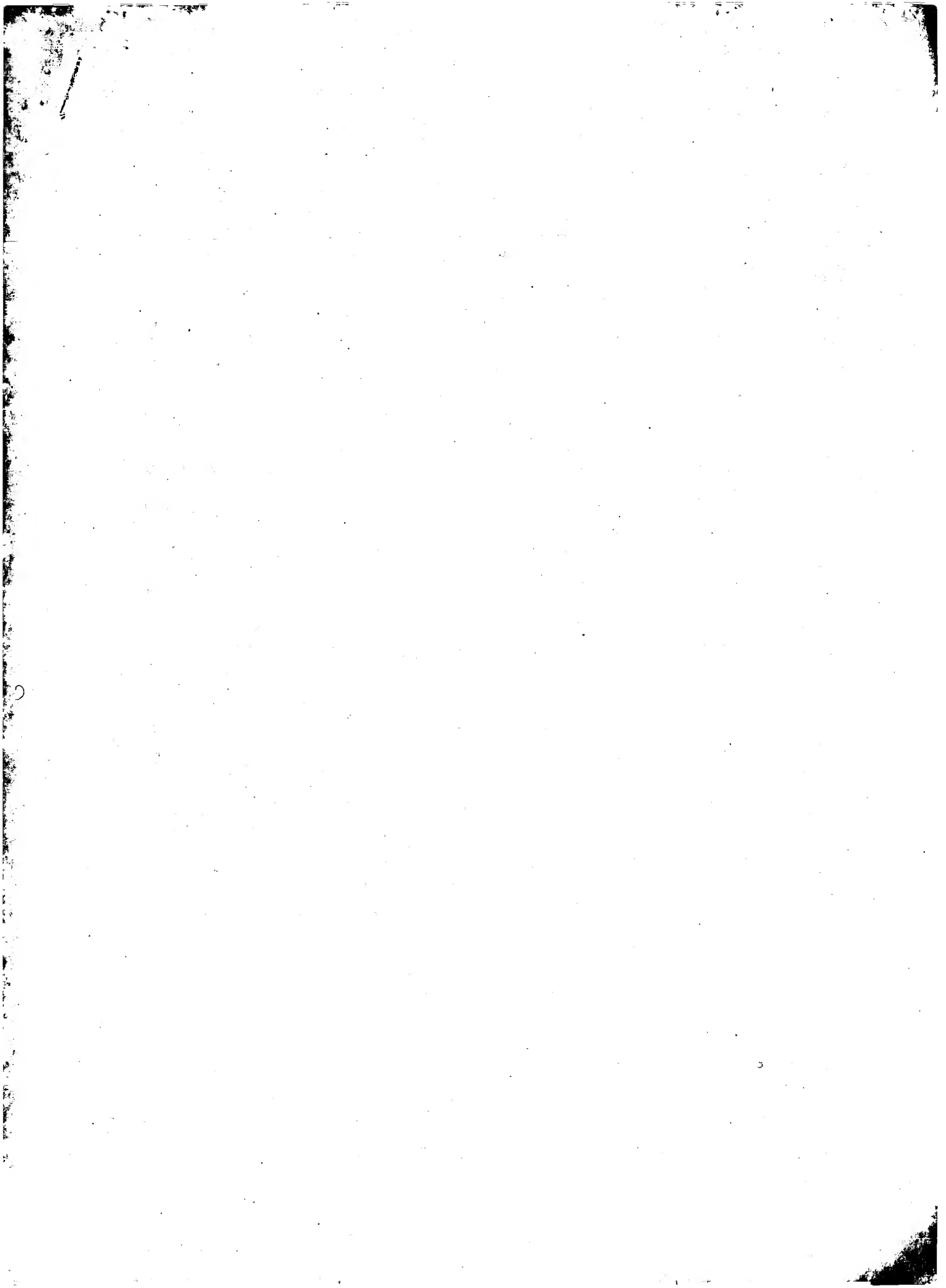
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RESULT 15
US-08-584-040-2521
/ Sequence 2521, Application US/08584040
/ Patent No. 6346398
/ GENERAL INFORMATION:
/ APPLICANT: Pavco, Pamela
/ APPLICANT: McSwiggen, James
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: METHOD AND REAGENT FOR THE
/ TITLE OF INVENTION: TREATMENT OF DISEASES OR
/ TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
/ TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
/ TITLE OF INVENTION: GROWTH FACTOR
/ NUMBER OF SEQUENCES: 8502
```

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Lyon & Lyon
/ STREET: 633 West Fifth Street
/ STREET: Suite 4700
/ CITY: Los Angeles
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 90071-2066
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ MEDIUM TYPE: storage
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: IBM P.C. DOS 5.0
/ SOFTWARE: Word Perfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/584,040
/ FILING DATE: January 11, 1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/005,974
/ FILING DATE: October 26, 1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Warburg, Richard J.
/ REGISTRATION NUMBER: 32,327
/ REFERENCE/DOCKET NUMBER: 218/064
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (213) 489-1600
/ TELEFAX: (213) 955-0440
/ TELEX: 67-3510
/ INFORMATION FOR SEQ ID NO: 2521:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-584-040-2521
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Query Match      83.3%; Score 10; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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QY      2 GTTCTCTTC 11
      |::||::|
Db      3 GUUCCUCUC 12
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Search completed: June 23, 2003, 10:17:03
Job time : 18.7888 secs



GenCore version 5.1.6
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OM-nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 96.4303 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-4
Perfect score: 12
Sequence: 1 CGTTCCTCTCC 12

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*

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- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
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- 6: /cgn2_6/prodata/1/pubpna/PCRUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
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- 11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	91.7	25	US-10-215-112-12736	Sequence 12736, A
C 2	11	91.7	25	US-10-098-263B-24096	Sequence 24096, A
C 3	11	91.7	25	US-10-098-263B-81647	Sequence 81647, A
C 4	11	91.7	25	US-10-098-263B-81648	Sequence 81648, A
C 5	11	91.7	25	US-10-098-263B-96226	Sequence 96226, A
C 6	11	91.7	25	US-10-098-263B-114611	Sequence 114611, A
C 7	10	83.3	17	US-09-818-875-899	Sequence 899, App
C 8	10	83.3	17	US-09-818-875-900	Sequence 900, App
C 9	10	83.3	17	US-10-163-552-930	Sequence 930, App
C 10	10	83.3	18	US-09-925-388-30	Sequence 30, Appl
C 11	10	83.3	18	US-09-969-373-3188	Sequence 3188, Ap
C 12	10	83.3	19	US-09-969-373-1794	Sequence 1794, Ap
C 13	10	83.3	20	US-10-139-496-25	Sequence 25, Appl
C 14	10	83.3	20	US-10-181-846-85	Sequence 85, Appl
C 15	10	83.3	20	US-09-953-047-40	Sequence 40, Appl
C 16	10	83.3	20	US-10-216-484-94	Sequence 94, Appl
C 17	10	83.3	20	US-10-216-484-98	Sequence 98, Appl
C 18	10	83.3	22	US-09-864-636A-1899	Sequence 1899, Ap
C 19	10	83.3	24	US-10-101-487-12	Sequence 12, Appl

C 20	10	83.3	24	US-10-101-487-13	Sequence 13, Appl
C 21	10	83.3	24	US-09-818-954A-4	Sequence 4, Appl
C 22	10	83.3	24	US-09-037-657-4	Sequence 4, Appl
C 23	10	83.3	25	US-09-943-388-16	Sequence 16, Appl
C 24	10	83.3	25	US-09-754-853A-686	Sequence 686, App
C 25	10	83.3	25	US-10-215-112-2936	Sequence 2936, Ap
C 26	10	83.3	25	US-10-215-112-4629	Sequence 4629, Ap
C 27	10	83.3	25	US-10-215-112-4630	Sequence 4630, Ap
C 28	10	83.3	25	US-10-215-112-13297	Sequence 13297, A
C 29	10	83.3	25	US-10-098-263B-2814	Sequence 2814, Ap
C 30	10	83.3	25	US-10-098-263B-17568	Sequence 17568, A
C 31	10	83.3	25	US-10-098-263B-19683	Sequence 19683, A
C 32	10	83.3	25	US-10-098-263B-24706	Sequence 24706, A
C 33	10	83.3	25	US-10-098-263B-25145	Sequence 25145, A
C 34	10	83.3	25	US-10-098-263B-26377	Sequence 26377, A
C 35	10	83.3	25	US-10-098-263B-39832	Sequence 39832, A
C 36	10	83.3	25	US-10-098-263B-40293	Sequence 40293, A
C 37	10	83.3	25	US-10-098-263B-40300	Sequence 40300, A
C 38	10	83.3	25	US-10-098-263B-44698	Sequence 44698, A
C 39	10	83.3	25	US-10-098-263B-52287	Sequence 52287, A
C 40	10	83.3	25	US-10-098-263B-67887	Sequence 67887, A
C 41	10	83.3	25	US-10-098-263B-84565	Sequence 84565, A
C 42	10	83.3	25	US-10-098-263B-86229	Sequence 86229, A
C 43	10	83.3	25	US-10-098-263B-95971	Sequence 95971, A
C 44	10	83.3	25	US-10-098-263B-95972	Sequence 95972, A
C 45	10	83.3	25	US-10-098-263B-96589	Sequence 96589, A

ALIGNMENTS

RESULT 1
US-10-215-112-12736/c
; Sequence 12736, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12736
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12736

Query Match 91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 2 GTTCTCTTCC 12
Db 18 GTTCTCTTCC 8

RESULT 2
US-10-098-263B-24096/c
; Sequence 24096, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16

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; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24096
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-24096
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Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 GTTCCTCTTCC 12
Db      16 GTTCCTCTTCC 6
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RESULT 3

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US-10-098-263B-81647
; Sequence 81647, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81647
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81647
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Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 GTTCCTCTTCC 12
Db      1 GTTCCTCTTCC 11
```

RESULT 4

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US-10-098-263B-81648
; Sequence 81648, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 81648
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-81648
```

```

Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 GTTCCTCTTCC 12
Db      1 GTTCCTCTTCC 11
```

```

US-10-098-263B-96226
; Sequence 96226, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 96226
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-96226
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RESULT 5

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US-10-098-263B-114611
; Sequence 114611, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-114611
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```

Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 GTTCCTCTTCC 12
Db      11 GTTCCTCTTCC 21
```

RESULT 6

```

US-10-098-263B-114611
; Sequence 114611, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-114611
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Query Match          91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 GTTCCTCTTCC 12
Db      6 GTTCCTCTTCC 16
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RESULT 7

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US-09-818-875-899/C
; Sequence 899, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamper, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
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PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedmann macro Napro4
SEQ ID NO 899
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-818-875-899

Query Match 83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTT 10
DB 17 CGTCTCTT 8

RESULT 8
US-09-818-875-900
Sequence 900, Application US/09818875
Publication No. US20030051270A1
GENERAL INFORMATION:
APPLICANT: Kmelec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedmann macro Napro4
SEQ ID NO 900
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-818-875-900

Query Match 83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTT 10
DB 1 CGTCTCTT 10

RESULT 9
US-10-163-552-930/c
Sequence 930, Application US/10163552
Publication No. US20030105051A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggan, Jim
TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level
TITLE OF INVENTION: HER2
FILE REFERENCE: MHB01-1653-A (400/014)

CURRENT APPLICATION NUMBER: US/10/163,552
CURRENT FILING DATE: 2002-06-06
NUMBER OF SEQ ID NOS: 1997
SOFTWARE: PatentIn version 3.0
SEQ ID NO 930
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-163-552-930

Query Match 83.3%; Score 10; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTC 11
DB 10 GTTCTCTTC 1

RESULT 10
US-09-925-388-30/c
Sequence 30, Application US/09925388
Publication No. US20030054523A1
GENERAL INFORMATION:
APPLICANT: HOSHINO, Tatsuo
APPLICANT: OJIMA, Kazuyuki
APPLICANT: SETOGUCHI, Yutaka
TITLE OF INVENTION: ISOPRENOL PRODUCTION
FILE REFERENCE: ISOPRENOL PRODUCTION
CURRENT APPLICATION NUMBER: US/09/925,388
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/306,595
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 30
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sense primer
OTHER INFORMATION: for cloning of 5'-adjacent region of MVK gene
US-09-925-388-30

Query Match 83.3%; Score 10; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12
DB 10 TTCTCTTCC 1

RESULT 11
US-09-969-373-318/c
Sequence 318, Application US/09969373
Patent No. US20020133852A1
GENERAL INFORMATION:
APPLICANT: Effeertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 318
LENGTH: 18

;; TYPE: DNA
;; ORGANISM: Glycine max
US-09-969-373-3188

Query Match
Best Local Similarity 100.0%; Score 10; DB 10; Length 18;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTCTCTTCC 11
DB 17 TTCTCTTCC 8

RESULT 12
US-09-969-373-1794
; Sequence 1794, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(32679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1794
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1794

Query Match
Best Local Similarity 100.0%; Score 10; DB 10; Length 19;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12
DB 6 TTCTCTTCC 15

RESULT 13
US-10-139-496-25/c
; Sequence 25, Application US/10139496
; Publication No. US20030082646A1
; GENERAL INFORMATION:
; APPLICANT: Carey, Thomas E.
; APPLICANT: Nair, Jennifer P.
; TITLE OF INVENTION: Antisense Targets of Autoimmune Sensorineural Hearing Loss (AISNL)
; FILE REFERENCE: UM-6982
; CURRENT APPLICATION NUMBER: US/10/139,496
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/222,179
; PRIOR FILING DATE: 1998-12-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-139-496-25

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12
DB 17 TTCTCTTCC 8

RESULT 14
US-10-181-846-85/c
; Sequence 85, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RSP-0363
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-85

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12
DB 10 TTCTCTTCC 1

RESULT 15
US-09-953-047-40
; Sequence 40, Application US/09953047
; Publication No. US20030087854A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR 3 EXP-
; FILE REFERENCE: RTS-0157
; CURRENT APPLICATION NUMBER: US/09/953,047
; CURRENT FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-953-047-40

Query Match
Best Local Similarity 100.0%; Score 10; DB 9; Length 20;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCC 12
DB 11 TTCTCTTCC 20

Search completed: June 23, 2003, 20:01:29
Job time : 97.4303 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1006.47 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564a-4
Perfect score: 12
Sequence: 1 CGTTCCTCTTCC 12

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Total number of hits satisfying chosen parameters: 12114646

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Post-processing: Listing first 45 summaries

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4	12	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appli
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Sequence 4, Appli

Sequence 3, Appli

Sequence 3, Appli

Sequence 81691, A

Sequence 18655, A

Sequence 81691, A

Sequence 45573, A

Sequence 52883, A

Sequence 39546, A

Sequence 2, Appli

Sequence 17, Appli

Sequence 62884, A

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Sequence 46617, A

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ALIGNMENTS

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 1..12
LOCATION:
OTHER INFORMATION: /note="oligo 14d"

RESULT 1
PCT-US97-23619-4
Sequence 4, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

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RESULT 1
PCT-US97-23619-4
Sequence 4, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US97-23619-4
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 1..12
LOCATION:
OTHER INFORMATION: /note="oligo 14d"

RESULT 2
US-08-770-564A-4
Sequence 4, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Krizan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

US-08-770-564A-4
Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PCT-US97-23619-3

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; Sequence 3, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorelila, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 14ab"
; PCT-US97-23619-3

Query Match 100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
Db 1 CGTTCCTCTTCC 12

RESULT 4
US-08-770-564A-3
; Sequence 3, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorelila, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-770-564A-3

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Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
Db 1 CGTTCCTCTTCC 12

RESULT 5
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; Sequence 81691, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819663
; US-09-954-427-81691

Query Match 100.0%; Score 12; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
Db 5 CGTTCCTCTTCC 16

RESULT 6
US-09-956-584-18655/c
; Sequence 18655, Application US/09956584

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: GENERAL INFORMATION:
: APPLICANT: Maltman, Michael
: TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
: FILE REFERENCE: 3115.1
: CURRENT APPLICATION NUMBER: US/09/956,584
: CURRENT FILING DATE: 2001-09-19
: PRIOR APPLICATION NUMBER: 60/234,017
: PRIOR FILING DATE: 2000-09-20
: NUMBER OF SEQ ID NOS: 605887
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ. ID NO. 18655
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Mus musculus
US-09-956-584-18655

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DB	18	CGTTCCTTC	7	

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RESULT 7
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Sequence 81691, Application US/60233166
GENERAL INFORMATION:
APPLICANT: Miltmann
APPLICANT: Aftemetric, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
TITLE OF INVENTION: Genome
FILE REFERENCE: 3112
CURRENT APPLICATION NUMBER: US/60/233.166
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 420907
SOFTWARE: Fastsqb for Windows Version 4.0
SEQ ID NO 81691
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank AA819663
US-60-233-166-81691

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Query Match 100.0% Score 12 DB 67 Length 25;
Best Local Similarity 100.0% Pred. No. 2e+04 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

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db

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RESULT 8
US-60-233-620-45573/c
Sequence 45573, Application US/60233620
GENERAL INFORMATION:
APPLICANT: Altman
APPLICANT: Altmetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
TITLE OF INVENTION: Arabidopsis thaliana
FILE REFERENCE: 316
CURRENT APPLICATION NUMBER: US/60/233,620
CURRENT FILING DATE: 2000-10-24
NUMBER OF SEQ ID NOS: 131820
SOFTWARE: Parseq for Windows Version 4.0
SEQ ID NO 45573
LENGTH: 25
TYPE: DNA
ORGANISM: Arabidopsis thaliana
PUBLICATION INFORMATION:

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1 DATABASE ACCESSION NUMBER: Genbank AL034567
US-60-233-620-45573

Query Match          100.0%; Score 12, DB 67, Length 25,
Best Local Similarity 100.0%; Prid. No. 2e+04;
Matches 12, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY      1 CATTCTCTCTTC 12
         |||||
Db       15 CATTCTCTCTTC 4

```

```

RESULT 9
US-60-234-017-52863/C
Sequence 52863, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Miltmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Musc
TITLE OF INVENTION: Musculus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234,017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52863
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
PUBLCATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U41285
US-60-234-017-52863

```

Query Match	100.0%	Score 12	DB 67	Length 25
Best Local Similarity	100.0%	Pred. No. 2e+04		
Matches 12	Conservative 0	Mismatches 0	Indels 0	Gaps 0
1	CGTTCCTCTTCC	12		
18	CGTTCCTCTTCC	7		
DB				

```

RESULT 10
US-60-353-987-396546/c
: Sequence 396546, Application US/60353987
: GENERAL INFORMATION:
: APPLICANT: Miltmann, Michael
: TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
: FILE REFERENCE: 3121
: CURRENT APPLICATION NUMBER: US/60/353,987
: CURRENT FILING DATE: 2002-02-01
: NUMBER OF SEQ ID NOS: 997516
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 396546
:
: LENGTH: 25
:
: TYPE: DNA
: ORGANISM: Homo sapien
US-60-353-987-396546

```

```
Query Match Score 12; DB 79; Length 25;
      Best Local Similarity 100.0%; Pwd. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF INVENTION: RNA Component of Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 14"
PCT-US97-23619-2
Query Match 100.0%; Score 12; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12
Db 1 CGTCTCTCTCC 12

RESULT 12
US-08-770-564a-2
Sequence 2, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Prizant, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
NUMBER OF INVENTION: Against the RNA Component of Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564a-2
Query Match 100.0%; Score 12; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCC 12
Db 1 CGTCTCTCTCC 12

RESULT 13
US-08-521-634-17/C
Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeneuve, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF INVENTION: 66
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/350,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-17

Query Match 100.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
|||
DB 31 CGTTCCTCTTCC 20

RESULT 14
PCT-US02-25943-62884/C
Sequence 62884, Application PC/TUS0225943
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 62884
LENGTH: 32
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (6132858)...(6132888)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 67367
PCT-US02-25943-62884

Query Match 100.0%; Score 12; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
|||
DB 22 CGTTCCTCTTCC 11

RESULT 15
US-10-227-565-62884/C
Sequence 62884, Application US/10227565
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 62884
LENGTH: 32
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (6132858)...(6132888)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectonObjectNumber = 6736
US-10-227-565-62884

Query Match 100.0%; Score 12; DB 42; Length 32;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
|||
DB 22 CGTTCCTCTTCC 11

Search completed: June 23, 2003, 16:08:17
Job time : 1006.55 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: June 23, 2003, 05:45:21 ; Search time 526.757 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564a-4
Perfect score: 12
Sequence: 1 CGTTCCTCTTCC 12

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Gapop 60.0, Gapext 60.0

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Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0
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10: /cgn2_6/prodata/1/pna/US10_NEW_COMB.seq3:*
11: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq:*
12: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq2:*
13: /cgn2_6/prodata/1/pna/US60_NEW_COMB.seq3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	12	100.0	25	7	US-09-954-445A-45573
C 2	12	100.0	25	9	US-10-355-577-396546
C 3	12	100.0	25	12	US-10-355-577-396546
C 4	11	91.7	17	11	US-10-303-778-7608
C 5	11	91.7	18	9	US-10-303-778-7627
C 6	11	91.7	18	9	US-10-310-188-65996
C 7	11	91.7	20	9	US-10-315-474-66
C 8	11	91.7	20	9	US-10-315-474-137
C 9	11	91.7	25	6	US-09-660-222-124398
C 10	11	91.7	25	6	US-09-660-222-124402
C 11	11	91.7	25	6	US-09-660-222-124403
C 12	11	91.7	25	6	US-09-660-222-124417
C 13	11	91.7	25	6	US-09-660-222-124417
C 14	11	91.7	25	7	US-09-953-570-131778
C 15	11	91.7	25	7	US-09-953-570-131778
C 16	11	91.7	25	7	US-09-954-445A-7403
C 17	11	91.7	25	7	US-09-954-445A-21805
C 18	11	91.7	25	7	US-09-954-445A-31524
C 19	11	91.7	25	7	US-09-954-445A-79209
C 20	11	91.7	25	7	US-09-954-445A-79210
C 20	11	91.7	25	9	US-10-098-263B-24096

21	11	91.7	25	9	US-10-098-263B-81647	Sequence 81647, A
22	11	91.7	25	9	US-10-098-263B-81648	Sequence 81648, A
23	11	91.7	25	9	US-10-098-263B-96226	Sequence 96226, A
24	11	91.7	25	9	US-10-098-263B-114611	Sequence 114611, A
C 25	11	91.7	25	9	US-10-355-577-96775	Sequence 96775, A
C 26	11	91.7	25	9	US-10-355-577-101273	Sequence 101273, A
C 27	11	91.7	25	9	US-10-355-577-101274	Sequence 101274, A
C 28	11	91.7	25	9	US-10-355-577-164671	Sequence 164671, A
C 29	11	91.7	25	9	US-10-355-577-178073	Sequence 178073, A
C 30	11	91.7	25	9	US-10-355-577-198249	Sequence 198249, A
C 31	11	91.7	25	9	US-10-355-577-318084	Sequence 318084, A
C 32	11	91.7	25	9	US-10-355-577-394493	Sequence 394493, A
C 33	11	91.7	25	9	US-10-355-577-394494	Sequence 394494, A
C 34	11	91.7	25	9	US-10-355-577-396545	Sequence 396545, A
C 35	11	91.7	25	9	US-10-355-577-498091	Sequence 498091, A
C 36	11	91.7	25	9	US-10-355-577-581372	Sequence 581372, A
C 37	11	91.7	25	9	US-10-355-577-581426	Sequence 581426, A
C 38	11	91.7	25	9	US-10-355-577-650483	Sequence 650483, A
C 39	11	91.7	25	9	US-10-355-577-650484	Sequence 650484, A
C 40	11	91.7	25	9	US-10-355-577-653296	Sequence 653296, A
C 41	11	91.7	25	9	US-10-355-577-658872	Sequence 658872, A
C 42	11	91.7	25	9	US-10-355-577-667847	Sequence 667847, A
C 43	11	91.7	25	9	US-10-355-577-667848	Sequence 667848, A
C 44	11	91.7	25	9	US-10-355-577-730882	Sequence 730882, A
C 45	11	91.7	25	9	US-10-355-577-734855	Sequence 734855, A

ALIGNMENTS

```

RESULT 1
US-09-954-445A-45573/c
; Sequence 45573, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-45573

Query Match
Best Local Similarity 100.0%; Score 12; DB 7; Length 25;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db      15 CGTTCCTCTTCC 4

RESULT 2
US-10-355-577-396546/c
; Sequence 396546, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

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Fri Jun 27 07:42:34 2003

us-08-770-564a-4.01lgo.rnps

Page 2

US-10-355-577-396546

Query Match 100.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCCTCTCC 12
|||
Db 24 CGTCCCTCTCC 13

RESULT 3
US-60-427-836-683575

Sequence 683575, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 683575
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus

Query Match 100.0%; Score 12; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCCTCTCC 12
|||
Db 12 CGTCCCTCTCC 23

RESULT 4
US-10-303-778-7608

Sequence 7608, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7608
LENGTH: 17
TYPE: DNA
ORGANISM: Avian infectious bronchitis virus

Query Match 91.7%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
|||
Db 7 GTTCCCTCTCC 17

RESULT 5
US-10-303-778-7627

Sequence 7627, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778

CURRENT FILING DATE: 2002-11-26

NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7627
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens

Query Match 91.7%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
|||
Db 7 GTTCCCTCTCC 17

RESULT 6
US-10-310-188-65996/c

Sequence 65996, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65996
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens

Query Match 91.7%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
|||
Db 12 GTTCCCTCTCC 2

RESULT 7
US-10-315-474-66/c

Sequence 66, Application US/10315474
GENERAL INFORMATION:
APPLICANT: Brett P. Montle
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REFERENCE: RTS-0338
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

Query Match 91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
|||
Db 12 GTTCCCTCTCC 2


```
RESULT 8
US-10-315-474-137
; Sequence 137, Application US/10315474
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0338
; CURRENT APPLICATION NUMBER: US/10/315,474
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-315-474-137

Query Match          91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCTCTCTTC 12
DB 9 GTTCTCTCTTC 19

RESULT 9
US-09-660-222-124398
; Sequence 124398, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124398

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTTC 11
DB 12 CGTCTCTCTTC 22

RESULT 10
US-09-660-222-124402
; Sequence 124402, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124402
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124402

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTTC 11
DB 6 CGTCTCTCTTC 16

RESULT 11
US-09-660-222-124403
; Sequence 124403, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124403

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTTC 11
DB 4 CGTCTCTCTTC 14

RESULT 12
US-09-660-222-124417
; Sequence 124417, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124417

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 618.693 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564a-4
Perfect score: 12
Sequence: 1 CGTTCCCTCTCC 12

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estnu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pla:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	91.7	46	13	BI488502 603021011
2	11	91.7	46	17	AL767395 Arabidops
3	10	83.3	26	17	AZ942099 2M0202C09
4	10	83.3	27	17	AZ630179 1M0483B10
5	10	83.3	28	14	N92455 2B63h01.81
6	10	83.3	33	17	BH850686 SALK_0716

C 7	10	83.3	37	17	A2392980	A2392980 1M0555P13
C 8	10	83.3	38	17	A2974736	A2974736 2M0249A03
C 9	10	83.3	43	17	A2419099	A2419099 1M0195N23
C 10	10	83.3	43	17	A2830358	A2830358 2M0109M04
C 11	10	83.3	46	9	AA052407	AA052407 mb70H06.r
C 12	10	83.3	49	9	AA902962	AA902962 OK44B09.f
C 13	10	83.3	50	9	AU102702	AU102702 A0102702
C 14	9	75.0	19	17	A2636812	A2636812 1M0495B21
C 15	9	75.0	26	17	A2799780	A2799780 2M0057K20
C 16	9	75.0	12	12	BG673330	BG673330 DRNBSF09
C 17	9	75.0	30	17	A2427759	A2427759 1M0209P20
C 18	9	75.0	30	17	A2604126	A2604126 1M0423O13
C 19	9	75.0	31	17	A2465005	A2465005 1M0274J09
C 20	9	75.0	32	17	A2587757	A2587757 1M0395P07
C 21	9	75.0	32	17	A2792853	A2792853 2M0045C07
C 22	9	75.0	32	17	BH847691	BH847691 SALK_0558
C 23	9	75.0	34	9	A1537243	A1537243 EP01E01.x
C 24	9	75.0	35	17	A2581591	A2581591 1M0370O23
C 25	9	75.0	36	17	A2828679	A2828679 2M0105K18
C 26	9	75.0	37	9	AA625816	AA625816 zV87a04.f
C 27	9	75.0	37	13	B1063841	B1063841 B1063841
C 28	9	75.0	37	17	A2474017	A2474017 1M0290A18
C 29	9	75.0	37	17	A2625706	A2625706 1M0465O23
C 30	9	75.0	37	17	A2761912	A2761912 1M0556D02
C 31	9	75.0	38	17	A2339873	A2339873 1M0071I04
C 32	9	75.0	38	17	A2949952	A2949952 2M0213J13
C 33	9	75.0	40	14	H51330	H51330 Y030B01.r1
C 34	9	75.0	40	17	A2597058	A2597058 1M0410M08
C 35	9	75.0	40	17	A2627381	A2627381 1M0469H09
C 36	9	75.0	41	17	A2848455	A2848455 1M0311M04
C 37	9	75.0	42	14	T17558	T17558 mp8 v145 Th
C 38	9	75.0	42	17	BH640418	BH640418 1008035G0
C 39	9	75.0	43	9	AA981631	AA981631 ua24b12.r
C 40	9	75.0	43	14	H41505	H41505 yp68h12.81
C 41	9	75.0	43	17	BH849028	BH849028 SALK_0691
C 42	9	75.0	44	14	W23377	W23377 SNAWCA702SK
C 43	9	75.0	44	17	A2761199	A2761199 1M0555G21
C 44	9	75.0	45	17	AZ423992	AZ423992 1M0203A16
C 45	9	75.0	45	17	A2657409	A2657409 1M0533M04

ALIGNMENTS

RESULT 1
LOCUS BI488502 46 bp mRNA linear EST 28-AUG-2001
DEFINITION 603021011F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191659 5',
mRNA sequence.
ACCESSION BI488502
VERSION BI488502.1 GI:15327730
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 46)
NIH-MGC <http://mgc.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
founded through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: L1AM11479 row: e column: 04
High quality sequence stop: 46.
Location/Qualifiers

FEATURES
source

1..46

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191659"
/clone_1lb="NH_MGC_114"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-Sport6; Site: 1; Not;
Site 2: ECoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yr. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Livtrogen). Research Genetics tracking code 019. Note:
this is a NH_MGC library."
This is a NH_MGC library."

BASE COUNT      9 a      8 c      25 g      4 t
ORIGIN

Query Match      91.7%; Score 11; DB 13; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 GTTCCCTCTCC 12
        |||||
        12 GTTCCCTCTCC 2

RESULT 2
AL767395      46 bp      DNA      linear      GSS 18-JUN-2002
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-219A03-014202,
genomic survey sequence.
ACCESSION
AL767395
VERSION
AL767395.1 GI:21520514
KEYWORDS
GSS.
SOURCE
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosid 11; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Strizhov, N., Li, Y., Rosso, M., Viehoveer, P., Dekker, K., Saedler, H.
and Weishaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weishaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 46)
JOURNAL
REFERENCE
AUTHORS
Li, Y., Rosso, M., Strizhov, N. and Weishaar, B.
TITLE
Direct Submission
JOURNAL
COMMENT
Submitted (17-JUN-2002) Weishaar, B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone fsk7. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mpg.de/GABI-Kat/.
http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1. 46
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-219A03-014202"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA

```

insertions. The DNA fragment(s) resulting from the PCR
 were directly sequenced to determine the genomic sequence
 flanking the insertion. Sequences displaying significant
 similarity to the A. thaliana nuclear genome sequence were
 processed for submission. T-DNA derived sequences were
 removed"

```

BASE COUNT      7 a      19 c      2 g      18 t
ORIGIN

Query Match      91.7%; Score 11; DB 17; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      2 GTTCCCTCTCC 12
        |||||
        29 GTTCCCTCTCC 39

RESULT 3
A2942099/c
LOCUS
DEFINITION
A2942099      26 bp      DNA      linear      GSS 26-APR-2001
2M0202C09F Mouse 10kb plasmid UNGC2M library Mus musculus genomic
clone UNGC2M0202C09 F, DNA sequence.
ACCESSION
A2942099
VERSION
A2942099.1 GI:13805115
KEYWORDS
GSS.
SOURCE
house mouse.
MUS musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0202 row: C column: 09
Seq primer: CCGTGTAAACGACGCGCACT
Clase: plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1. 26
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UNG2M0202C09"
/clone_1lb="Mouse 10kb plasmid UNGC2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resilient, F-"
/notes="Vector: pMDA2ny; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMDA2 (g11473211419b|AF129072.1), a copy-number

```

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 0 c 16 g 0 t

Query Match 83.3%; Score 10; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTCTCC 12
12 TTCCTCTCC 3

RESULT 4
A2630179 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0483B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGCIM0483B10 R, DNA sequence.

ACCESSION A2630179.1 GI:11752369
VERSION A2630179
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weis, R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0483 row: B column: 10
Seq primer: CACACAGAAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source 1..27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0483B10"
/clone_1ib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 9 g 0 t

Query Match 83.3%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTCTCC 12
4 TTCCTCTCC 13

RESULT 5
N92455 28 bp mRNA linear EST 20-AUG-1996
LOCUS zb63h01.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:308305.3', similar to gb:X06323_cds1 MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);, mRNA sequence.

ACCESSION N92455
VERSION N92455.1 GI:1264764
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chappelli, B., Chisoe, S., Dietrich, N., Dubugue, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucada, T., Lacey, M., Le, M., Le, N., Martis, B., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevasis, E., Underwood, K., Woldmann, P., Waterston, R., Wilson, R. and Merra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LNL; contact the IMAG Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 866 Std Error: 0.00
Seq primer: mob.RGA+ET
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source 1..28
/organism="Homo sapiens"
/db_xref="GDB:1251718"
/db_xref="taxon:9606"
/clone="IMAGE:308305"
/clone_1ib="Soares fetal_lung_NBHL19W"
/dev_stage="19 weeks"
/lab_host="PH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5'-GTGACATCTGAGTGGAGCGCCGACATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares

BASE COUNT fetal heart NbhH19W."
 ORIGIN 7 a 9 c 4 g 8 t

Query Match 83.3%; Score 10; DB 14; Length 28;
 Best Local Similarity 100.0%; Pred. No. 7.8e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TTCTCTTTC 11
 |||||
 3 TTCTCTTTC 12

RESULT 6
 BH850686 33 bp DNA linear GSS 13-JUN-2002
 LOCUS
 DEFINITION Arabidopsis thaliana genomic clone SALK_071692.32.90.x, DNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadriah, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE
 JOURNAL
 COMMENT

Arabidopsis Genome
 Unpublished (2001)
 Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.

FEATURES
 source

Location/Qualifiers
 1..33
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_071692.32.90.x"
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocol used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 5 a 16 c 1 g 11 t

Query Match 83.3%; Score 10; DB 17; Length 33;
 Best Local Similarity 100.0%; Pred. No. 8.1e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTTC 12
 |||||
 19 TTCTCTTTC 28

RESULT 7
 AZ392980/c 37 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0155P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Dunn, D., Aoyagi, A., Barber, M., Baerns, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Kelly, M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE
 JOURNAL
 COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0155 row: P column: 13
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence scop: 37.

FEATURES
 source

Location/Qualifiers
 1..37
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0155P13"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114[9b]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 15 a 0 c 22 g 0 t

Query Match 83.3%; Score 10; DB 17; Length 37;
 Best Local Similarity 100.0%; Pred. No. 8.4e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCTCTTTC 12
 |||||
 16 TTCTCTTTC 7

RESULT 8
 AZ974736 38 bp DNA linear GSS 27-APR-2001
 LOCUS
 DEFINITION ZM0249A03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic

ACCESSION clone UGCG2M0249A03 R, DNA sequence.
 VERSION A2974736
 KEYWORDS GI:13845963
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 38)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0249 row: A column: 03
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 38.
 Location/Qualifiers
 1..38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0249A03"
 /clone_1lb="Mouse 10kb plasmid UGCG2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 14 a 8 c 9 g 7 t
 ORIGIN
 Query Match 83.3%; Score 10; DB 17; Length 38;
 Best Local Similarity 100.0%; Pred. No. 8.4e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCC 12
 Db 19 TTCTCTTCC 10
 RESULT 9
 AZA19099/c 43 bp DNA linear GSS 03-OCT-2000
 LOCUS
 DEFINITION IM0195N23F Mouse 10kb plasmid UGCG2M library Mus musculus genomic

ACCESSION clone UGCG1M0195N23 F, DNA sequence.
 VERSION A2419099
 KEYWORDS GI:10543112
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weis,R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0195 row: N column: 23
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 43.
 Location/Qualifiers
 1..43
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0195N23"
 /clone_1lb="Mouse 10kb plasmid UGCG1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 BASE COUNT 21 a 0 c 22 g 0 t
 ORIGIN
 Query Match 83.3%; Score 10; DB 17; Length 43;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCC 12
 Db 33 TTCTCTTCC 24
 RESULT 10
 AZB30358 43 bp DNA linear GSS 20-FEB-2001
 LOCUS
 DEFINITION 2M0109M04R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone U062M0109M04 R, DNA sequence.

ACCESSION A2830358
 VERSION A2830358.1 GI:13000266
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 43)
 Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhuesern, A. and Wright, D., Weiser, R., von Niederhuesern, A.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0109 row: M column: 04
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 43.
 Location/Qualifiers
 1..43
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U062M0109M04"
 /clone_1lb="Mouse 10kb plasmid U062M0109M04"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 10 c 8 g 18 t
 ORIGIN

Query Match 83.3%; Score 10; DB 17; Length 43;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTCTTC 12
 |||||
 |||||
 Db 23 TTCTCTCTTC 32

RESULT 11
 AA052407/c 46 bp mRNA linear EST 13-SEP-1996
 LOCUS
 DEFINITION mb70H06.r1 Soares mouse p3JMF19.5 Mus musculus cDNA clone

IMAGE:334811.5' similar to SW:IN35_HUMAN P80217 INTERFERON-INDUCED 35 KD PROTEIN ;, mRNA sequence.

ACCESSION AA052407
 VERSION AA052407.1 GI:1543262
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 46)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kuchta, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellendberg, K., Sepulchre, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lemon, G., Soares, B., Wilson, R. and Waterston, R.
 The WashU-HMNI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMNI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MG1:216211
 Trace considered overall poor quality
 Putative full length read
 vector to vector length is
 possible reversed clone: similarity on wrong strand
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..46
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:334811"
 /clone_1lb="Soares mouse p3JMF19.5"
 /dev_stage="19.5 dpc total fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: p773D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified p773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bernaldo. RNA was kindly provided by Dr. Mithun Ko (Wayne State University)."

BASE COUNT 14 a 7 c 15 g 10 t
 ORIGIN

Query Match 83.3%; Score 10; DB 9; Length 46;
 Best Local Similarity 100.0%; Pred. No. 8.8e+04;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTC 11
 |||||
 |||||
 Db 23 GTTCTCTTC 14

RESULT 12
 AA902962 49 bp mRNA linear EST 08-APR-1996
 LOCUS
 DEFINITION OK44B09.s1 NCI CGAP Le12 Homo sapiens cDNA clone IMAGE:1516793 3' similar to TR:004118 Q0418 SALIVARY PROLINE-RICH GLYCOPROTEIN G1 PRECURSOR. ;, mRNA sequence.

ACCESSION AA902962.1 GI:3038085
 VERSION
 KEYWORDS EST.


```

SOURCE
ORGANISM      human.
REFERENCE     Homo sapiens
AUTHORS       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE         1 (bases 1 to 49)
              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
              Email: cgaps-remail.nih.gov
              unknown library type
              Trace considered overall poor quality
              Seq primer: -40ml3 fwd. RT from Amersham
              High quality sequence stop: 1.
FEATURES
source
1..49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1516793"
/clone_1lb="NCI CGAP L612"
/tissue_type="t1ciomyosarcoma"
/lab_host="DH10B"
/note="Organ: soft tissue; Vector: pTT3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dt) primer
[5'-AACTGAGAGATTCGGCGCGCAATGTTTGTGTGTGTGTGT-3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT
ORIGIN
19 a      15 c      15 g      0 t
Query Match      83.3%; Score 10; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCTCTTCC 12
Db      17 TTCTCTTCC 8

RESULT 13
LOCUS      AU102702/c      50 bp      mRNA      linear      EST 30-AUG-2001
DEFINITION      AU102702 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION      CAS08541, mRNA sequence.
VERSION        AU102702
KEYWORDS       AU102702.1 GI:13552223
SOURCE        EST.
ORGANISM      human.
REFERENCE     Homo sapiens
              Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
              1 (bases 1 to 50)
              Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
              'H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
              'Y., Nakamura, Y., Suyama, A. and Sugano, S.
              Diverse transcriptional initiation revealed by fine, large-scale
              mapping of mRNA start sites
              EMBO Rep. 2 (5), 388-393 (2001)
TITLE         21270072
JOURNAL       Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp
              Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
              'S. Construction and characterization of a full length-enriched and
              a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers

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1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_1lb="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfluminate treated U937 cells"
BASE COUNT
ORIGIN
13 a      12 c      18 g      7 t
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Best Local Similarity 100.0%; Pred. No. 9e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCTCTTC 11
Db      12 GTTCTCTTC 3

RESULT 14
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DEFINITION      AZ636812
              1M045B21R Mouse 10kb plasmid UGCIM library Mus musculus genomic
              clone UGCIM0495B21 R. DNA sequence.
ACCESSION      AZ636812
VERSION        AZ636812
KEYWORDS       GSS.
SOURCE        AZ636812.1 GI:11759002
ORGANISM      house mouse.
REFERENCE     Mus musculus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 19)
              Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
              Islam, H., Longacre, S., Mahmoud, M., Meenen, B., Pedersen, T., Rellily
              'M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
              and Wright, D., Weis, R.
              Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
              Unpublished (2000)
JOURNAL       Contact: Robert B. Weiss
              University of Utah Genome Center
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert length: 10000 Std Error: 0.00
              Plate: 0495 row: B column: 21
              Seq primer: CACACAGAAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 19.
FEATURES
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1..19
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIM0495B21"
/clone_1lb="Mouse 10kb plasmid UGCIM library"
/lab_host="Male"
/note="Vector: PMD29v. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydridynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

6 a 2 c 9 g 2 t

ORIGIN

of pMD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 75.0%; Score 9; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 75.0%; Score 9; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

AZ799780

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ799780 26 bp DNA linear GSS 16-FEB-2001
2M0057K20F Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM0057K20 F, DNA sequence.
AZ799780
AZ799780.1 GI:12951241
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std. Error: 0.00
Plate: 0057 Row: K Column: 20
Seq primer: CGTGTAAACGACGCCAGT
Class: Plasmid ends
High quality sequence stop: 26.
Location/Qualifiers
1..26
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCM0057K20"
/clone_1bp="Mouse 10kb plasmid UUGCM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

Search completed: June 23, 2003, 10:10:17
Job time : 620.647 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 18.2151 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-4
Perfect score: 12
Sequence: 1 CGTTCCTCTCC 12

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: *
1: /cgn2_6/ptodata/2/ina/5A COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PTCUS COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	100.0	12	2	US-08-770-565-4
2	12	100.0	20	2	US-08-770-565-3
3	12	100.0	20	2	US-08-833-377-7
4	12	100.0	30	2	US-08-770-565-2
5	11	91.7	20	1	US-08-031-143B-6
6	11	91.7	20	1	US-08-031-143B-33
7	11	91.7	20	2	US-08-833-377-14
8	11	91.7	20	5	PCT-US94-02891-6
9	11	91.7	20	5	PCT-US94-02891-33
10	10.4	86.7	15	1	US-08-363-240A-690
11	10.4	86.7	18	1	US-08-363-240A-1209
12	10.4	86.7	20	3	US-08-418-641-39
13	10.4	86.7	24	1	US-08-211-202-16
14	10.4	86.7	24	1	US-08-211-202-36
15	10.4	86.7	24	1	US-08-307-619-7
16	10.4	86.7	24	2	US-08-350-260A-53
17	10.4	86.7	24	3	US-08-983-607-2
18	10.4	86.7	24	3	US-08-983-607-2
19	10.4	86.7	26	4	US-08-859-998-684
20	10.4	86.7	26	4	US-09-225-928-684
21	10.4	86.7	42	1	US-08-487-037-8
22	10.4	86.7	45	1	US-08-211-202-11
23	10.4	86.7	45	1	US-08-211-202-15
24	10.4	86.7	45	1	US-08-307-619-22
25	10.4	86.7	45	2	US-08-350-260A-68
26	10.4	86.7	45	3	US-09-050-783-22
27	10.4	86.7	45	4	US-09-287-936-8

28	10.4	86.7	45	4	US-08-669-656A-26	Sequence 26, Appl
29	10.4	86.7	47	4	US-09-641-638-892	Sequence 892, App
30	10	83.3	14	1	US-08-294-424-33	Sequence 33, Appl
31	10	83.3	15	4	US-08-584-040-8457	Sequence 8457, Ap
32	10	83.3	17	3	US-08-988-706-54	Sequence 54, Appl
33	10	83.3	17	4	US-08-584-040-2519	Sequence 2519, Ap
34	10	83.3	17	4	US-08-584-040-2520	Sequence 2520, Ap
35	10	83.3	17	4	US-08-584-040-2521	Sequence 2521, Ap
36	10	83.3	17	4	US-08-584-040-2522	Sequence 2522, Ap
37	10	83.3	18	4	US-09-306-595C-30	Sequence 30, Appl
38	10	83.3	20	2	US-08-534-479-1	Sequence 1, Appl
39	10	83.3	20	4	US-09-490-692-85	Sequence 85, Appl
40	10	83.3	20	4	US-09-258-377-30	Sequence 30, Appl
41	10	83.3	20	4	US-09-203-895-5	Sequence 5, Appl
42	10	83.3	21	4	US-08-949-344C-18	Sequence 18, Appl
43	10	83.3	22	1	US-07-820-412-8	Sequence 8, Appl
44	10	83.3	22	1	US-08-488-144-4	Sequence 4, Appl
45	10	83.3	22	1	US-08-611-155B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-4
; Sequence 4, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Puzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-4
Query Match 100.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCC 12

Fri Jun 27 07:42:35 2003

us-08-770-564a-4.rn1

Page 2

Db 1 CGTTCCTCTCC 12

RESULT 2
US-08-770-565-3
Sequence 3, Application US/0870565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-3
Query Match 100.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
RESULT 3
US-08-833-377-7
Sequence 7, Application US/0883377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtesteiner, Serge P.
APPLICANT: Vaseetot, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "Oligo 14ab"
US-08-833-377-7
Query Match 100.0%; Score 12; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCC 12
Db 1 CGTTCCTCTCC 12
RESULT 4
US-08-770-565-2
Sequence 2, Application US/0870565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565

INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-6
Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTTCCCTCTCC 12
DB 18 GTTCCCTCTCC 8
RESULT 6
US-08-031-143B-33
Sequence 33, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CURRENT APPLICATION DATA:
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN

US-08-031-143B-6/c
Sequence 6, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CURRENT APPLICATION DATA:
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN

Query Match
Best Local Similarity 100.0%; Score 12; DB 2; Length 30;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCC 12
DB 1 CGTTCCTCTCC 12
RESULT 5
US-08-031-143B-6/c
Sequence 6, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CURRENT APPLICATION DATA:
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN

INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-6
Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTTCCCTCTCC 12
DB 18 GTTCCCTCTCC 8
RESULT 6
US-08-031-143B-33
Sequence 33, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
ATTORNEY/AGENT INFORMATION:
NAME: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CURRENT APPLICATION DATA:
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-33
Query Match
Best Local Similarity 91.7%; Score 11; DB 1; Length 20;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTTCCCTCTCC 12
DB 3 GTTCCCTCTCC 13
RESULT 7
US-08-833-377-14
Sequence 14, Application US/08833377

Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinlich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vasselet, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "biotinylated oligo 14ab"
US-08-833-377-14
Query Match 91.7%; Score 11; DB 2; length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GTTCCTCTCC 12
Db 2 GTTCCTCTCC 12
RESULT 8
PCT-US94-02891-6/c
Sequence 6, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: XSCID
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: YES
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-6
Query Match 91.7%; Score 11; DB 5; length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GTTCCTCTCC 12
Db 18 GTTCCTCTCC 8
RESULT 9
PCT-US94-02891-33
Sequence 33, Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FELTER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-33

Query Match 91.7%; Score 11; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCC 12
DB 3 GTTCCTCTTCC 13

RESULT 10
US-08-363-240A-690
Sequence 690, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaler, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 690:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-363-240A-690

Query Match 86.7%; Score 10.4; DB 1; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
DB 4 CGTTCCTCTTCC 15

RESULT 11
US-08-363-240A-1209
Sequence 1209, Application US/08363240A
Patent No. 5705388
GENERAL INFORMATION:
APPLICANT: Couture, Larry
APPLICANT: McSwiggen, James
APPLICANT: Bisgaler, Charles
APPLICANT: Pape, Michael
TITLE OF INVENTION: METHOD AND REAGENT FOR
PREVENTION, INHIBITION OF
PROGRESSION AND REGRESSION
TITLE OF INVENTION: OF VASCULAR DISEASES
NUMBER OF SEQUENCES: 1243
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,240A
FILING DATE: December 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 210/096
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1209:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-363-240A-1209

Query Match 86.7%; Score 10.4; DB 1; Length 18;
Best Local Similarity 58.3%; Pred. No. 1.9e+03;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
||:||||:|
DB 2 CQVCCGCUCC 13

RESULT 12
US-08-418-641-39
Sequence 39, Application US/09418641A
Patent No. 6124133
GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
APPLICANT: Lex M. Cowbert
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
FILE REFERENCE: RTS-0105
CURRENT APPLICATION NUMBER: US/09/418,641A
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-418-641-39

Query Match 86.7%; Score 10.4; DB 3; Length 20;
Best Local Similarity 91.7%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
||:|||||
DB 4 CGTTCCTCTCC 15

RESULT 13
US-08-211-202-16/c
Sequence 16, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Bornn
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
FILING DATE: 23-SEP-1992

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-211-202-16

Query Match 86.7%; Score 10.4; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+03;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
||:|||||
DB 13 CGTTCCTCTCC 2

RESULT 14
US-08-211-202-36/c
Sequence 36, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGENBOOM, Hendricus Reneus Jacobus Matheus
APPLICANT: BAIER, Michael
APPLICANT: JESPEERS, Laurent Stephane Anne Therese
APPLICANT: WINTER, Gregory Paul
TITLE OF INVENTION: Production of chimeric antibodies - a
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
ADDRESSER: Bornn
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATE: 23-SEP-1992

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
FILING DATE: 23-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120377.8
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206372.6
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/31960
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-211-202-36

Query Match 86.7%; Score 10.4; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCTCTCTCC 12
Db 13 CGTCTCTCTCC 2

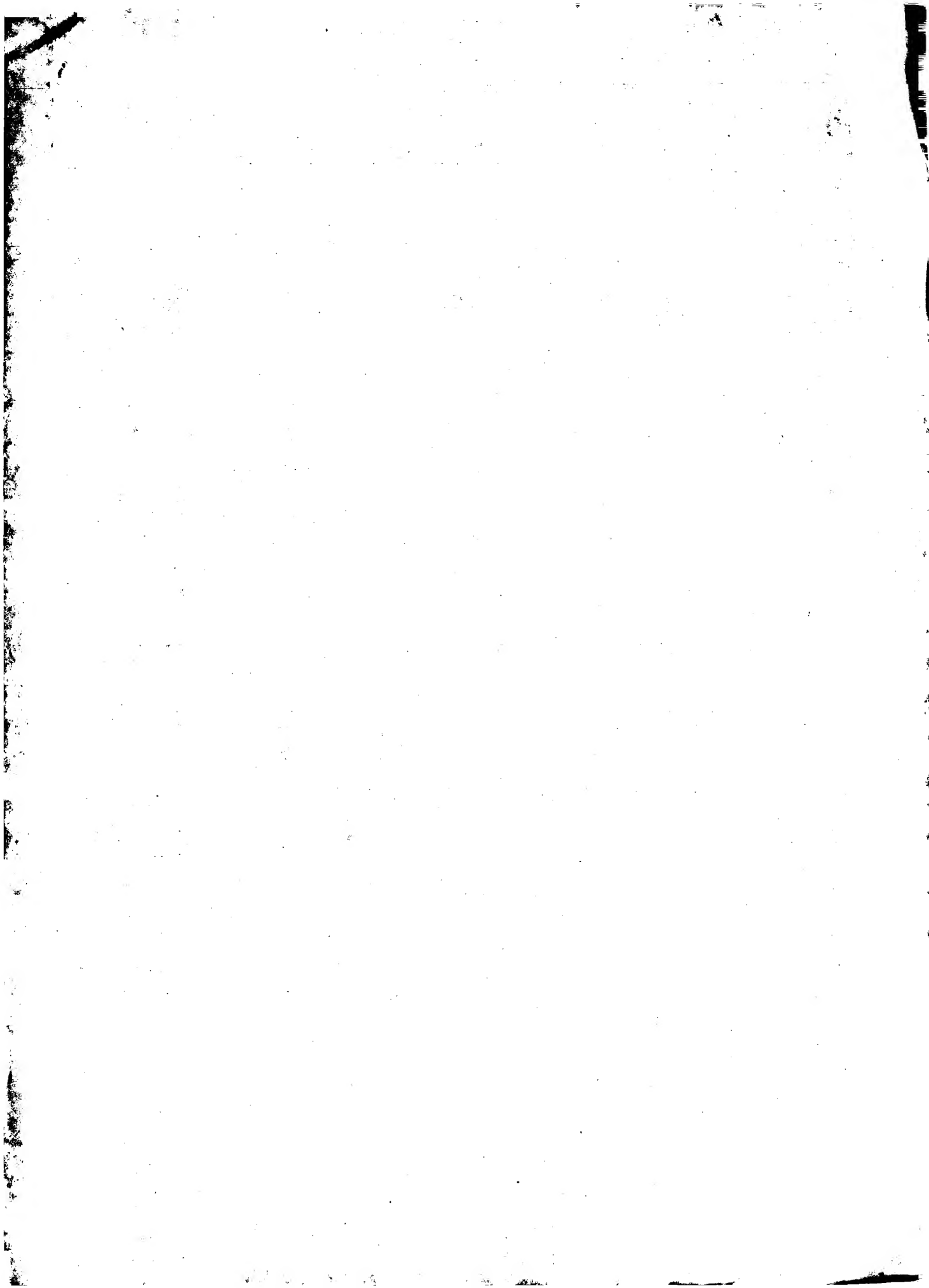
RESULT 15
US-08-307-619-7/c
Sequence 7, Application us/08307619
Patent No. 5733743
GENERAL INFORMATION:
APPLICANT: Johnson, Kevin S
APPLICANT: Winter, Gregory P
APPLICANT: Griffiths, Andrew D
APPLICANT: Smith, Andrew JH
APPLICANT: Waterhouse, P
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: us/08/307,619
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
CLASSIFICATION: G01N 33/531, G01N 33/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
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FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32238
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-307-619-7

Query Match 86.7%; Score 10.4; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTCTCTCTCC 12
Db 13 CGTCTCTCTCC 2

Search completed: June 25, 2003, 00:24:35
Job time : 18.2151 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1018.23 Seconds
(Without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-4
Perfect score: 12
Sequence: 1 CGTTCCTCTTCC 12

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	12	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appli
4	12	100.0	20	US-08-770-564A-3	Sequence 3, Appli
5	12	100.0	25	36 US-09-954-427-81691	Sequence 81691, A
6	12	100.0	25	36 US-09-956-584-18655	Sequence 18655, A
7	12	100.0	25	67 US-60-233-166-81691	Sequence 81691, A
8	12	100.0	25	67 US-60-233-620-45573	Sequence 45573, A
9	12	100.0	25	67 US-60-234-017-52883	Sequence 52883, A
10	12	100.0	30	79 US-60-353-987-396546	Sequence 396546, A
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14	12	100.0	32	1 PCT-US02-25943-62884	Sequence 62884, A
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 23 11 91.7 25 17 US-09-396-196F-95195 Sequence 95195, A
 24 11 91.7 25 17 US-09-396-196F-95206 Sequence 95206, A
 25 11 91.7 25 17 US-09-396-196F-119937 Sequence 119937, A
 26 11 91.7 25 17 US-09-396-196G-95194 Sequence 95194, A
 27 11 91.7 25 17 US-09-396-196G-95195 Sequence 95195, A
 28 11 91.7 25 17 US-09-396-196G-95206 Sequence 95206, A
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 31 11 91.7 25 26 US-09-660-220-124403 Sequence 124403, A
 32 11 91.7 25 26 US-09-660-220-124417 Sequence 124417, A
 33 11 91.7 25 26 US-09-660-220-124418 Sequence 124418, A
 34 11 91.7 25 36 US-09-954-427-51992 Sequence 51992, A
 35 11 91.7 25 36 US-09-954-427-56129 Sequence 56129, A
 36 11 91.7 25 36 US-09-954-427-56139 Sequence 56139, A
 37 11 91.7 25 36 US-09-954-427-77982 Sequence 77982, A
 38 11 91.7 25 36 US-09-954-427-149911 Sequence 149911, A
 39 11 91.7 25 36 US-09-954-427-149920 Sequence 149920, A
 40 11 91.7 25 36 US-09-954-427-291192 Sequence 291192, A
 41 11 91.7 25 36 US-09-954-427-291202 Sequence 291202, A
 42 11 91.7 25 36 US-09-954-427-291352 Sequence 291352, A
 43 11 91.7 25 36 US-09-954-427-377727 Sequence 377727, A
 44 11 91.7 25 36 US-09-956-584-14807 Sequence 14807, A
 45 11 91.7 25 36 US-09-956-584-100805 Sequence 100805, A

ALIGNMENTS

RESULT 1
 PCT-US97-23619-4
 ; Sequence 4, Application PC/TUS9723619
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; APPLICANT:
 ; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/23619
 ; FILING DATE: Not yet assigned
 ; CLASSIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,564
 ; FILING DATE: 20-DEC-1996
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/770,565
 ; FILING DATE: 20-DEC-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 15389-27PC
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:

LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: 1.12
 LOCATION: 1.12
 OTHER INFORMATION: /note="oligo 14d"
 PCT-US97-23619-4
 Query Match 100.0%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
 US-08-770-564a-4
 ; Sequence 4, Application US/08770564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ron
 ; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
 ; AGAINST THE RNA COMPONENT OF TELOMERASE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,564A
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-770-564a-4

Query Match 100.0%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 PCT-US97-23619-3

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; Sequence 3, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 14ab"
PCT-US97-23619-3

Query Match          100.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 CGTCTCTCTCC 12

RESULT 4
US-08-770-564a-3
; Sequence 3, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-770-564a-3
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Query Match          100.0%; Score 12; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
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; Sequence 81691, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Miltmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819663
US-09-954-427-81691
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Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      5 CGTCTCTCTCC 16
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RESULT 6
US-09-956-584-18655/c
; Sequence 18655, Application US/09956584
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; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-18655

Query Match          100.0%; Score 12; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTCTCTTCC 12
Db 18 CGTCTCTTCC 7

RESULT 7
US-60-233-166-81691
; Sequence 81691, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81691
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AA819663
US-60-233-166-81691

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTCTCTTCC 12
Db 5 CGTCTCTTCC 16

RESULT 8
US-60-233-620-45573/c
; Sequence 45573, Application US/60233620
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of
; TITLE OF INVENTION: Arabidopsis thaliana
; FILE REFERENCE: 3116
; CURRENT APPLICATION NUMBER: US/60/233,620
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; PUBLICATION INFORMATION:
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; DATABASE ACCESSION NUMBER: Genbank AL034567
US-60-233-620-45573

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTCTCTTCC 12
Db 15 CGTCTCTTCC 4

RESULT 9
US-60-234-017-52883/c
; Sequence 52883, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; TITLE OF INVENTION: musculus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank U41285
US-60-234-017-52883

Query Match          100.0%; Score 12; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTCTCTTCC 12
Db 18 CGTCTCTTCC 7

RESULT 10
US-60-353-987-396546/c
; Sequence 396546, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-396546

Query Match          100.0%; Score 12; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGTCTCTTCC 12
Db 24 CGTCTCTTCC 13

RESULT 11
PCT-US97-23619-2
; Sequence 2, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
TITLE OF INVENTION: RNA Component of Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..30
OTHER INFORMATION: /note= "oligo 14"
PCT-US97-23619-2
Query Match 100.0%; Score 12; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTCTCTCTCC 12
DB 1 CGTCTCTCTCC 12
RESULT 12
US-08-770-564a-2
Sequence 2, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Prizant, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
CITY: Two Embarcadero Center, 8th Floor
CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564a-2
Query Match 100.0%; Score 12; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTCTCTCTCC 12
DB 1 CGTCTCTCTCC 12
RESULT 13
US-08-521-634-17/C
Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
CITY: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:

Fri Jun 27 07:42:37 2003

us-08-770-564a-4.rnqm

Page 6

APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-17

Query Match
Best Local Similarity 100.0%; Score 12; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
|||
DB 31 CGTTCCTCTCC 20

RESULT 14
PCT-US02-25943-62884/c
Sequence 62884, Application PC/TUS0225943
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25943
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 62884
LENGTH: 32
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (6132858) ... (6132888)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 67367
PCT-US02-25943-62884

Query Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
|||
DB 22 CGTTCCTCTCC 11

RESULT 15
US-10-227-565-62884/c
Sequence 62884, Application US/10227565
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Pseudomonas aeruginosa PA01, complete genome.
FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/227,565
CURRENT FILING DATE: 2002-08-26
NUMBER OF SEQ ID NOS: 64158
SOFTWARE: Proprietary
SEQ ID NO 62884
LENGTH: 32
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa PA01, complete genome.
FEATURE:
LOCATION: (6132858) ... (6132888)

OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 6736
US-10-227-565-62884
Query Match
Best Local Similarity 100.0%; Score 12; DB 42; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCC 12
|||
DB 22 CGTTCCTCTCC 11

Search completed: June 25, 2003, 06:20:21
Job time : 1018.85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: June 25, 2003, 13:28:54 ; Search time 36.4781 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564a-4
Perfect score: 12
Sequence: 1 GGTTCCTCTCC 12

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 6: /cgn2_6/ptodata/1/pubpna/PCRUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	91.7	25	US-10-215-112-12736	Sequence 12736, A
C 2	11	91.7	25	US-10-098-263B-24096	Sequence 24096, A
C 3	11	91.7	25	US-10-098-263B-81647	Sequence 81647, A
C 4	11	91.7	25	US-10-098-263B-81648	Sequence 81648, A
C 5	11	91.7	25	US-10-098-263B-96226	Sequence 96226, A
C 6	11	91.7	25	US-10-098-263B-114611	Sequence 114611, A
C 7	10.4	86.7	17	US-09-818-875-899	Sequence 899, App
C 8	10.4	86.7	17	US-09-818-875-900	Sequence 900, App
C 9	10.4	86.7	20	US-09-854-883-302	Sequence 302, App
C 10	10.4	86.7	22	US-09-864-636A-1899	Sequence 1899, App
C 11	10.4	86.7	24	US-09-818-954A-4	Sequence 4, Appl
C 12	10.4	86.7	24	US-09-988-899-9	Sequence 9, Appl
C 13	10.4	86.7	25	US-09-943-388-16	Sequence 16, Appl
C 14	10.4	86.7	25	US-10-045-631A-12	Sequence 12, Appl
C 15	10.4	86.7	25	US-10-098-263B-9063	Sequence 9063, Ap
C 16	10.4	86.7	25	US-10-098-263B-9064	Sequence 9064, Ap
C 17	10.4	86.7	25	US-10-098-263B-21621	Sequence 21621, A
C 18	10.4	86.7	25	US-10-098-263B-22257	Sequence 22257, A
C 19	10.4	86.7	25	US-10-098-263B-23782	Sequence 23782, A

20	10.4	86.7	25	US-10-098-263B-25281	Sequence 25281, A
21	10.4	86.7	25	US-10-098-263B-48100	Sequence 48100, A
22	10.4	86.7	25	US-10-098-263B-57561	Sequence 57561, A
23	10.4	86.7	25	US-10-098-263B-81106	Sequence 81106, A
24	10.4	86.7	25	US-10-098-263B-84565	Sequence 84565, A
25	10.4	86.7	25	US-10-098-263B-85942	Sequence 85942, A
26	10.4	86.7	25	US-10-098-263B-95403	Sequence 95403, A
27	10.4	86.7	25	US-10-098-263B-117167	Sequence 117167, A
28	10.4	86.7	25	US-10-098-263B-117168	Sequence 117168, A
29	10.4	86.7	25	US-10-098-263B-120874	Sequence 120874, A
30	10.4	86.7	25	US-10-098-263B-120939	Sequence 120939, A
31	10.4	86.7	30	US-09-987-456-129	Sequence 129, App
32	10.4	86.7	31	US-10-052-942-80	Sequence 80, Appl
33	10.4	86.7	31	US-09-987-456-128	Sequence 128, App
34	10.4	83.3	17	US-10-163-552-930	Sequence 930, App
35	10.4	83.3	18	US-09-925-388-30	Sequence 30, Appl
36	10.4	83.3	18	US-09-969-373-3188	Sequence 3188, Ap
37	10.4	83.3	19	US-10-139-496-25	Sequence 1794, Ap
38	10.4	83.3	20	US-10-181-846-85	Sequence 85, Appl
39	10.4	83.3	20	US-09-953-047-40	Sequence 40, Appl
40	10.4	83.3	20	US-10-216-484-94	Sequence 94, Appl
41	10.4	83.3	20	US-10-216-484-98	Sequence 98, Appl
42	10.4	83.3	24	US-10-101-487-12	Sequence 12, Appl
43	10.4	83.3	24	US-10-101-487-13	Sequence 13, Appl
44	10.4	83.3	24	US-10-101-487-13	Sequence 13, Appl
45	10.4	83.3	24	US-09-037-657-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-215-112-12736/c
; Sequence 12736, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12736
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-12736

Query Match 91.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTCTCC 12
DB 18 GTTCCCTCTCC 8

RESULT 2
US-10-098-263B-24096/c
; Sequence 24096, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16


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; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 899
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-818-875-899

Query Match      86.7%; Score 10.4; DB 9; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db      17 CGTTCCTCTTCC 6

RESULT 8
US-09-818-875-900
; Sequence 900, Application US/09818875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gamet, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; TITLE OF INVENTION: Stranded Oligonucleotides
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/208,538
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/244,989
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 4385
; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 900
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-818-875-900

Query Match      86.7%; Score 10.4; DB 9; Length 17;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db      1 CGTTCCTCTTCC 12

RESULT 9
US-09-854-883-302/c
; Sequence 302, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
```

```

; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 302
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-302

Query Match      86.7%; Score 10.4; DB 10; Length 20;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db      20 CGTTCCTCTTCC 9

RESULT 10
US-09-864-636A-1899/c
; Sequence 1899, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Alwai, Hachim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1899
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-1899

Query Match      86.7%; Score 10.4; DB 9; Length 22;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGTTCCTCTTCC 12
Db      12 CTTCTCTTCC 1

RESULT 11
US-09-818-954A-4
; Sequence 4, Application US/09818954A
; Patent No. US20020015981A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher
; APPLICANT: Cao, Jin
; APPLICANT: Danilenko, Dmitry
; APPLICANT: Gong, Jianhua
; APPLICANT: Hill, David
; TITLE OF INVENTION: Beta-like Glycoprotein Hormone Polypeptide and Heterodimer
; FILE REFERENCE: A-676B
; CURRENT APPLICATION NUMBER: US/09/818,954A
; CURRENT FILING DATE: 2001-03-27
```

;; PRIOR APPLICATION NUMBER: 09/723,970
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/199,211
;; PRIOR FILING DATE: 2000-04-24
;; PRIOR APPLICATION NUMBER: 60/192,654
;; PRIOR FILING DATE: 2000-03-28
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO: 4
;; LENGTH: 24
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-818-954A-4

Query Match 86.7%; Score 10.4; DB 10; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 11 CATTCTCTCC 22

RESULT 12
US-09-968-899-9/c
; Sequence 9, Application US/09988899
; Patent No. US20020102613A1
; GENERAL INFORMATION:
; APPLICANT: HOOGENDOORN, HENDRICUS R.J.M.
; TITLE OF INVENTION: NOVEL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
; FILE REFERENCE: DX/003 CON
; CURRENT APPLICATION NUMBER: US/09/988,899
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: PCT/US00/13682
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 99201558.6
; PRIOR FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-968-899-9

Query Match 86.7%; Score 10.4; DB 10; Length 24;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 13 CGTTCCTCTCC 2

RESULT 13
US-09-943-388-16
; Sequence 16, Application US/09943388
; Patent No. US20020160953A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; APPLICANT: Webster, Philippa J.
; APPLICANT: Thayer, Edward C.
; TITLE OF INVENTION: Mammalian Glycoprotein Hormone-1
; FILE REFERENCE: 00-34
; CURRENT APPLICATION NUMBER: US/09/943,388
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/839,706
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US 60/199,498
; PRIOR APPLICATION NUMBER: 2000-04-25
; NUMBER OF SEQ ID NOS: 44

;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 16
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-943-388-16

Query Match 86.7%; Score 10.4; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 11 CATTCTCTCC 22

RESULT 14
US-10-045-631A-12
; Sequence 12, Application US/10045631A
; Publication No. US20030044300A1
; GENERAL INFORMATION:
; APPLICANT: Berand, Christophe
; APPLICANT: Onishi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugene
; APPLICANT: Wood, Ken
; APPLICANT: Yu, Ming
; APPLICANT: CytoKinetix, Inc.
; TITLE OF INVENTION: HUMAN KINESINS AND METHODS OF PRODUCING AND PURIFYING
; FILE REFERENCE: 020552-000410US
; CURRENT APPLICATION NUMBER: US/10/045,631A
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: WO PCT/US00/10870
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/295,612
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 12
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: (Spanning 22-2274)
US-10-045-631A-12

Query Match 86.7%; Score 10.4; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCC 12
Db 2 CGTTCCTCTCC 13

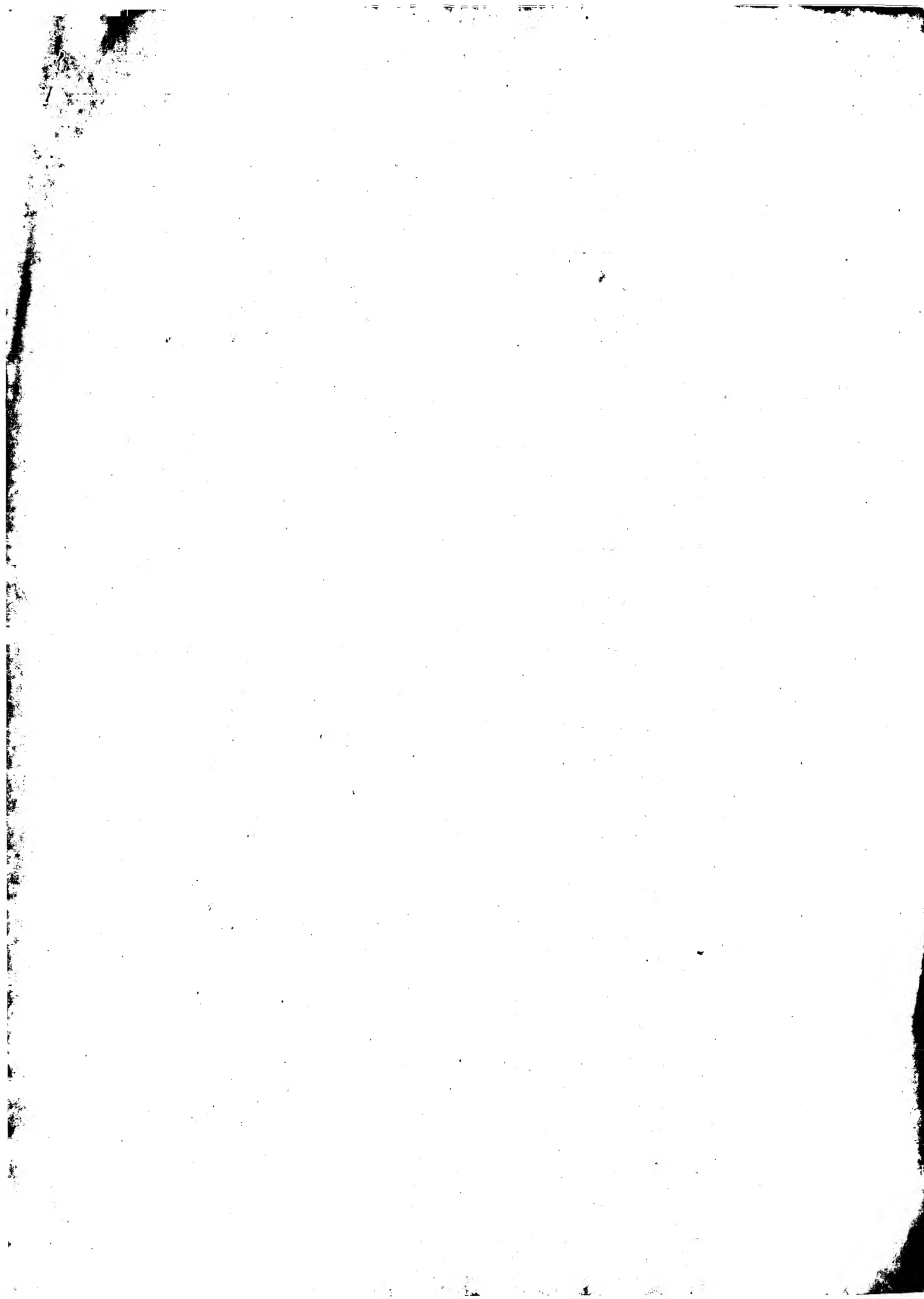
RESULT 15
US-10-098-263B-9063
; Sequence 9063, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; APPLICANT: Human Microarray
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118-1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO: 9063
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-9063

Query Match 86.7%; Score 10.4; DB 9; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.4e+04;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTTCCTCTTC 12
|||
Db 1 CGTTCCTCTTC 12

Search completed: June 25, 2003, 22:25:02
Job time : 37.4781 secs



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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20

Sequence: 1 CGTTCCTCTCTGCGGCT 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEM_PUB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEM_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.2	71.0	25	US-10-098-263B-114611	Sequence 114611, App1
2	14.2	71.0	39	US-09-832-355A-71	Sequence 71, App1
3	13.8	69.0	25	US-10-098-263B-23782	Sequence 23782, A
4	13.6	68.0	25	US-10-098-263B-69585	Sequence 69585, A
5	13.4	67.0	31	US-09-912-263-428	Sequence 428, App
6	13.2	66.0	23	US-09-439-429-17	Sequence 17, App1
7	13.2	66.0	25	US-10-098-263B-24011	Sequence 24011, A
8	13.2	66.0	25	US-10-098-263B-48100	Sequence 48100, A
9	13.2	65.0	31	US-09-801-274-1791	Sequence 1791, App
10	12.8	64.0	17	US-09-780-533A-58	Sequence 58, App1
11	12.8	64.0	17	US-09-780-533A-59	Sequence 59, App1
12	12.8	64.0	25	US-09-944-160-26	Sequence 26, App1
13	12.8	64.0	25	US-09-944-160-40	Sequence 40, App1
14	12.8	64.0	25	US-10-098-263B-49318	Sequence 49318, A
15	12.8	64.0	25	US-10-098-263B-116559	Sequence 116559, A
16	12.8	64.0	25	US-10-098-263B-116560	Sequence 116560, App
17	12.8	64.0	28	US-09-225-201-40	Sequence 40, App1
18	12.8	64.0	38	US-09-780-533A-3290	Sequence 3290, App
19	12.8	64.0	38	US-09-930-423-1849	Sequence 1849, App

C 20	12.8	64.0	42	9	US-09-500-700-58	Sequence 58, App1
C 21	12.6	63.0	20	9	US-10-060-301-189	Sequence 189, App
C 22	12.6	63.0	25	9	US-10-098-263B-114612	Sequence 114612, App
C 23	12.6	63.0	25	10	US-09-866-108-5348	Sequence 5348, App
C 24	12.6	63.0	25	10	US-09-866-108-5349	Sequence 5349, App
C 25	12.6	63.0	25	10	US-09-866-108-5350	Sequence 5350, App
C 26	12.6	63.0	25	10	US-09-866-108-5351	Sequence 5351, App
C 27	12.6	63.0	25	10	US-09-866-108-5352	Sequence 5352, App
C 28	12.6	63.0	25	10	US-09-866-108-5353	Sequence 5353, App
C 29	12.6	63.0	25	10	US-09-866-108-5354	Sequence 5354, App
C 30	12.4	62.0	18	10	US-09-969-373-1923	Sequence 1923, App
C 31	12.4	62.0	25	9	US-10-215-112-326	Sequence 326, App
C 32	12.4	62.0	25	9	US-10-215-112-3587	Sequence 3587, App
C 33	12.4	62.0	25	9	US-10-098-263B-46242	Sequence 46242, A
C 34	12.4	62.0	25	9	US-10-098-263B-47500	Sequence 47500, A
C 35	12.4	62.0	38	9	US-09-780-533A-3556	Sequence 3556, App
C 36	12.4	62.0	38	9	US-09-780-533A-3688	Sequence 3688, App
C 37	12.4	62.0	38	9	US-09-848-754A-5600	Sequence 5600, App
C 38	12.4	62.0	38	9	US-09-780-533A-954	Sequence 954, App
C 39	12.2	61.0	17	9	US-09-866-108-2417	Sequence 2417, App
C 40	12.2	61.0	20	10	US-09-854-883-127	Sequence 127, App
C 41	12.2	61.0	23	9	US-10-061-395-97	Sequence 97, App1
C 42	12.2	61.0	23	9	US-09-818-921-62	Sequence 62, App1
C 43	12.2	61.0	23	9	US-10-052-942-140	Sequence 140, App
C 44	12.2	61.0	23	9	US-09-987-456-108	Sequence 108, App
C 45	12.2	61.0	23	10		

ALIGNMENTS

RESULT 1
US-10-098-263B-114611
Sequence 114611, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION: Michael
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276, 759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 114611
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-114611

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 6 GTTCTCTCTCTAGGACTT 24
2 GTTCTCTCTCTAGGACTT 20

RESULT 2
US-09-832-355A-71/c
Sequence 71, Application US/0982355A
Publication No. US20030027751A1
GENERAL INFORMATION: Imre
APPLICANT: Kovacs, Imre
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832, 355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: PatentIn version 3.0

SEQ ID NO 71
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (..)
OTHER INFORMATION: Synthetic
US-09-832-355A-71

Query Match
Best Local Similarity 71.0%; Score 14.2; DB 9; Length 39;
84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCTCTGCGGCT 20
DB 32 GTTCCTCTTCTCTGCGGCT 14

RESULT 3
US-10-098-263B-23782/c
Sequence 23782, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23782
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-23782

Query Match
Best Local Similarity 69.0%; Score 13.8; DB 9; Length 25;
88.2%; Pred. No. 2.6e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCTGCGG 17
DB 20 CGTTCCTCTTCTCTGCGG 4

RESULT 4
US-10-098-263B-69585/c
Sequence 69585, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 69585
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-69585

Query Match
Best Local Similarity 68.0%; Score 13.6; DB 9; Length 25;
80.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCTGCGGCT 20

DB 21 CGTTCCTCTTCTCTGCGGACT 2

RESULT 5
US-09-912-263-428/c
Sequence 428, Application US/09912263
Publication No. US20030039973A1
GENERAL INFORMATION:
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.
TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 2825.2017-001
CURRENT APPLICATION NUMBER: US/09/912,263
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US 60/220,315
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 552
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 428
LENGTH: 31
TYPE: DNA
ORGANISM: Homo sapiens
US-09-912-263-428

Query Match
Best Local Similarity 67.0%; Score 13.4; DB 9; Length 31;
82.4%; Pred. No. 3.9e+03;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCCTCTTCTCTGCGGC 19
DB 28 TGCCTCTTCTCTGCGGC 12

RESULT 6
US-09-439-429-17/c
Sequence 17, Application US/09439429
Publication No. US20030083275A1
GENERAL INFORMATION:
APPLICANT: Power, Christopher
APPLICANT: Mayne, Michael B.
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
FILE REFERENCE: 3045.00002
CURRENT APPLICATION NUMBER: US/09/439,429
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 60/062,718
PRIOR FILING DATE: 1997-10-22
PRIOR APPLICATION NUMBER: 09/176,862
PRIOR FILING DATE: 1998-10-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-439-429-17

Query Match
Best Local Similarity 66.0%; Score 13.2; DB 9; Length 23;
83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCTGCGGC 18
DB 18 CGCTCTTCTCTCTGCTGC 1

RESULT 7
US-10-098-263B-24011
Sequence 24011, Application US/10098263B


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; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24011
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-24011

Query Match      66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCTCTGCGGC 19
Db      8 GTTCCTCTCTCTGCTCC 25

RESULT 8
; US-10-098-263B-48100
; Sequence 48100, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-098-263B-48100

Query Match      66.0%; Score 13.2; DB 9; Length 25;
Best Local Similarity 83.3%; Pred. No. 4.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 CGTTCCTCTCTGCGGC 18
Db      5 CGGTCTCTCTCTGTGAC 22

RESULT 9
; US-09-801-274-1791
; Sequence 1791, Application US/09801274
; Patent No. US20020032319A1
; GENERAL INFORMATION:
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Lander, Eric S.
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: 2825.2009-001
; CURRENT APPLICATION NUMBER: US/09/801,274
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/187,510
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 60/206,129
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 1802
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 1791
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-801-274-1791

Query Match      65.0%; Score 13; DB 10; Length 31;
Best Local Similarity 86.7%; Pred. No. 5.8e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GTTCCTCTCTCTGCG 16
Db      6 GGTCCTCTCTCTGCG 20

RESULT 10
; US-09-780-533A-58
; Sequence 58, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 58
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-58

Query Match      64.0%; Score 12.8; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      3 TTCCTCTCTCTGCGGC 18
Db      2 UUCUCUCUCUCGUCG 17

RESULT 11
; US-09-780-533A-59
; Sequence 59, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH800, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 59
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-09-780-533A-59

Query Match      64.0%; Score 12.8; DB 9; Length 17;
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Fri Jun 27 07:42:27 2003

us-08-770-564a-3.rnpb

Page 4

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Best Local Similarity 50.0%; Pred. No. 7.7e+03;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
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Qy	3	TTCCCTCTTCCTGCGGC	18
		::: :: :: :: ::	
Db	1	TUGCUCUUCGCGCUGC	16

RESULT 12

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US-09-944-160-26
/ Sequence 26, Application US/09944160
/ Patent No. US20020174452A1
/ GENERAL INFORMATION:
/ APPLICANT: Lewis, No. US20020174452A1man
/ APPLICANT: Davin, Laurence
/ APPLICANT: .. Huang, Ming
/ TITLE OF INVENTION: Monocot Seeds with Increased Lignan
/ TITLE OF INVENTION: Content
/ FILE REFERENCE: MSUR117983
/ CURRENT APPLICATION NUMBER: US/09/944,160
/ PRIORITY FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/230,652
/ PRIOR FILING DATE: 2000-09-07
/ NUMBER OF SEQ. ID NOS.: 49
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ. ID NO. 25
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: primer
US-09-944-160-26

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Query Match	64.0%;	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Dy 3 TTCTCTTCCTGGGC 18
 |||||
Db 10 TTCCTCTCATGCTGC 25

RESULT 13

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Sequence 40, Application US/09944160
Patent No. US20020174452A1
GENERAL INFORMATION:
APPLICANT: Lewis, No. US20020174452A1man
APPLICANT: Davlin, Laurence
APPLICANT: .. Huang, Ning
TITLE OF INVENTION: Monococ Seeds with Increased Lignan
TITLE OF INVENTION: Content
FILE REFERENCE: WSUR117983
CURRENT APPLICATION NUMBER: US/09/944,160
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/230,632
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Parseq for Windows Version 4.0
SEQ ID NO 40
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-944-160-40

```

Query Match	64.0%	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

3 TTCCTCTTCCTGCGC 18

Db 10 TTCCTCTTCATGCTGC 25

RESULT 14
US-10-098-263B-49318/C

APPLIC

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? TITLE OF INVENTION: Human Microarray
? FILE REFERENCE: 3118.1
? CURRENT APPLICATION NUMBER: US/10/098,263B
? CURRENT FILING DATE: 2003-01-08
? PRIOR APPLICATION NUMBER: 60/276,759
? PRIOR FILING DATE: 2001-03-16
? NUMBER OF SEQ ID NOS: 131066
? SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
? SEQ ID NO 49318
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Homo sapien
? US-10-098-263B-49318

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Query Match	64.0%	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	2	GTTCTCTCTTCCTGCGG	17
Db	18	GTGACTCTTCTCCTGCCG	3

RESULT 15

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US-10-098-263B-116559/c
? Sequence 116559, Application US/10098263B
? Publication No. US20030104410A1
? GENERAL INFORMATION:
? APPLICANT: Mclennan, Michael
? TITLE OF INVENTION: Human Microarray
? FILE REFERENCE: 3118.1
? CURRENT APPLICATION NUMBER: US/10/098,263B
? CURRENT FILING DATE: 2003-01-08
? PRIOR APPLICATION NUMBER: 60/276,759
? PRIOR FILING DATE: 2001-03-16
? NUMBER OF SEQ ID NOS: 131066
? SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
? SEQ ID NO 116559
? LENGTH: 25
? TYPE: DNA
? ORGANISM: Homo sapien
? US-10-098-263B-116559

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Query Match 64.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 7.4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCCTGCG 16
||| ||| ||| |||
Db 18 CGTTCCTCTTCCCTGCG 3

Search completed: June 25, 2003, 22:25:01
Job time : 61.7968 secs

US-09-944-160-40

Query Match	64.0%	Score 12.8;	DB 9;	Length 25;
Best Local Similarity	87.5%	Pred. No. 7.4e+03;		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

3 TTCCTCTTCCTGCGC 18

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1697.05 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564a-3
Perfect score: 20
Sequence: 1 CGTTCCTCTCTGCGGCTT 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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11: /cgn2_6/ptodata/2/pna/US09610_COMB.seq.*
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1	20	100.0	20	1 PCT-US97-23619-3	Sequence 3, Appl1
2	20	100.0	20	US-08-770-564a-3	Sequence 3, Appl1
3	20	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
4	20	100.0	30	11 US-08-770-564a-2	Sequence 2, Appl1
5	20	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
6	15.8	79.0	20	41 US-10-174-020-71	Sequence 71, Appl1
7	15.8	79.0	20	41 US-10-174-020-118	Sequence 138, Appl1
8	15.2	76.0	24	1 PCT-US01-30828-5	Sequence 8, Appl1
9	15.2	76.0	24	1 PCT-US01-42431-18	Sequence 18, Appl1
10	14.4	72.0	25	36 US-09-956-584-18655	Sequence 18655, A
11	14.4	72.0	25	67 US-06-234-017-52883	Sequence 52883, A
12	14.4	72.0	29	13 US-08-913-665-14	Sequence 14, Appl1
13	14.4	71.0	42	26 US-09-671-346-8	Sequence 8, Appl1
14	14.2	71.0	25	79 US-06-353-987-421837	Sequence 421837, A
15	14.2	71.0	39	32 US-09-832-355A-71	Sequence 71, Appl1
16	14.2	71.0	47	3 US-07-972-453-31	Sequence 31, Appl1
17	14.2	71.0	47	3 US-07-972-453-38	Sequence 38, Appl1
18	14.2	71.0	49	3 US-07-972-453-34	Sequence 34, Appl1
19	14.2	71.0	49	3 US-07-972-453-40	Sequence 40, Appl1
20	14	70.0	25	17 US-09-396-196F-119937	Sequence 119937, A
21	14	70.0	25	17 US-09-396-196G-119937	Sequence 119937, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 13.8 69.0 20 1 PCT-US00-27954A-39 Sequence 39, Appl
23 13.8 69.0 20 18 US-09-418-641-39 Sequence 39, Appl
24 13.8 69.0 20 40 US-10-110-514-39 Sequence 39, Appl
25 13.8 69.0 25 26 US-09-660-220-118104 Sequence 118104
26 13.8 69.0 25 36 US-09-856-584-257212 Sequence 257212
27 13.8 69.0 25 67 US-09-234-017-252876 Sequence 252876
28 13.8 69.0 25 79 US-09-353-987-593121 Sequence 593121
29 13.8 69.0 25 79 US-09-353-987-593121 Sequence 593121
30 13.8 69.0 25 79 US-09-353-987-593121 Sequence 593121
31 13.8 69.0 27 27 US-09-687-246A-2 Sequence 2, Appl
32 13.8 69.0 27 27 US-09-687-246A-2 Sequence 2, Appl
33 13.8 69.0 31 18 US-09-454-623-15 Sequence 15, Appl
34 13.8 69.0 31 17 US-09-367-170-23 Sequence 23, Appl
35 13.8 69.0 33 18 US-09-407-402-8 Sequence 44, Appl
36 13.8 69.0 33 18 US-09-407-402-8 Sequence 44, Appl
37 13.8 69.0 33 18 US-09-481-620-6 Sequence 6, Appl
38 13.8 69.0 33 18 US-09-481-620-6 Sequence 6, Appl
39 13.8 69.0 33 32 US-09-852-370-38 Sequence 38, Appl
40 13.8 69.0 33 32 US-09-852-370-38 Sequence 38, Appl
41 13.8 69.0 33 38 US-10-002-244-8 Sequence 8, Appl
42 13.8 69.0 33 38 US-10-002-244-8 Sequence 8, Appl
43 13.8 69.0 33 38 US-10-002-244A-8 Sequence 8, Appl
44 13.8 69.0 33 38 US-10-002-244A-8 Sequence 8, Appl
45 13.8 69.0 33 39 US-10-087-286-30 Sequence 30, Appl

ALIGNMENTS

RESULT 1
PCT-US97-23619-3
Sequence 3, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Method for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 14ab"
PCT-US97-23619-3

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTCCTTCTCGGCGCT 20
Db 1 CGTTCCTTCTCGGCGCT 20

RESULT 2
US-08-770-564A-3
Sequence 3, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinlich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGTTCCTTCTCGGCGCT 20
Db 1 CGTTCCTTCTCGGCGCT 20

RESULT 3
PCT-US97-23619-2

Sequence 2, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..30
OTHER INFORMATION: /note= "oligo 14"
PCT-US97-23619-2
Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCGCGGCT 20
DB 1 CGTTCCTTCTCGCGGCT 20

RESULT 4
US-08-770-564A-2
Sequence 2, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-2

Query Match 100.0%; Score 20; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCGCGGCT 20
DB 1 CGTTCCTTCTCGCGGCT 20

RESULT 5
US-08-521-634-17/c
Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-17

Query Match          100.0%; Score 20; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTCGGCGCT 20
DB 31 CGTTCCTTCTCTCGGCGCT 12

RESULT 6
US-10-174-020-71
; Sequence 71, Application US/10174020
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: RTS-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-10-174-020-71

Query Match          79.0%; Score 15.8; DB 41; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTCGGCGCT 19
DB 2 CGTTCCTTCTCTGTGGCC 20

RESULT 7
US-10-174-020-138/C
; Sequence 138, Application US/10174020
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: RTS-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
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; FEATURE:
; US-10-174-020-138

Query Match          79.0%; Score 15.8; DB 41; Length 20;
Best Local Similarity 89.5%; Pred. No. 7.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTCGGCGCT 19
DB 19 CGTTCCTTCTCTGTGGCC 1

RESULT 8
PCT-US01-30828-5/C
; Sequence 5, Application PC/TUS0130828
; GENERAL INFORMATION:
; APPLICANT: Keck Graduate Institute
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Galas, David J.
; APPLICANT: Garrison, Lori K.
; TITLE OF INVENTION: GENOTYPING BY LIQUID CHROMATOGRAPHIC ANALYSIS OF SHORT
; FILE REFERENCE: 480189.403PC
; CURRENT APPLICATION NUMBER: PCT/US01/30828
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/300,350
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primers
; PCT-US01-30828-5

Query Match          76.0%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTCGGCGCT 20
DB 22 CGTTCCTATCTGTGCTT 3

RESULT 9
PCT-US01-42432-18/C
; Sequence 18, Application PC/TUS0142432
; GENERAL INFORMATION:
; APPLICANT: Keck Graduate Institute
; APPLICANT: Van Ness, Jeffrey
; APPLICANT: Galas, David J.
; APPLICANT: Garrison, Lori K.
; TITLE OF INVENTION: METHODS FOR PARALLEL MEASUREMENT OF GENETIC VARIATIONS
; FILE REFERENCE: 480189.402PC
; CURRENT APPLICATION NUMBER: PCT/US01/42432
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/269,244
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
; PCT-US01-42432-18

Query Match          76.0%; Score 15.2; DB 1; Length 24;
Best Local Similarity 85.0%; Pred. No. 1.4e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CGTTCCTCTCTGCGGCT 20
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 Db 22 CGTTCCTCATCTGTGCTT 3

RESULT 10
 US-09-956-584-18655/c
 ; Sequence 18655, Application US/09956584
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltman, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
 ; FILE REFERENCE: 3115.1
 ; CURRENT APPLICATION NUMBER: US/09/956,584
 ; CURRENT FILING DATE: 2001-09-19
 ; PRIOR APPLICATION NUMBER: 60/234,017
 ; PRIOR FILING DATE: 2000-09-20
 ; NUMBER OF SEQ ID NOS: 605887
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO.18655
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-09-956-584-18655

Query Match 72.0%; Score 14.4; DB 36; Length 25;
 Best Local Similarity 93.8%; Pred. No. 3.1e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTGCGG 16
 |||||
 Db 18 CGTTCCTCTCTGCGG 3

RESULT 11
 US-60-234-017-52883/c
 ; Sequence 52883, Application US/60234017
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltman, M
 ; APPLICANT: Affymetrix, Inc.
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
 ; FILE REFERENCE: 3115
 ; CURRENT APPLICATION NUMBER: US/60/234,017
 ; CURRENT FILING DATE: 2000-09-20
 ; NUMBER OF SEQ ID NOS: 605887
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 52883
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank U41285
 US-60-234-017-52883

Query Match 72.0%; Score 14.4; DB 67; Length 25;
 Best Local Similarity 93.8%; Pred. No. 3.1e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTGCG 16
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 Db 18 CGTTCCTCTCTGCGG 3

RESULT 12
 US-08-913-665-14/c
 ; Sequence 14, Application US/08913665
 ; GENERAL INFORMATION:
 ; APPLICANT: Saiga, Akihiko
 ; APPLICANT: Oriita, Satoshi
 ; APPLICANT: Igarashi, Hisanaga
 ; APPLICANT: Okumura, Kouichi
 ; APPLICANT: Sakaguchi, Gaku

;; TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
 ;; TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
 ;; NUMBER OF SEQUENCES: 20
 ;; CORRESPONDENCE ADDRESS:
 ;; ADDRESSEE: FISH & NEAVE
 ;; STREET: 1251 Avenue of the Americas
 ;; CITY: New York
 ;; STATE: New York
 ;; COUNTRY: USA
 ;; ZIP: 10020
 ;; COMPUTER READABLE FORM:
 ;; MEDIUM TYPE: Floppy disk
 ;; COMPUTER: IBM PC compatible
 ;; OPERATING SYSTEM: PC-DOS/MS-DOS
 ;; SOFTWARE: Patent In Release #1.0, Version #1.30
 ;; CURRENT APPLICATION DATA:
 ;; APPLICATION NUMBER: US/08/913,665
 ;; FILING DATE: 19-SEP-1997
 ;; CLASSIFICATION: 536
 ;; ATTORNEY/AGENT INFORMATION:
 ;; NAME: Haley, James F.
 ;; REGISTRATION NUMBER: 27,794
 ;; REFERENCE/DOCKET NUMBER: SHGN-12
 ;; TELECOMMUNICATION INFORMATION:
 ;; TELEPHONE: 212-596-9000
 ;; TELEFAX: 212-596-9090
 ;; INFORMATION FOR SEQ ID NO: 14:
 ;; SEQUENCE CHARACTERISTICS:
 ;; LENGTH: 29 base pairs
 ;; TYPE: nucleic acid
 ;; STRANDEDNESS: single
 ;; TOPOLOGY: linear
 ;; MOLECULE TYPE: other nucleic acid
 ;; DESCRIPTION: /desc = "synthetic DNA"
 US-08-913-665-14

Query Match 72.0%; Score 14.4; DB 13; Length 29;
 Best Local Similarity 93.8%; Pred. No. 3.2e+04;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCGGCC 19
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 Db 21 TACTCTCTCTGCGGCC 6

RESULT 13
 US-09-671-346-8/c
 ; Sequence 8, Application US/09671346
 ; GENERAL INFORMATION:
 ; APPLICANT: Wolf, David L.
 ; APPLICANT: Siba, Uma
 ; TITLE OF INVENTION: Agents Affecting Thrombosis and Hemostasis
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Morgan, Lewis & Bockius LLP
 ; STREET: 1111 Pennsylvania Avenue, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/671,346
 ; FILING DATE: 27-Sep-2000
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/578,646
 ; FILING DATE: 1990-09-04
 ; APPLICATION NUMBER: US 07/808,329
 ; FILING DATE: 1991-12-16

Fri Jun 27 07:42:28 2003

us-08-770-564a-3. rrom

Page 6

APPLICATION NUMBER: US 08/249,777
 FILING DATE: 1994-05-26
 APPLICATION NUMBER: US 08/266,003
 FILING DATE: 1994-06-29
 APPLICATION NUMBER: US 08/469,301
 FILING DATE: 1995-06-06
 APPLICATION NUMBER: US 09/016,403
 FILING DATE: 1998-01-30
 APPLICATION NUMBER: US 09/366,207
 FILING DATE: 1999-07-28
 ATTORNEY/AGENT INFORMATION:
 NAME: Michael S. Tuccan, Ph.D.
 REGISTRATION NUMBER: 43,210
 REFERENCE/DOCKET NUMBER: 44461-5002-15-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 739-3000
 TELEFAX: (202) 739-3001
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 18-09-671-346-8

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? SEQ ID NO 71
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? LENGTH: 39
? TYPE: DNA
? ORGANISM: Artificial sequence
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1..7)
? OTHER INFORMATION: Synthetic
US-09-832-355A-71

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Best Local Similarity 84.2%; Freq. No. 4e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0,

QY      2 GTTCCTCTCTCTCGAGCCT 20
      ||| ||| ||| ||| |||
Db      32 GTTCCTCTCTCTCGGCCT 14

Search completed: June 25, 2003, 06:20:21
Job time : 1698.67 secs

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Best Local Similarity	93.8%	Pred. No. 3.3e+04		
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RESULT 14
US-60-353-987-421837/c
/ Sequence 421837, Application US/60353987
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U13
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/60/353,987
/ CURRENT FILING DATE: 2002-02-01
/ NUMBER OF SEQ ID NOS: 997516
/ SEQ ID NO 421837
/ SEQ ID NO 421837
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
/ US-60-353-987-421837

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Best Local Similarity 84.2%; Pred. No. 3.8e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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RESULT 15
 US-09-832-355A-71/c
 Sequence 71, Application US/09832355A
 GENERAL INFORMATION:
 APPLICANT: Kovesdi, Imre
 APPLICANT: Keesler, Paul
 TITLE OF INVENTION: VEGF FUSION PROTEINS
 FILE REFERENCE: 205654
 CURRENT APPLICATION NUMBER: US/09/832,355A
 CURRENT FILING DATE: 2001-04-10
 NUMBER OF SEQ ID NOS: 126
 SOFTWARE: PatentIn version 3.0

Search completed: June 25, 2003, 06:20:21
Job time : 1698.67 secs.

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Best Local Similarity	84.2%	Pred No. 4e+04		
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DB	32	GTTCCTTCTTCGCGGCT	14	

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? SEQ ID NO 71
? LENGTH: 39
? TYPE: DNA
? ORGANISM: Artificial sequence
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1..7)
? OTHER INFORMATION: Synthetic
US-09-832-355A-71

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20
Sequence: 1 CGTTCCCTCTCTCGCGGCT 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	20	100.0	20	2	US-08-770-565-2
4	19	95.0	20	2	US-08-833-377-14
5	14.4	72.0	29	3	US-09-121-321-14
6	14.4	72.0	29	4	US-08-933-803A-14
7	14.4	72.0	42	1	US-08-487-037-8
8	13.8	69.0	20	3	US-09-418-641-39
9	13.8	69.0	31	2	US-08-576-626A-15
10	13.8	69.0	33	4	US-08-672-213-8
11	13.8	69.0	33	4	US-08-672-213-49
12	13.8	69.0	33	4	US-08-973-131-38
13	13.4	67.0	20	2	US-08-534-479-1
14	13.2	66.0	20	3	US-09-009-913-173
15	13.2	66.0	23	3	US-09-176-862-17
16	13.2	66.0	45	1	US-08-211-202-11
17	13.2	66.0	45	1	US-08-211-202-15
18	13.2	66.0	45	1	US-08-307-619-22
19	13.2	66.0	45	2	US-08-350-260A-68
20	13.2	66.0	45	3	US-09-050-783-22
21	13	65.0	45	1	US-08-487-037-9
22	12.8	64.0	20	2	US-08-206-790A-18
23	12.8	64.0	20	5	PCT-US95-02943-18
24	12.8	64.0	21	1	US-08-303-009-8
25	12.8	64.0	21	2	US-08-691-123-8
26	12.8	64.0	21	3	US-09-107-075-8
27	12.8	64.0	21	3	US-08-866-544-1

C 28	12.8	64.0	28	2	US-08-859-998-40	Sequence 40, Appl
C 29	12.8	64.0	28	4	US-09-225-928-40	Sequence 40, Appl
C 30	12.8	64.0	42	3	US-08-863-813A-58	Sequence 58, Appl
C 31	12.6	63.0	30	4	US-08-348-548-48	Sequence 48, Appl
C 32	12.6	63.0	30	5	PCT-US95-15716-48	Sequence 48, Appl
C 33	12.6	63.0	37	1	US-08-431-080-10	Sequence 10, Appl
C 34	12.6	63.0	37	2	US-08-938-534-10	Sequence 10, Appl
C 35	12.6	63.0	37	4	US-09-345-294-10	Sequence 10, Appl
C 36	12.6	63.0	49	4	US-09-538-709-935	Sequence 935, App
C 37	12.6	63.0	49	4	US-09-538-709-978	Sequence 978, App
C 38	12.4	62.0	20	1	US-08-031-143B-6	Sequence 6, Appl
C 39	12.4	62.0	20	1	US-08-031-143B-33	Sequence 6, Appl
C 40	12.4	62.0	20	5	PCT-US94-02891-6	Sequence 6, Appl
41	12.4	62.0	20	5	PCT-US94-02891-33	Sequence 33, Appl
42	12.2	61.0	20	4	US-09-487-368A-127	Sequence 127, App
43	12.2	61.0	20	4	US-09-851-896-86	Sequence 86, Appl
44	12.2	61.0	24	3	US-08-936-632B-16	Sequence 16, Appl
45	12.2	61.0	33	1	US-08-078-683A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-3
Sequence 3, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-3
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CGTTCCCTCTCTCGCGGCT 20

Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 2
US-08-833-377-7
Sequence 7, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtshteyner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "Oligo 14ab"
US-08-833-377-7
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 3
US-08-770-565-2
Sequence 2, Application US/0870565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 32,944
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2
Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
Db 1 CGTTCCTCTCTCGGCGCT 20

RESULT 4
US-08-833-377-14
Sequence 14, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtshteyner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377

FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"
US-08-833-377-14

Query Match 95.0%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GTTCCTTCTCGGCGCT 20

RESULT 5
US-09-121-321-14/c
Sequence 14, Application US/09121321
Patent No. 6090783
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,321
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/933,803
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-121-321-14

Query Match 72.0%; Score 14.4; DB 3; Length 29;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TTCTCTCTCGGCGCC 19
DB 21 TACTCTTCTCGGCGCC 6

RESULT 6
US-08-933-803A-14/c
Sequence 14, Application US/08933803A
Patent No. 6218522
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,803A
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-933-803A-14

Query Match 72.0%; Score 14.4; DB 4; Length 29;
Best Local Similarity 93.8%; Pred. No. 3.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Fri Jun 27 07:42:27 2003

us-08-770-564a-3.rn1

Page 4

QY 4 TCTCTTCTCTCGGCC 19
DB 21 TACTCTCTCTCGGCC 6

RESULT 7

US-08-487-037-8/c
Sequence 8, Application US/08487037
Patent No. 5795863

GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-037-8

Query Match 72.0%; Score 14.4; DB 1; Length 42;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCTCGCG 16
DB 25 CGATCTCTCTCTCGG 10

RESULT 8

US-09-418-641-39
Sequence 39, Application US/09418641A
Patent No. 6124133

GENERAL INFORMATION:
APPLICANT: Jennifer K. Taylor
TITLE OF INVENTION: ANTISENSE MODULATION OF FRA-1 EXPRESSION
FILE REFERENCE: R15-0105
CURRENT APPLICATION NUMBER: US/09/418,641A
CURRENT FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 39
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-09-418-641-39

Query Match 69.0%; Score 13.8; DB 3; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 4 CGCTCTCTCTCTCGG 20

RESULT 9

US-08-576-626A-15/c
Sequence 15, Application US/08576626A
Patent No. 5998194

GENERAL INFORMATION:
APPLICANT: Summers, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Staver, M.J.
TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casato
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857-US.O1
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-576-626A-15

Query Match 69.0%; Score 13.8; DB 2; Length 31;
Best Local Similarity 88.2%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 TCTCTTCTCTCGGCC 20
DB 23 TCTCTTCTCTCGGCC 7

RESULT 10

US-08-672-213-8/c
Sequence 8, Application US/08672213
Patent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.

APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
STREET: 26 Landedowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 346B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-672-213-8

Query Match 69.0%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 11
US-08-672-213-49/c
Sequence 49, Application US/08672213
Patent No. 6306649
GENERAL INFORMATION:
APPLICANT: GILMAN, Michael Z.
APPLICANT: NATESAN, Sridaran
TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
FACTORS IN GENE THERAPY
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Gene Therapeutics, Inc.
STREET: 26 Landedowne Street
CITY: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02139-4234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,213
FILING DATE: 27-JUN-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,553
FILING DATE: 27-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,614
FILING DATE: 29-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERSTEIN, David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: ARIAD 346B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-672-213-49

Query Match 69.0%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 12
US-08-973-131-38/c
Sequence 38, Application US/08973131
Patent No. 6326166
GENERAL INFORMATION:
APPLICANT: Pomerantz, Joel L.
APPLICANT: Sharp, Phillip A.
TITLE OF INVENTION: Chimeric DNA-binding proteins
FILE REFERENCE: APV-022.02
CURRENT APPLICATION NUMBER: US/08/973,131
EARLIER FILING DATE: 1998-03-16
EARLIER APPLICATION NUMBER: PCT/US95/16982
EARLIER FILING DATE: 1995-12-29
EARLIER APPLICATION NUMBER: 08/366,083
EARLIER FILING DATE: 1994-12-29
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-08-973-131-38

Query Match 69.0%; Score 13.8; DB 4; Length 33;
Best Local Similarity 88.2%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTCTCTTCTGCGGCC 19
Db 23 TTCTCTCTCTGCGGCC 7

RESULT 13
US-08-534-479-1
Sequence 1, Application US/08534479

Patent No. 5851769
GENERAL INFORMATION:
APPLICANT: GRAY, JOE W.
TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/534,479
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, KAMRIN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: LBL-01754
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-534-479-1
Query Match 67.0%; Score 13.4; DB 2; Length 20;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 TTCCTCTTCCTGCGG 17
DB 1 TTCCTCTTCCTGCGG 15
RESULT 14
US-09-009-913-173/c
Sequence 173, Application US/09009913
GENERAL INFORMATION:
APPLICANT: AXYS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Ave, Suite 200
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELEPHONE: 650-327-3231
TELEFAX: 650-327-3231
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-913-173

Query Match 66.0%; Score 13.2; DB 3; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTCCTCTTCCTGCGGCT 20
DB 20 TTCCTCTTCCTGCGGCT 3

RESULT 15
US-09-176-862-17/c
Sequence 17, Application US/09176862B
Patent No. 6046319
GENERAL INFORMATION:
APPLICANT: Power, Christopher
TITLE OF INVENTION: ANTISENSE OLIGODEOXYNUCLEOTIDES REGULATING EXPRESSION
FILE REFERENCE: 3045,00002
CURRENT APPLICATION NUMBER: US/09/176,862B
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: 60/062,718
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 17
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-176-862-17

Query Match 66.0%; Score 13.2; DB 3; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTTCCTGCGGC 18
DB 18 CGCTCTTCCTGCGGC 1

Search completed: June 25, 2003, 00:24:35
UOB time : 51.586 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-3

Perfect score: 20

Sequence: 1 CGTTCCTCTCTCGCGGCT 20

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hlc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hlc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vit:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	38	AZ974736	AZ974736 2M0249A03
C 2	12	60.0	43	AZ830358	AZ830358 2M0109M04
C 3	12	60.0	46	AZ767395	AZ767395 Arabidops
C 4	11	55.0	26	AZ942099	AZ942099 2M0202C09
C 5	11	55.0	33	BH850686	BH850686 SALX_0716
C 6	11	55.0	37	AZ392980	AZ392980 IM0155P13

Result No.	Score	Query Match	Length	ID	Description
C 7	11	55.0	40	AZ627381	AZ627381 IM0469H09
C 8	11	55.0	43	AZ419099	AZ419099 IM0195N23
C 9	11	55.0	45	AZ423992	AZ423992 IM0203A16
C 10	11	55.0	46	B1488502	B1488502 603021011
C 11	11	55.0	50	AU102628	AU102628 AU102629
C 12	11	55.0	50	B1685073	B1685073 603310058
C 13	10	50.0	27	AZ630179	AZ630179 IM0483B10
C 14	10	50.0	28	N92455	N92455 zb63h01.s1
C 15	10	50.0	29	AZ794049	AZ794049 2M0047H08
C 16	10	50.0	32	AZ587757	AZ587757 IM0395F07
C 17	10	50.0	32	AZ792853	AZ792853 2M0045C07
C 18	10	50.0	32	BH847691	BH847691 SALX_0558
C 19	10	50.0	35	AZ581591	AZ581591 IM0370O23
C 20	10	50.0	37	AZ625706	AZ625706 IM0456O23
C 21	10	50.0	37	AZ761912	AZ761912 IM0555G21
C 22	10	50.0	41	AZ608460	AZ608460 IM0432J07
C 23	10	50.0	41	BH625029	BH625029 100710280
C 24	10	50.0	42	BH640418	BH640418 1008035G0
C 25	10	50.0	43	H41505	H41505 yp68h12.s1
C 26	10	50.0	43	T77849	T77849 yd16f04.s1
C 27	10	50.0	44	AZ761199	AZ761199 IM0555G21
C 28	10	50.0	45	AZ657409	AZ657409 IM0533M04
C 29	10	50.0	45	AZ843544	AZ843544 2M0142O22
C 30	10	50.0	45	AL754108	AL754108 Arabidops
C 31	10	50.0	46	AA052407	AA052407 mb70h06.x
C 32	10	50.0	46	A1003193	A1003193 an12a01.s
C 33	10	50.0	46	R87862	R87862 yoa5f03.r1
C 34	10	50.0	47	H80650	H80650 yu77a07.r1
C 35	10	50.0	47	AZ784478	AZ784478 2M0027K02
C 36	10	50.0	47	AZ845343	AZ845343 2M0145B07
C 37	10	50.0	48	AZ443723	AZ443723 IM0238D11
C 38	10	50.0	48	BH840628	BH840628 KG05923-5
C 39	10	50.0	49	AA902962	AA902962 ok44b09.s
C 40	10	50.0	50	A1252059	A1252059 qy39f04.x
C 41	10	50.0	50	AU102702	AU102702 AU102702
C 42	10	50.0	50	AU104073	AU104073 AU104073
C 43	10	50.0	50	AU104281	AU104281 AU104281
C 44	10	50.0	50	AU104282	AU104282 AU104282
C 45	10	50.0	50	AU104283	AU104283 AU104283

ALIGNMENTS

RESULT 1

LOCUS AZ974736/c 38 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0249A03R Mouse 10kb plasmid UGCG2M library Mus musculus genomic

ACCESSION AZ974736

VERSION AZ974736.1 GI:13645963

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 38)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiser,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SUC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00

Fri Jun 27 07:42:26 2003

us-08-770-564a-3.oligo.rst

Page 2

Plate: 0249 row: A column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.

BASE COUNT	14 a	8 c	9 g	7 b
ORIGIN				

Query Match	60.0%	Score 12	DB 17	Length 38
Best Local Similarity	100.0%	Pred. No. 2.2e+04		
Matches 12, Conservative	0	Mismatches 0	Indels 0	Gaps 0

[illegible]

Plate: 0109 row: M column: 04
Seq primer: CACACAGAAACAGCTATGACCC
Class: plasmid ends
High quality sequence stop: 43.

BASE COUNT	7 a	10 c	8 g	18 t
ORIGIN	.			

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Query Match      60.0%; Score 12; DB 17; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

[illegible]

COMMENT

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f5k7. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

SOURCE

Location/Qualifiers

1..46
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-219A03-014202"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 7 a 19 c 2 g 18 t
ORIGIN

Query Match 60.0%; Score 12; DB 17; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 TTCCTCTTCT 13
|||||
Db 29 TTCCTCTTCT 40

RESULT 4
AZ942099/c

LOCUS

26 bp DNA linear GSS 26-APR-2001
DEFINITION clone UUGC2M020C09 F, DNA sequence.

ACCESSION

AZ942099

VERSION

AZ942099.1 GI:13805115

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

COMMENT

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0202 row: C column: 09
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid
High quality sequence stop: 26.
Location/Qualifiers

FEATURES

SOURCE

1..26
/organism="Mus musculus"
/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="UUGC2M020C09"
/clone_1lb="Mouse 10kb plasmid UUGC2M 1library"
/sex="Female"

/lib_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: FMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|g14732114|g14732114), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptor complementary to the insert adaptor and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 10 a 0 c 16 g 0 t
ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 6.3e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCCTCTTCT 13
|||||
Db 12 TTCCTCTTCT 2

RESULT 5
BH850686

LOCUS

33 bp DNA linear GSS 13-JUN-2002
DEFINITION SALK_071692.32.90 x Arabidopsis thaliana TDNA insertion lines

ACCESSION

BH850686

VERSION

BH850686.1 GI:21421557

KEYWORDS

GSS.

SOURCE

thale cress.

ORGANISM

Arabidopsis thaliana

REFERENCE

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS

1 (bases 1 to 33)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J., and Ecker, J.R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL

Unpublished (2001)
Contact: Joseph R. Ecker

COMMENT

Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

SOURCE

1..33
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_071692.32.90.x"

/clone.lib="Arabidopsis thaliana TDNA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tDNA_protocol.html"

BASE COUNT 5 a 16 c 1 g 11 t
 ORIGIN
 Query Match 55.0%; Score 11; DB 17; Length 33;
 Best Local Similarity 100.0%; Pred. No. 6.6e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCT 13
 Db 19 TTCTCTTCT 29

RESULT 6
 LOCUS A2392980 37 bp. DNA linear GSS 03-OCT-2000
 DEFINITION 1M0155P13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 accession A2392980
 version A2392980
 keywords A2392980.1 GI:10508052
 source GSS.
 organism house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 37)
 Authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0155 row: P column: 13
 Seq primer: CACGACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 37.
 Location/Qualifiers

FEATURES

source

1. 37
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0155P13"
 /clone.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: FMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 15 a 0 c 22 g 0 t
 ORIGIN
 Query Match 55.0%; Score 11; DB 17; Length 37;
 Best Local Similarity 100.0%; Pred. No. 6.7e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCT 13
 Db 16 TTCTCTTCT 6

RESULT 7
 LOCUS A2627381 40 bp. DNA linear GSS 13-DEC-2000
 DEFINITION 1M0469H09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 accession A2627381
 version A2627381
 keywords A2627381.1 GI:11749571
 source GSS.
 organism house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 40)
 Authors Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 unpublished (2000)

JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0469 row: H column: 09
 Seq primer: CGTGTAAACGACGCGCAT
 Class: plasmid ends
 High quality sequence stop: 40.
 Location/Qualifiers

FEATURES

source

1. 40
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0469H09"
 /clone.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: FMD42ny; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 11 c 6 g 20 t

Query Match 55.0%; Score 11; DB 17; Length 45;
Best Local Similarity 100.0%; Pred. No. 6.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTG 14
|||||
18 TCCTCTCTCTG 28

RESULT 10
LOCUS B1488502 46 bp mRNA linear EST 28-AUG-2001
DEFINITION 603021011F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191659 5',
mRNA sequence.
ACCESSION B1488502
VERSION B1488502.1 GI:15327730
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 46)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M1479 row: e column: 04
High quality sequence strip: 46.
Location/Qualifiers

FEATURES
source 1..46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5191659"
/clone_1ib="NIH_MGC_114"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: BcoRI (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (BcoRI site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

BASE COUNT 9 a 8 c 25 g 4 t

Query Match 55.0%; Score 11; DB 13; Length 46;
Best Local Similarity 100.0%; Pred. No. 6.9e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12
|||||
12 GTTCTCTTCC 2

RESULT 11
LOCUS AU102629 50 bp mRNA linear EST 30-AUG-2001
DEFINITION AU102629 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
CAS04232, mRNA sequence.
ACCESSION AU102629
VERSION AU102629.1 GI:13552150
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, Y., Hara, H., Oka, T., Isegai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers

FEATURES
source 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS04232"
/clone_1ib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylsulfoxide treated U937 cells"
Location/Qualifiers

BASE COUNT 13 a 10 c 18 g 9 t

Query Match 55.0%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTG 14
|||||
19 TCCTCTCTCTG 9

RESULT 12
LOCUS B1685073 50 bp mRNA linear EST 18-SEP-2001
DEFINITION 60310058F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345950 5',
mRNA sequence.
ACCESSION B1685073
VERSION B1685073.1 GI:15647701
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 50)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov
Plate: L1AM11879 row: c column: 15
High quality sequence stop: 50.
Location/Qualifiers

FEATURES

source

1. 50
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345990"
/clone_lib="NCI CGAP Mam6"
/sex="Female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 3 a 20 c 17 g 10 t
ORIGIN

Query Match 55.0%; Score 11; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TCCTGCGGCT 20
Db 6 TCCTGCGGCT 16

RESULT 13

AZ630179

LOCUS

1M0483B10R Mouse 10kb plasmid UGCG1M library Mus musculus genomic

clone UGCG1M0483B10 R, DNA sequence.

AZ630179.1 GI:11752369

VERSION

GSS.

KEYWORDS

house mouse.

SOURCE

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 27)

REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamll, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.

and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0483 row: B column: 10

Seq primer: CACACAGCAACAGCTATGAC

Class: plasmid ends

High quality sequence stop: 27.

Location/Qualifiers

1. 27

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UGCG1M0483B10"

/clone_lib="Mouse 10kb plasmid UGCG1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (g14732114[GB|AF129072.1]), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 9 t
ORIGIN

Query Match 50.0%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTTCC 12
Db 4 TTCCCTTCC 13

RESULT 14

N92455

LOCUS

28 bp mRNA linear EST 20-AUG-1996

263301.81 Soares fetal_lung_NbHL19w Homo sapiens cDNA clone

IMAGE:308305 3, similar to gb:X06322.cdsl MITOCHONDRIAL 605

RIBOSOMAL PROTEIN L3 (HUMAN); mRNA sequence.

VERSION

N92455

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

1 (bases 1 to 28)

REFERENCE

Hillier, L., Lennon, G., Becker, M., Bonaldi, M.F., Chippelli, B.,

Chissee, S., Dietrich, N., Dubque, T., Favello, A., Gish, W., Hawkins

M., Hultman, M., Kucada, T., Lacy, M., Le, M., De, N., Mardis, E., Moore

B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevisan, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

Contact: Wilson RK

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.wustl.edu

This clone is available royalty-free through LINT; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 866 Std Error: 0.00

Seq primer: mob.RBGA+RT

High quality sequence stop: 1.

Location/Qualifiers

1. 28

/organism="Homo sapiens"

/db_xref="GDB:1251718"

/db_xref="taxon:9606"

/clone="IMAGE:308305"

/clone_lib="Soares fetal_lung_NbHL19w"

/dev_stage="19 weeks"

/lab-host="DH10B (ampicillin resistant)"
 /note="Organ: lung; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer
 [5'-TGTACCAATCTGAAGGAGCGCGCAATTTTCTTTTCTTTT-3'],
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Bento
 Soares and M. Fatima Bonaldi. This library was constructed
 from the same fetus as the fetal heart library, Soares
 fetal heart NBH119W."

BASE COUNT

7 a 9 c 4 g 8 t

BASE COUNT

5 a 11 c 7 g 6 t

Query Match 50.0%; Score 10; DB 14; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 50.0%; Score 10; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCCTCTTC 11
 |||||
 3 GTTCCTCTTC 12

OY 11 CCTGCGGCGCT 20
 |||||
 27 CCTGCGGCGCT 18

RESULT 15

A2794049/c

29 bp DNA linear GSS 16-FEB-2001

LOCUS

DEFINITION

2M0047H08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

A2794049

UUGC2M0047H08 R, DNA sequence.

VERSION

A2794049.1

GI:12939621

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus.

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A.
 and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000

Std Error: 0.00

Seq primer: CACACGAGAAACACCTATGACC

Class: plasmid ends

High quality sequence step: 29.

Location/Qualifiers

1..29

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC2M0047H08"

/clone_11b="Mouse 10kb plasmid UUGC1M library"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA

Search completed: June 23, 2003, 10:10:15
 Job time : 1032.31 secs

was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI4732114[GB|AF129072.1]), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20
Sequence: 1 CGTTCCTCTCTGCGGCTT 20

Scoring table:
OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending Patents_NA_New:*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq2:*
7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq3:*
8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2:*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq3:*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq2:*
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14	70.0	19	1	PCT-US03-04088-26
C 2	14	70.0	19	1	PCT-US03-04088-290
C 3	13	65.0	20	6	US-09-905-688-11
C 4	13	65.0	20	9	US-10-310-188-14029
C 5	13	65.0	21	4	US-08-825-746-11
C 6	13	65.0	25	7	US-09-954-454-45573
C 7	13	65.0	25	9	US-10-355-577-198249
C 8	13	65.0	25	9	US-10-355-577-223567
C 9	13	65.0	25	9	US-10-355-577-498091
C 10	13	65.0	25	12	US-60-417-190-13946
C 11	13	65.0	25	12	US-60-417-190-13947
C 12	13	65.0	25	12	US-60-417-190-48932
C 13	13	65.0	25	12	US-60-417-190-48933
C 14	13	65.0	25	12	US-60-417-190-48939
C 15	13	65.0	25	12	US-60-417-190-48940
C 16	13	65.0	25	12	US-60-427-808-172999
C 17	13	65.0	25	12	US-60-427-808-218754
C 18	13	65.0	25	12	US-60-427-808-275929
C 19	13	65.0	25	12	US-60-427-808-469548
C 20	13	65.0	25	12	US-60-427-808-564830

C 21	13	65.0	25	12	US-60-427-836-440978	Sequence 440978,
C 22	13	65.0	25	12	US-60-427-836-549003	Sequence 549003,
C 23	13	65.0	25	12	US-60-427-836-599225	Sequence 599225,
C 24	13	65.0	25	12	US-60-427-836-683575	Sequence 683575,
C 25	13	65.0	25	13	US-60-470-475-51737	Sequence 51737, A
C 26	13	65.0	25	13	US-60-470-475-51738	Sequence 51738, A
C 27	13	65.0	25	13	US-60-470-475-55703	Sequence 55703, A
C 28	13	65.0	25	13	US-60-470-475-57853	Sequence 57853, A
C 29	13	65.0	25	13	US-60-470-475-61267	Sequence 61267, A
C 30	13	65.0	25	13	US-60-470-475-61272	Sequence 61272, A
C 31	13	65.0	25	13	US-60-470-475-73706	Sequence 73706, A
C 32	13	65.0	25	13	US-60-470-475-98981	Sequence 98981, A
C 33	13	65.0	25	9	US-10-294-719-499	Sequence 499, App
C 34	13	65.0	50	5	US-09-749-8808-7801	Sequence 7801, Ap
C 35	13	65.0	50	9	US-10-325-899-3869	Sequence 3869, Ap
C 36	12	60.0	20	9	US-10-103-778-15311	Sequence 15311, A
C 37	12	60.0	20	9	US-10-310-188-28440	Sequence 28440, A
C 38	12	60.0	20	10	US-10-289-762-3651	Sequence 3651, Ap
C 39	12	60.0	25	7	US-09-953-570-13178	Sequence 13178,
C 40	12	60.0	25	7	US-09-954-445A-7403	Sequence 7403, Ap
C 41	12	60.0	25	7	US-09-954-445A-13116	Sequence 13116, A
C 42	12	60.0	25	7	US-09-954-445A-21805	Sequence 21805, A
C 43	12	60.0	25	9	US-10-098-263B-49318	Sequence 49318, A
C 44	12	60.0	25	9	US-10-098-263B-114611	Sequence 114611,
C 45	12	60.0	25	9	US-10-355-577-80134	Sequence 80134, A

ALIGNMENTS

RESULT 1
PCT-US03-04088-26/c
Sequence 26, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-26

Query Match 70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 TCTTCTCGGCGCT 20
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 Db 19 TCTTCTCGGCGCT 6

RESULT 2
 PCT-US03-04088-290
 ; Sequence 290, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwigen, James
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; PRIOR FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 290
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense
 PCT-US03-04088-290

Query Match 70.0%; Score 14; DB 1; Length 19;
 Best Local Similarity 64.3%; Pred. No. 1.7e+03;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 7 TCTTCTCGGCGCT 20
 |||||
 Db 1 UCUUCUGCGGCTU 14

RESULT 3
 US-09-905-688-11
 ; Sequence 11, Application US/09905688
 ; GENERAL INFORMATION:
 ; APPLICANT: CERNIAK, BOGDAN
 ; TITLE OF INVENTION: METHODS OF DETECTING AND DIAGNOSING BLADDER CANCER AND
 ; FILE REFERENCE: UTSC:663US
 ; CURRENT APPLICATION NUMBER: US/09/905,688
 ; CURRENT FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Primer
 US-09-905-688-11

Query Match 65.0%; Score 13; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTCTGC 15
 |||||
 Db 1 TTCTCTTCTCTGC 13

RESULT 4
 US-10-310-188-34029/c
 ; Sequence 34029, Application US/10310188
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosetadonics
 ; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN
 ; FILE REFERENCE: 47487
 ; CURRENT APPLICATION NUMBER: US/10/310,188
 ; CURRENT FILING DATE: 2002-12-15
 ; NUMBER OF SEQ ID NOS: 86841
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 34029
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-310-188-34029

Query Match 65.0%; Score 13; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTCTGC 15
 |||||
 Db 19 TTCTCTTCTCTGC 7

RESULT 5
 US-08-825-746-11
 ; Sequence 11, Application US/08825746
 ; GENERAL INFORMATION:
 ; APPLICANT: Vogelstein, Bert
 ; APPLICANT: Baker, Suzanne
 ; APPLICANT: Pearson, Eric
 ; TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function
 ; FILE REFERENCE: 001107.05677
 ; CURRENT APPLICATION NUMBER: US/08/825,746
 ; CURRENT FILING DATE: 1997-04-03
 ; PRIOR APPLICATION NUMBER: 08/035,366
 ; PRIOR FILING DATE: 1993-03-22
 ; PRIOR APPLICATION NUMBER: 07/860,758
 ; PRIOR FILING DATE: 1992-03-21
 ; PRIOR APPLICATION NUMBER: 07/715,182
 ; PRIOR FILING DATE: 1991-06-14
 ; PRIOR APPLICATION NUMBER: 07/928,661
 ; PRIOR FILING DATE: 1992-08-17
 ; PRIOR APPLICATION NUMBER: 07/446,584
 ; PRIOR FILING DATE: 1989-12-06
 ; PRIOR APPLICATION NUMBER: 07/350,566
 ; PRIOR FILING DATE: 1989-03-29
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-08-825-746-11

Query Match 65.0%; Score 13; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTGTC 15
 |||||
 1 TTCTCTTCTGTC 13

RESULT 6
 US-09-954-445A-45573/c

```
; Sequence 45573, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954, 445A
; CURRENT FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233, 620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-45573
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Query Match 65.0%; Score 13; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTTCTCTTCTCT 13
 |||||
 15 GTTCTCTTCTCT 3

RESULT 7
 US-10-355-577-198249

```
; Sequence 198249, Application US/103555577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355, 577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 198249
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-198249
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Query Match 65.0%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCTCTTCTG 14
 |||||
 9 GTTCTCTTCTG 21

RESULT 8
 US-10-355-577-223567/c

```
; Sequence 223567, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355, 577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 223567
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Homo sapien
 US-10-355-577-223567

Query Match 65.0%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CCTCTCTGCGG 17
 |||||
 25 CCTCTCTGCGG 13

RESULT 9
 US-10-355-577-498091

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; Sequence 498091, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355, 577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 498091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-498091
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Query Match 65.0%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCTCTTCTG 14
 |||||
 3 GTTCTCTTCTG 15

RESULT 10
 US-60-417-190-13946

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; Sequence 13946, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417, 190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-13946
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Query Match 65.0%; Score 13; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TTCTCTTCTGCG 16
 |||||
 2 TTCTCTTCTGCG 14

RESULT 11
 US-60-417-190-13947

```
; Sequence 13947, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
```

```
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 13947
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-13947
```

```
Query Match
Best Local Similarity 100.0%; Score 13; DB 12; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 TTCCTTCTCTGCG 16
    |||
Db 1 TCCCTTCTCTGCG 13
```

```
RESULT 12
US-60-417-190-48932
/ Sequence 48932, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48932
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48932
```

```
Query Match
Best Local Similarity 100.0%; Score 13; DB 12; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 TTCCTTCTCTGCG 15
    |||
Db 13 TTCCTTCTCTGCG 25
```

```
RESULT 13
US-60-417-190-48933
/ Sequence 48933, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48933
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48933
```

```
Query Match
Best Local Similarity 100.0%; Score 13; DB 12; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 TTCCTTCTCTGCG 15
```

```
Db 12 TTCCTTCTCTGCG 24
    |||
```

```
RESULT 14
US-60-417-190-48939
/ Sequence 48939, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48939
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48939
```

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 3 TTCCTTCTCTGCG 15
    |||
Db 13 TTCCTTCTCTGCG 25
```

```
RESULT 15
US-60-417-190-48940
/ Sequence 48940, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Giulia Kennedy
/ APPLICANT: Hajime Matsuzaki
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ CURRENT FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 48940
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-48940
```

```
Query Match
Best Local Similarity 100.0%; Score 13; DB 12; Length 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||
Db 12 TTCCTTCTCTGCG 24
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Job time : 877.926 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-3

Perfect score: 20
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Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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2	20	100.0	20	1 US-08-770-564A-3	Sequence 3, Appli
3	20	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appli
4	20	100.0	30	1 US-08-770-564A-2	Sequence 2, Appli
5	20	100.0	31	9 US-08-521-634-17	Sequence 17, Appli
6	20	100.0	31	17 US-09-396-1966-119937	Sequence 119937,
7	20	100.0	25	17 US-09-396-1966-119937	Sequence 119937,
8	20	100.0	25	36 US-09-356-584-18655	Sequence 18655, A
9	20	100.0	25	67 US-60-234-017-52883	Sequence 52883, A
10	20	100.0	29	13 US-08-913-665-14	Sequence 14, Appli
11	20	100.0	20	1 PCT-US01-47856-3869	Sequence 11, Appli
12	20	100.0	20	41 US-10-167-241-11	Sequence 11, Appli
13	20	100.0	21	41 US-10-157-058-11	Sequence 11, Appli
14	20	100.0	25	67 US-60-233-620-45573	Sequence 45573, A
15	20	100.0	25	79 US-60-353-987-198249	Sequence 198249,
16	20	100.0	25	79 US-60-353-987-198249	Sequence 223567,
17	20	100.0	25	79 US-60-353-987-198249	Sequence 498091,
18	20	100.0	31	18 US-09-454-623-15	Sequence 15, Appli
19	20	100.0	42	26 US-09-671-346-8	Sequence 8, Appli
20	20	100.0	45	26 US-09-671-346-9	Sequence 9, Appli
21	20	100.0	50	1 PCT-US01-47856-3869	Sequence 3869, Ap

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Fri Jun 27 07:42:23 2003

us-08-770-564a-3.oligo.rnp

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C. 22-13 65.0 50 40 US-10-131-827-3869
Sequence 3869, Ap
C 23-13 65.0 50 40 US-10-131-831-3869
Sequence 3869, Ap
C 24-12 60.0 12 11 PCT-US97-23619-4
Sequence 4, Appl
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Sequence 4, Appl
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Sequence 1021, Ap
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Sequence 1585, Ap
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Sequence 95195, A
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Sequence 22718, A
C 44-12 60.0 25 17 US-09-396-186G-34054
Sequence 34054, A
C 45-12 60.0 25 17 US-09-396-186G-95194
Sequence 95194, A

ALIGNMENTS

RESULT 1
PCT-US97-23619-3
Sequence 3, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "oligo 14ab"
PCT-US97-23619-3
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTTCTCTTCTCGGCGCT 20
Db 1 CGTTCTCTTCTCGGCGCT 20

RESULT 2
US-08-770-564A-3
Sequence 3, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
AGAINST THE RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGTTCTCTTCTCGGCGCT 20
Db 1 CGTTCTCTTCTCGGCGCT 20

RESULT 3
PCT-US97-23619-2

Sequence 2, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 14"
PCT-US97-23619-2

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCGGCGCT 20

RESULT 4
US-08-770-564A-2
Sequence 2, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-2

Query Match 100.0%; Score 20; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGCGCT 20
DB 1 CGTTCCTCTCTCGGCGCT 20

RESULT 5
US-08-521-634-17/c
Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 7-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dunn, Tracy J.
/ REGISTRATION NUMBER: 34,587
/ REFERENCE/DOCKET NUMBER: 15389-000850
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-17

Query Match          100.0%; Score 20; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCTCGGCGCT 20
DB 31 CGTTCCTCTTCCTCGGCGCT 12

RESULT 6
US-09-396-196F-119937/C
/ Sequence 119937, Application US/09396196F
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196F
/ PRIOR FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 60/100,678
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 119937
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196F-119937

Query Match          70.0%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGC 15
DB 25 GTTCTCTTCTCTGC 12

RESULT 7
US-09-396-196G-119937/C
/ Sequence 119937, Application US/09396196G
/ GENERAL INFORMATION:
/ APPLICANT: Michael Miltmann
/ APPLICANT: David Mack
/ APPLICANT: David Lockhart
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis
/ FILE REFERENCE: 3101.1
/ CURRENT APPLICATION NUMBER: US/09/396,196G
/ CURRENT FILING DATE: 1999-09-15
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/ PRIOR APPLICATION NUMBER: 60/100,678
/ PRIOR FILING DATE: 1998-09-17
/ NUMBER OF SEQ ID NOS: 127806
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 119937
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-396-196G-119937

Query Match          70.0%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGC 15
DB 25 GTTCTCTTCTCTGC 12

RESULT 8
US-09-956-584-18655/C
/ Sequence 18655, Application US/09956584
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
/ FILE REFERENCE: 3115.1
/ CURRENT APPLICATION NUMBER: US/09/956,584
/ PRIOR FILING DATE: 2001-09-19
/ PRIOR APPLICATION NUMBER: 60/234,017
/ NUMBER OF SEQ ID NOS: 605887
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 18655
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: mus musculus
US-09-956-584-18655

Query Match          70.0%; Score 14; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTG 14
DB 18 CGTTCCTTCTCTG 5

RESULT 9
US-60-234-017-52883/C
/ Sequence 52883, Application US/60234017
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, M
/ APPLICANT: Affymetrix, Inc.
/ TITLE OF INVENTION: Methods of Genetic Analysis of Mus
/ FILE REFERENCE: 3115
/ CURRENT APPLICATION NUMBER: US/60/234,017
/ PRIOR FILING DATE: 2000-09-20
/ NUMBER OF SEQ ID NOS: 605887
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52883
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Mus musculus
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: GenBank U41285
US-60-234-017-52883

Query Match          70.0%; Score 14; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTCTG 14
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Db 18 CGTCTCTCTCTG 5

RESULT 10

US-08-913-665-14/C
Sequence 14, Application US/08913665
GENERAL INFORMATION:
APPLICANT: Saiga, Atsuhiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/913,665
APPLICATION NUMBER: US/08/913,665
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHN-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-913-665-14
Query Match 70.0%; Score 14; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 CTCTTCTGCGGC 19
Db 19 CTCTTCTGCGGC 6

RESULT 11

PCT-US02-18427-11
Sequence 11, Application PC/TUS0218427
GENERAL INFORMATION:
APPLICANT: CZERNIAK, BOGDAN
APPLICANT: JOHNSTON, DENNIS
TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER
TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION
FILE REFERENCE: UFGC:712-WO
CURRENT APPLICATION NUMBER: PCT/US02/18427
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 60/297,813
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
PCT-US02-18427-11

Query Match 65.0%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTGCGC 15
Db 1 TTCTCTTCTGCGC 13

RESULT 12

US-10-167-241-11
Sequence 11, Application US/10167241
GENERAL INFORMATION:
APPLICANT: CZERNIAK, BOGDAN
APPLICANT: JOHNSTON, DENNIS
TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER
TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION
FILE REFERENCE: UFGC:712US
CURRENT APPLICATION NUMBER: US/10/167,241
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 60/297,813
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Primer
US-10-167-241-11

Query Match 65.0%; Score 13; DB 41; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTGCGC 15
Db 1 TTCTCTTCTGCGC 13

RESULT 13

US-10-157-058-11
Sequence 11, Application US/10157058
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function
FILE REFERENCE: 001107.00257
CURRENT APPLICATION NUMBER: US/10/157,058
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 08/825,746
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/035,366
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/928,661
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/860,758
PRIOR FILING DATE: 1992-03-31
PRIOR APPLICATION NUMBER: 07/715,182
PRIOR FILING DATE: 1991-06-14

PRIOR APPLICATION NUMBER: 07/446,584
 PRIOR FILING DATE: 1989-12-06
 PRIOR APPLICATION NUMBER: 07/330,566
 PRIOR FILING DATE: 1989-03-29
 NUMBER OF SEQ ID NOS: 17
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 11
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-157-058-11

Query Match 65.0%; Score 13; DB 41; Length 21;
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCTG 15
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 1 TTCTCTTCTG 13

RESULT 14
 US-60-233-620-45573/C
 Sequence 45573, Application US/60233620
 GENERAL INFORMATION:
 APPLICANT: Altmeyer, Inc.
 TITLE OF INVENTION: Methods of Genetic Analysis of
 FILE REFERENCE: 3116
 CURRENT APPLICATION NUMBER: US/60/233,620
 CURRENT FILING DATE: 2000-10-24
 NUMBER OF SEQ ID NOS: 131820
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 45573
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: GenBank AL034567
 US-60-233-620-45573

Query Match 65.0%; Score 13; DB 67; Length 25;
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCT 13
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 15 CGTCTCTTCT 3

RESULT 15
 US-60-353-987-198249
 Sequence 198249, Application US/60353987
 GENERAL INFORMATION:
 APPLICANT: Hiltmann, Michael
 TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U13
 FILE REFERENCE: 3121
 CURRENT APPLICATION NUMBER: US/60/353,987
 CURRENT FILING DATE: 2002-02-01
 NUMBER OF SEQ ID NOS: 997516
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 198249
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-60-353-987-198249

Query Match 65.0%; Score 13; DB 79; Length 25;
 Best Local Similarity 100.0%; Pred.No. 2.1e+04;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTTCTG 14

Db 9 GTTCCTTCTG 21
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 Job time: 1678.53 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 / Search time 160.717 Seconds
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182.610 Million cell updates/sec

Title: US-08-770-564A-3

Perfect score: 20
Sequence: 1 CGTTCCTTCTCTGCGGCT 20

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Gapop 60.0, Gapext 60.0

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Word size: 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Published Applications NA:*

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- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	20	US-10-139-496-25	Sequence 25, Appl
C 2	12	60.0	25	US-09-754-853A-686	Sequence 686, Ap
C 3	12	60.0	25	US-10-098-263B-49318	Sequence 49318, A
C 4	12	60.0	25	US-10-098-263B-114611	Sequence 114611, A
C 5	11	55.0	12	US-09-938-744-2	Sequence 2, Appl
C 6	11	55.0	19	US-09-969-373-1923	Sequence 1923, Ap
C 7	11	55.0	19	US-09-879-389B-4	Sequence 4, Appl
C 8	11	55.0	19	US-09-902-563-38	Sequence 38, Appl
C 9	11	55.0	19	US-09-902-563-41	Sequence 41, Appl
C 10	11	55.0	19	US-10-096-255-38	Sequence 38, Appl
C 11	11	55.0	19	US-10-096-255-41	Sequence 41, Appl
C 12	11	55.0	19	US-09-947-770-26	Sequence 26, Appl
C 13	11	55.0	20	US-09-919-197-23	Sequence 23, Appl
C 14	11	55.0	24	US-10-101-487-12	Sequence 12, Appl
C 15	11	55.0	24	US-10-101-487-13	Sequence 13, Appl
C 16	11	55.0	24	US-09-818-954A-4	Sequence 4, Appl
C 17	11	55.0	25	US-09-943-388-16	Sequence 16, Appl
C 18	11	55.0	25	US-09-990-940-48	Sequence 48, Appl
C 19	11	55.0	25	US-10-215-112-2042	Sequence 2042, Ap

20	11	55.0	25	9	US-10-215-112-10695	Sequence 10695, A
C 21	11	55.0	25	9	US-10-215-112-12736	Sequence 12736, A
C 22	11	55.0	25	9	US-10-098-263B-9249	Sequence 9249, Ap
C 23	11	55.0	25	9	US-10-098-263B-17568	Sequence 17568, A
C 24	11	55.0	25	9	US-10-098-263B-24096	Sequence 24096, A
C 25	11	55.0	25	9	US-10-098-263B-48043	Sequence 48043, A
C 26	11	55.0	25	9	US-10-098-263B-48044	Sequence 48044, A
C 27	11	55.0	25	9	US-10-098-263B-48100	Sequence 48100, A
C 28	11	55.0	25	9	US-10-098-263B-50057	Sequence 50057, A
C 29	11	55.0	25	9	US-10-098-263B-50058	Sequence 50058, A
C 30	11	55.0	25	9	US-10-098-263B-56723	Sequence 56723, A
C 31	11	55.0	25	9	US-10-098-263B-56724	Sequence 56724, A
C 32	11	55.0	25	9	US-10-098-263B-67054	Sequence 67054, A
C 33	11	55.0	25	9	US-10-098-263B-81647	Sequence 81647, A
C 34	11	55.0	25	9	US-10-098-263B-81648	Sequence 81648, A
C 35	11	55.0	25	9	US-10-098-263B-96226	Sequence 96226, A
C 36	11	55.0	27	10	US-09-898-541-26	Sequence 26, Appl
C 37	11	55.0	29	9	US-10-210-327A-9	Sequence 9, Appl
C 38	11	55.0	37	12	US-10-014-927-14	Sequence 14, Appl
C 39	11	55.0	38	9	US-09-930-423-3068	Sequence 3068, Ap
C 40	11	55.0	38	9	US-10-104-943-86	Sequence 86, Appl
C 41	11	55.0	45	9	US-09-938-744-1	Sequence 1, Appl
C 42	11	55.0	45	9	US-10-013-803A-10	Sequence 10, Appl
C 43	11	55.0	45	10	US-09-482-520-2	Sequence 2, Appl
C 44	11	55.0	45	10	US-09-773-882-8	Sequence 8, Appl
C 45	11	55.0	46	9	US-10-085-108-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-139-496-25/C
Sequence 25, Application US/10139496
Publication No. US2003082646A1
GENERAL INFORMATION:
APPLICANT: Carey, Thomas E.
APPLICANT: Gray, Jennifer P.
TITLE OF INVENTION: Anticancer Targets of Autoimmune Sensorineural Hearing Loss (AISHL)
FILE REFERENCE: UM-6982
CURRENT FILING DATE: 2002-09-10
PRIORITY FILING DATE: 1998-12-29
PRIORITY APPLICATION NUMBER: 09/222,179
PRIORITY FILING DATE: 1998-12-29
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-139-496-25

Query Match 60.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 17 TTCTCTTCTCTG 6

RESULT 2
US-09-754-853A-686/C
Sequence 686, Application US/09754853A
Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.

```

; APPLICANT: Wang, Ming Li
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-10(15810)B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/114,880
; NUMBER OF SEQ ID NOS: 1119
; SEQ ID NO 686
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 318013_region_A3_151839_17_Reverse_Primer_Seq
US-09-754-853A-686

Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTCTCTG 14
DB 12 TTCTCTCTCTG 1

RESULT 3
US-10-098-263B-49318/c
; Sequence 49318, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 49318
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-49318

Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCTCTCTGCGG 17
DB 14 CTCTCTCTGCGG 3

RESULT 4
US-10-098-263B-114611
; Sequence 114611, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-10-098-263B-114611
Query Match          60.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTCT 13
DB 6 GTTCCCTTCTCT 17

RESULT 5
US-09-938-744-2/c
; Sequence 2, Application US/09938744
; Patent No. US20020172954A1
; GENERAL INFORMATION:
; APPLICANT: Mao, Yumin
; APPLICANT: Xie, Yi
; TITLE OF INVENTION: METHOD FOR LARGE SCALE CDNA CLONING AND
; FILE REFERENCE: A34606-PCT-USA-A 072975.0111
; CURRENT APPLICATION NUMBER: US/09/938,744
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/CN00/00036
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: CN 99102450.8
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-938-744-2

Query Match          55.0%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TTCTCTGCGGCC 19
DB 11 TTCTCTGCGGCC 1

RESULT 6
US-09-969-373-1923/c
; Sequence 1923, Application US/09969373
; Patent No. US20020135852A1
; GENERAL INFORMATION:
; APPLICANT: Eifert, Roger J.
; APPLICANT: Haug, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1923
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1923

Query Match          55.0%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 CCTCTCTCTGC 15
| | | | |
Db 14 CCTCTCTCTGC 4

RESULT 7
US-09-879-389B-4/c
; Sequence 4, Application US/09879389B
; Publication No. US20030032165A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030032165A1ocymee A/S
; APPLICANT: Wu, Wenzheng
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Kauppinen, Markus Sakari
; TITLE OF INVENTION: ASPARTIC ACID PROTEASES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 6123.200-US
; CURRENT APPLICATION NUMBER: US/09/879,389B
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-879-389B-4

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 TTCTCGCGGCC 19
| | | | |
Db 11 TTCTCGCGGCC 1

RESULT 8
US-09-902-563-38/c
; Sequence 38, Application US/09902563
; Publication No. US2003009654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-902-563-38

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCTG 14
| | | | |
Db 17 TCCTCTTCTCTG 7

RESULT 9
US-09-902-563-41
; Sequence 41, Application US/09902563
; Publication No. US2003009654A1

; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-902-563-41

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCTG 14
| | | | |
Db 8 TCCTCTTCTCTG 18

RESULT 10
US-10-096-255-38/c
; Sequence 38, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537
; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-096-255-38

Query Match 55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCTG 14
| | | | |
Db 17 TCCTCTTCTCTG 7

RESULT 11
US-10-096-255-41
; Sequence 41, Application US/10096255
; Publication No. US20030103974A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; APPLICANT: Clark, David A.
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-52
; CURRENT APPLICATION NUMBER: US/10/096,255
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/046,537

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; PRIOR FILING DATE: 1997-05-17
; PRIOR APPLICATION NUMBER: US 60/061,684
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-10-036-255-41

Query Match          55.0%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 TCCTCTTCTG 14
         |||||
Db      8 TCCTCTTCTG 18

RESULT 12
; US-09-947-770-26
; Sequence 26, Application US/09947770
; Patent No. US20020068715A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Ruiz, Pedro
; TITLE OF INVENTION: DNA Vaccination for Treatment of
; FILE REFERENCE: SPAN123CIP
; CURRENT APPLICATION NUMBER: US/09/947,770
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/06233
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/267,590
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IFN-gamma primer
; US-09-947-770-26

Query Match          55.0%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 TCCTGCGGCT 20
         |||||
Db      1 TCCTGCGGCT 11

RESULT 13
; US-09-919-197-23/c
; Sequence 23, Application US/09919197
; Patent No. US20030083484A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF SHORT HETERODIMER PARTNER-1 EXPRESSION
; FILE REFERENCE: ISPH-0593
; CURRENT APPLICATION NUMBER: US/09/919,197
; PRIOR FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 20

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-919-197-23

Query Match          55.0%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 CCTCTTCTGC 15
         |||||
Db      20 CCTCTTCTGC 10

RESULT 14
; US-10-101-487-12/c
; Sequence 12, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUJIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: MAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-101-487-12

Query Match          55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 TTCCCTTCTCT 13
         |||||
Db      22 TTCCCTTCTCT 12

RESULT 15
; US-10-101-487-13
; Sequence 13, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUJIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: MAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-10-101-487-13

Query Match 55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCT 13
Db 7 TTCTCTTCT 17

Search completed: June 23, 2003, 20:01:28
Job time : 160.717 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds
(without alignments)
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Title: US-08-770-564A-3

Perfect score: 20
Sequence: 1 CGTTCCTCTCTCGCGCCT 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

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Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	2	US-08-770-565-3
2	20	100.0	20	2	US-08-833-377-7
3	20	100.0	20	2	US-08-770-565-2
4	19	95.0	20	2	US-08-833-377-14
5	14	70.0	29	3	US-09-121-321-14
6	14	70.0	29	4	US-08-933-803A-14
7	13	65.0	20	2	US-08-534-479-1
8	13	65.0	31	2	US-08-576-626A-15
9	13	65.0	42	1	US-08-487-037-8
10	13	65.0	45	1	US-08-487-037-9
11	12	60.0	12	2	US-08-770-565-4
12	12	60.0	20	1	US-08-031-143B-6
13	12	60.0	20	1	US-08-031-143B-3
14	12	60.0	20	5	PCT-US94-02891-6
15	12	60.0	20	5	PCT-US94-02891-33
16	12	60.0	33	4	US-08-090-369-15
17	12	60.0	33	4	US-09-482-971-15
18	11	55.0	11	1	US-08-126-594-5
19	11	55.0	11	1	US-08-465-811A-5
20	11	55.0	11	2	US-08-619-542B-5
21	11	55.0	11	2	US-08-619-542B-48
22	11	55.0	12	1	US-08-126-594-6
23	11	55.0	12	1	US-08-465-811A-6
24	11	55.0	12	2	US-08-619-542B-6
25	11	55.0	14	1	US-08-294-424-33
26	11	55.0	18	4	US-09-251-645-21
27	11	55.0	19	4	US-09-442-143A-38

28	11	55.0	19	4	US-09-442-143A-41	Sequence 41, Appli
29	11	55.0	20	1	US-08-068-945A-8	Sequence 8, Appli
30	11	55.0	20	1	US-08-442-806-8	Sequence 8, Appli
31	11	55.0	20	2	US-08-206-790A-18	Sequence 18, Appli
32	11	55.0	20	3	US-08-589-939-40	Sequence 40, Appli
33	11	55.0	20	4	US-09-258-377-30	Sequence 30, Appli
34	11	55.0	20	4	US-09-851-896-86	Sequence 86, Appli
35	11	55.0	20	5	PCT-US95-02943-18	Sequence 18, Appli
36	11	55.0	21	6	5177193-10	Patent No. 5177193
37	11	55.0	22	1	US-07-820-412-8	Sequence 8, Appli
38	11	55.0	22	1	US-08-611-155B-1	Sequence 1, Appli
39	11	55.0	22	1	US-08-611-155B-2	Sequence 2, Appli
40	11	55.0	22	1	US-08-611-155B-3	Sequence 3, Appli
41	11	55.0	22	1	US-08-611-155B-4	Sequence 4, Appli
42	11	55.0	22	1	US-08-611-155B-5	Sequence 5, Appli
43	11	55.0	22	1	US-08-611-155B-6	Sequence 6, Appli
44	11	55.0	22	2	US-08-916-120A-1	Sequence 1, Appli
45	11	55.0	22	2	US-08-916-120A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-770-565-3
Sequence 3, Application US/08770565
Patent No. 5846723

GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-3

Query Match 100.0%; Score 20; DB 2; Length 20;
Best local Similarity 100.0%; Pred. No. 0.061;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCTCGCGCCT 20

Db 1 CGTTCCTCTTCTCGGGCCT 20

RESULT 2
US-08-833-377-7
Sequence 7, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="Oligo 14ab"
US-08-833-377-7
Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTCCTCTTCTCGGGCCT 20
Db 1 CGTTCCTCTTCTCGGGCCT 20
RESULT 3
US-08-770-565-2
Sequence 2, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770.565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-2
Query Match 100.0%; Score 20; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.061; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 CGTTCCTCTTCTCGGGCCT 20
Db 1 CGTTCCTCTTCTCGGGCCT 20
RESULT 4
US-08-833-377-14
Sequence 14, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.377

FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note= "N = 5' biotinylated cytidine"
US-08-833-377-14

Query Match 95.0%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTCTCGCGCCT 20
Db 2 GTTCTCTCTCGCGCCT 20

RESULT 5
US-09-121-321-14/C
Sequence 14, Application US/09121321
Patent No. 6090783
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121.321
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/933,803
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.

REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-121-321-14

Query Match 70.0%; Score 14; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCTTCTCGCGCC 19
Db 19 CTCTTCTCGCGCC 6

RESULT 6
US-08-933-803A-14/C
Sequence 14, Application US/08933803A
Patent No. 6218522
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,803A
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-933-803A-14

Query Match 70.0%; Score 14; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Page 4

QY 6 CTCTCTCTCGGCC 19
DB 19 CTCTCTCTCGGCC 6

RESULT 7
US-08-534-479-1
Sequence 1, Application US/08534479

GENERAL INFORMATION:
APPLICANT: GREY, HEINZ-URICH G.
TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/534,479
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MACKNIGHT, KAREN T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: IBL-01754
TELEPHONE: (415) 978-8338
TELEFAX: (415) 705-8410
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-534-479-1

Query Match 65.0%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0

QY 3 TTCTCTCTCTGC 15
DB 1 TTCTCTCTCTGC 13

RESULT 8
US-08-576-626A-15/c
Sequence 15, Application US/08576626A

GENERAL INFORMATION:
APPLICANT: Sumner, R.G.
APPLICANT: Katz, L.
APPLICANT: Donadio, S.
APPLICANT: Scaver, W.J.
TITLE OF INVENTION: POLYMERIDE-ASSOCIATED SUGAR
TITLE OF INVENTION: BIOSYNTHESIS GENES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: Illinois

COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,626A
FILING DATE: 21 435
CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dittie Casulo
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 5857-US.01
TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-576-626A-15

Query Match 65.0%; Score 13; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0

QY 8 CTCTCTCTCGGCC 20
DB 19 CTCTCTCTCGGCC 7

RESULT 9
US-08-487-037-8/c
Sequence 8, Application US/08487037

GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FORSTER
STREET: 2000 Pennysylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/487,037
APPLICATION NUMBER: 1995
FILING DATE: 07-JUN-1995
CLASSIFICATION: 344
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Robert G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-037-8

Query Match 65.0%; Score 13; DB 1; Length 42;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCG 16
|||||
DB 22 TCCTCTCTCTGCG 10

RESULT 10
US-08-487-037-9/C
Sequence 9, Application US/08487037
Patent No. 5795863

GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487.037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-037-9

Query Match 65.0%; Score 13; DB 1; Length 45;
Best Local Similarity 100.0%; Pred.No. 1.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCG 16
|||||
DB 22 TCCTCTCTCTGCG 10

RESULT 11
US-08-770-565-4
Sequence 4, Application US/08770565
Patent No. 5846723

GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770.565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-4

Query Match 60.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred.No. 6.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCC 12
|||||
DB 1 CGTTCCTCTTCC 12

RESULT 12
US-08-031-143B-6/C
Sequence 6, Application US/08031143B
Patent No. 5518880

GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
APPLICANT: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031.143B
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER

REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-6

Query Match 60.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCT 13
|||
18 GTTCTCTTCTCT 7

Db

RESULT 13
US-08-031-143B-33
Sequence 33; Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
APPLICANT: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,143B
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-6

ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-33

Query Match 60.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCT 13
|||
3 GTTCTCTTCTCT 14

Db

RESULT 14
PCT-US94-02891-6/c
Sequence 6; Application PC/TUS9402891
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL
APPLICANT: INSTITUTES OF HEALTH, BOX 071, BETHESDA, MARYLAND 20892 USA
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: XSCID
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-6

Query Match 60.0%; Score 12; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 31.3147 secs

Qy 2 GTTCTCTTCT 13
|||
Db 18 GTTCTCTTCT 7

RESULT 15
PCT-US94-02891-33

; Sequence 33, Application PC/TUS9402891

; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

; APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN

; APPLICANT: SERVICES

; APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL

; APPLICANT: INSTITUTES OF HEALTH, BOX 077, BETHESDA, MARYLAND 20892 USA

; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: XSCID

; NUMBER OF SEQUENCES: 69

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN

; STREET: 345 PARK AVE.

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10154

; COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK

; COMPUTER: IBM PC COMPATIBLE

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORD PERFECT # 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/02891

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/031,143

; FILING DATE: 12-MAR-1993

; APPLICATION NUMBER: 08/121,435

; FILING DATE: 14-SEPT-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAM S. FEILER

; REGISTRATION NUMBER: 26,728

; REFERENCE/DOCKET NUMBER: 2026-4061

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; TELEX: 421792

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE:

; DESCRIPTION: OLIGONUCLEOTIDE

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: HUMAN

; INDIVIDUAL ISOLATE: IL-2R

; PCT-US94-02891-33

; Query Match

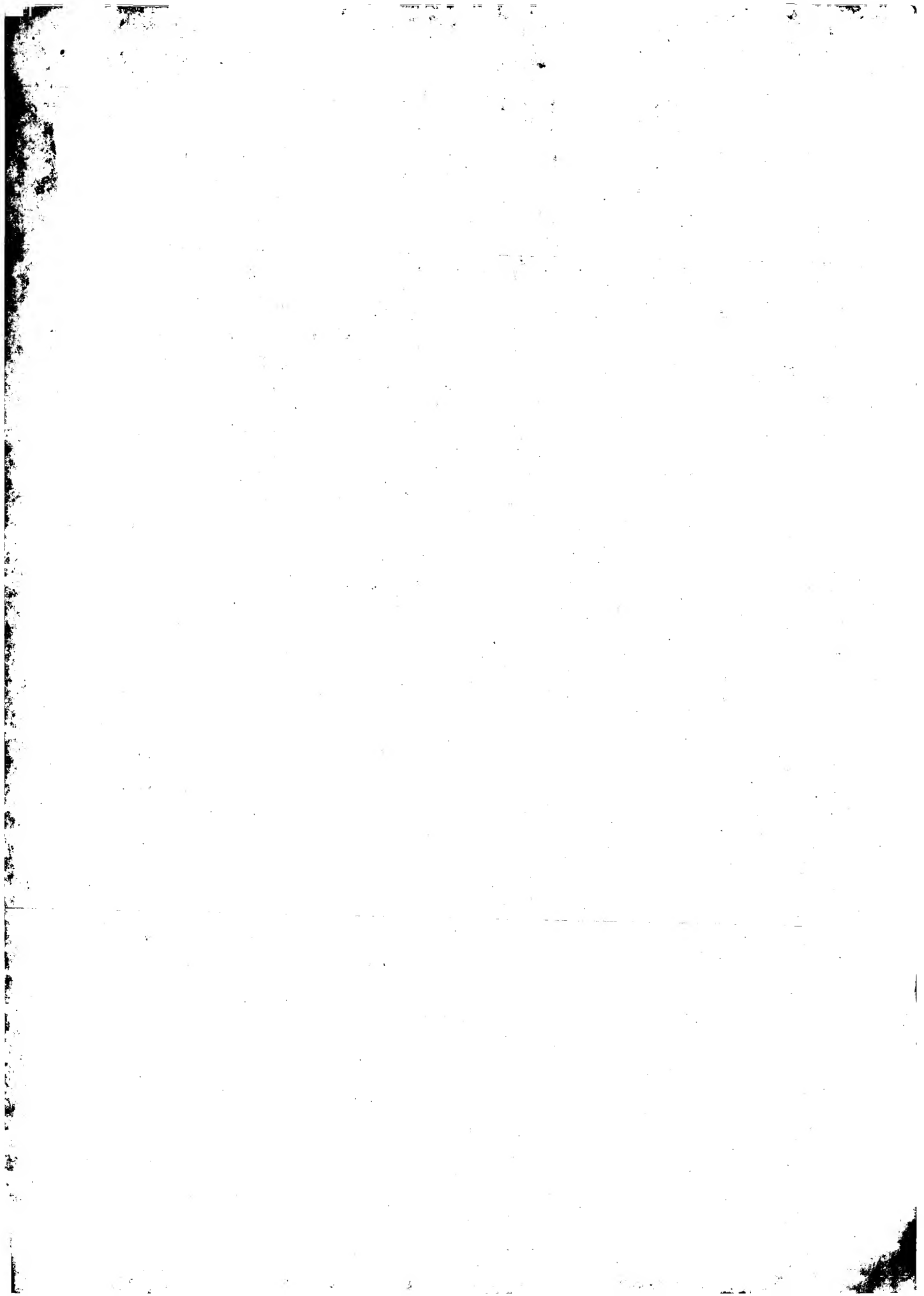
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; Matches 12; Conservative 100.0%; Pred.No. 5.9e+02;

; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCT 13
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Db 3 GTTCTCTTCT 14

Search completed: June 23, 2003, 10:17:03



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564a-3

Perfect score: 20
Sequence: 1 CGTTCCTCTCTCGCGCCT 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database : N.GeneSeq.101002.*

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23: /SIDS2/gcgdata/geneSeq/geneSeqn-emb1/NA2001B.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	19	AAV71226
2	20	100.0	20	19	AAV71226
3	20	100.0	20	19	AAV41170
4	20	100.0	20	20	AAZ23632
5	20	100.0	20	20	AAZ23636
6	20	100.0	20	22	AAZ09477
7	20	100.0	20	22	AAZ09480
8	20	100.0	30	19	AAV41169
9	14	70.0	29	17	AAZ42916
	13	65.0	21	17	AAZ36484

10	13	65.0	21	21	AAZ72585	Upstream PCR prime
11	13	65.0 <td>21</td> <td>22</td> <td>AAZ74842</td> <td>Human p53 PCR prim</td>	21	22	AAZ74842	Human p53 PCR prim
12	13	65.0 <td>21</td> <td>18</td> <td>AAZ72696</td> <td>Sugar biosynthesis</td>	21	18	AAZ72696	Sugar biosynthesis
13	13	65.0 <td>50</td> <td>22</td> <td>AAZ34593</td> <td>Human SNP oligonuc</td>	50	22	AAZ34593	Human SNP oligonuc
14	12	60.0 <td>12</td> <td>19</td> <td>AAV41171</td> <td>RNA component of h</td>	12	19	AAV41171	RNA component of h
15	12	60.0 <td>20</td> <td>15</td> <td>AAQ71941</td> <td>Human IL-2R gamma</td>	20	15	AAQ71941	Human IL-2R gamma
16	12	60.0 <td>20</td> <td>15</td> <td>AAQ71914</td> <td>Human IL-2R gamma</td>	20	15	AAQ71914	Human IL-2R gamma
17	12	60.0 <td>20</td> <td>19</td> <td>AAV45148</td> <td>Human saptiens P-TEN</td>	20	19	AAV45148	Human saptiens P-TEN
18	12	60.0 <td>20</td> <td>20</td> <td>AAZ94325</td> <td>PCR primer used to</td>	20	20	AAZ94325	PCR primer used to
19	12	60.0 <td>21</td> <td>22</td> <td>AAZ62356</td> <td>RBP2 polymorphism</td>	21	22	AAZ62356	RBP2 polymorphism
20	12	60.0 <td>24</td> <td>15</td> <td>AAQ57316</td> <td>Enzymatic RNA mole</td>	24	15	AAQ57316	Enzymatic RNA mole
21	12	60.0 <td>25</td> <td>22</td> <td>AAI62055</td> <td>Soybean 318013 reg</td>	25	22	AAI62055	Soybean 318013 reg
22	12	60.0 <td>27</td> <td>22</td> <td>AAZ87709</td> <td>Human glutathione</td>	27	22	AAZ87709	Human glutathione
23	12	60.0 <td>31</td> <td>21</td> <td>AAZ79024</td> <td>Human genomic DNA</td>	31	21	AAZ79024	Human genomic DNA
24	12	60.0 <td>33</td> <td>14</td> <td>AAQ49474</td> <td>Primer "a332" to a</td>	33	14	AAQ49474	Primer "a332" to a
25	12	60.0 <td>37</td> <td>24</td> <td>ABA01509</td> <td>EryCIII PCR primer</td>	37	24	ABA01509	EryCIII PCR primer
26	12	60.0 <td>40</td> <td>17</td> <td>AAZ70784</td> <td>Stenotic carotid a</td>	40	17	AAZ70784	Stenotic carotid a
27	12	60.0 <td>40</td> <td>17</td> <td>AAZ70788</td> <td>Stenotic carotid a</td>	40	17	AAZ70788	Stenotic carotid a
28	12	60.0 <td>40</td> <td>17</td> <td>AAZ70789</td> <td>Stenotic carotid a</td>	40	17	AAZ70789	Stenotic carotid a
29	11	55.0 <td>14</td> <td>13</td> <td>AAZ026598</td> <td>Predicted HPV-18 e</td>	14	13	AAZ026598	Predicted HPV-18 e
30	11	55.0 <td>15</td> <td>22</td> <td>AAZ04286</td> <td>ASO primer #2 for</td>	15	22	AAZ04286	ASO primer #2 for
31	11	55.0 <td>15</td> <td>22</td> <td>AAZ04288</td> <td>ASO primer #4 for</td>	15	22	AAZ04288	ASO primer #4 for
32	11	55.0 <td>19</td> <td>24</td> <td>AAZ27185</td> <td>Pseudozyma species</td>	19	24	AAZ27185	Pseudozyma species
33	11	55.0 <td>20</td> <td>15</td> <td>AAQ54225</td> <td>BSSL/CEL Exon 10/1</td>	20	15	AAQ54225	BSSL/CEL Exon 10/1
34	11	55.0 <td>20</td> <td>16</td> <td>AAQ91339</td> <td>DNA antisense prim</td>	20	16	AAQ91339	DNA antisense prim
35	11	55.0 <td>20</td> <td>20</td> <td>AAZ23347</td> <td>Bacillus amyloliqu</td>	20	20	AAZ23347	Bacillus amyloliqu
36	11	55.0 <td>20</td> <td>20</td> <td>AAZ95176</td> <td>PCR primer used to</td>	20	20	AAZ95176	PCR primer used to
37	11	55.0 <td>20</td> <td>21</td> <td>AAZ68884</td> <td>Dog genomic marker</td>	20	21	AAZ68884	Dog genomic marker
38	11	55.0 <td>20</td> <td>21</td> <td>AAZ07908</td> <td>He-UNC-53/2 specif</td>	20	21	AAZ07908	He-UNC-53/2 specif
39	11	55.0 <td>20</td> <td>21</td> <td>AAZ88913</td> <td>Human wolframin ex</td>	20	21	AAZ88913	Human wolframin ex
40	11	55.0 <td>20</td> <td>22</td> <td>AAZ09927</td> <td>Short consensus am</td>	20	22	AAZ09927	Short consensus am
41	11	55.0 <td>20</td> <td>22</td> <td>AAZ40301</td> <td>Human cathepsin 6 an</td>	20	22	AAZ40301	Human cathepsin 6 an
42	11	55.0 <td>20</td> <td>24</td> <td>ABA01570</td> <td>HLA class I micros</td>	20	24	ABA01570	HLA class I micros
43	11	55.0 <td>21</td> <td>21</td> <td>AAZ75837</td> <td>Human biallelic ma</td>	21	21	AAZ75837	Human biallelic ma
44	11	55.0 <td>21</td> <td>21</td> <td>AAZ76054</td> <td>Human biallelic ma</td>	21	21	AAZ76054	Human biallelic ma
45	11	55.0 <td>21</td> <td>21</td> <td>AAA11686</td> <td>Human GABA-B recep</td>	21	21	AAA11686	Human GABA-B recep

ALIGNMENTS

RESULT 1
AAV71226
ID AAV71226 standard; DNA; 20 BP.
AC AAV71226;
DT 15-FEB-1999 (first entry)
XX
DE Antisense oligonucleotide 14ab for human telomerase RNA component.
XX Human; telomerase RNA component; anticancer therapy; purification;
KW assay; vaccine; cancer; antisense oligonucleotide; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT FT /tag= a
FT FT /note= "biotinylated"
XX
PN W09845450-A1.
XX
PD 15-OCT-1998.
XX
PF 04-APR-1997; 97WO-US06012.
XX
PR 04-APR-1997; 97WO-US06012.
XX (GERO-) GERON CORP.
PA
XX Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;

PI Vassero AP, Weinrich SL,
 XX
 DR WPI; 1998-594485/50.
 XX
 PT Purification of telomerase on affinity material - useful for, e.g.
 PT diagnosis and treatment of cancer
 XX
 PS Claim 6; Page 61; 76pp; English.

XX The present sequence represents an antisense oligonucleotide
 CC directed against the human telomerase RNA component gene sequences.
 CC The oligonucleotide can be used as an affinity agent in the methods of
 CC the invention, which are used to purify human telomerase. The methods
 CC involve the use of several sequential steps, including the use of two
 CC matrices that bind molecules bearing negative charges, a matrix that
 CC binds molecules bearing positive charges, an affinity purification step
 CC and a size separation. Telomerase is a particular target of anticancer
 CC therapies, and is useful in assays for characterizing (pre)cancerous
 CC cells. Telomerase can also be used to screen for specific modulators,
 CC for biochemical analysis of its activity, and in preparation of
 CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
 CC are used in vaccines, and for treating over expression of telomerase,
 CC particularly in cancer.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTTCTCGGCGCT 20
 DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 2
 ID AAV41170
 XX AAV41170 standard; DNA; 20 BP.

AC AAV41170;

DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) antisense oligo 14ab.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

PD 02-JUL-1998.

PP 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

PI Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F;

DR WPI; 1998-377670/32.

XX New polynucleotide(s) anti-sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX Claim 11; Page 65; 80pp; English.

XX Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridise to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridise to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.45;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGTTCCTCTTCTCGGCGCT 20
 DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 3
 ID AAZ23632
 XX AAZ23632 standard; DNA; 20 BP.

AC AAZ23632;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide 14ab.

XX Telomerase; human; immune response; cancer; vaccine; treatment;
 KW disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5968506-A.

PD 19-OCT-1999.

PP 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;

DR Vassero AP;

XX WPI; 1999-590379/50.

XX Compositions comprising human telomerase, useful for treating diseases
 PT associated with overexpression of telomerase e.g. cancer -

XX Disclosure; Column 45-46; 34pp; English.

XX This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from

CC adenovirus-transformed kidney cell line. The composition is useful for
CC eliciting an immune response in animals and may therefore be used as a
CC vaccine for treating diseases associated with the overexpression of
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used
CC in the isolation of human clone 28-1 which contains a fragment of the
CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCT 20
DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 4
AA223636
ID AA223636 standard; DNA; 20 BP.

AC AA223636;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide oligo 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;
KW disease; primer; ss.

OS Synthetic.
OS Homo sapiens.

FT Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-biotinylated cytidine"

PN US968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;

PS Vassero AP;

DR WPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases

XX associated with overexpression of telomerase e.g. cancer -

XX Disclosure; Column 49-50; 34pp; English.

CC This invention describes a novel composition comprising human telomerase
CC having at least 2000-fold (preferably at least 6000-fold) increased
CC relative purity compared with crude extract of cells from
CC adenovirus-transformed kidney cell line. The composition is useful for
CC eliciting an immune response in animals and may therefore be used as a
CC vaccine for treating diseases associated with the overexpression of
CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used
CC in the isolation of human clone 28-1 which contains a fragment of the
CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.45;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTTCTCGGCGCT 20
DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 5
AAS09477
ID AAS09477 standard; DNA; 20 BP.

AC AAS09477;

DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

KW Human; Telomerase; vaccine; antibody; cancer; EF2H;
KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

PN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;

PS Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in

XX animals, comprises several thousand folds increased purity compared

XX with cytoplasmic crude cell preparations -

XX Disclosure; Column 2; 29pp; English.

CC The sequence represents an antisense oligonucleotide used in
CC the purification of human telomerase. The invention relates
CC to a purified human telomerase core enzyme protein comprising
CC 2000-fold increased purity compared with a crude extract of cells from
CC adenovirus-transformed kidney cell line (293 cells) and when associated
CC with telomerase RNA component has DNA polymerase activity and a molecular
CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
CC for inducing a humoral or cell-mediated immune response in an animal.
CC Purified telomerase or immunogenic fragments are useful as vaccines for
CC treating diseases associated with over-expression of telomerase, such as
CC cancer and for producing antibodies that recognize telomerase, which are
CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EF2H with
CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.45; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCT 20
DB 1 CGTTCCTCTTCTCGGCGCT 20

```

RESULT 6
ID AAS09480 standard; DNA; 20 BP.
XX
AC AAS09480;
XX
DT 24-OCT-2001 (first entry)
XX
DE Antisense oligonucleotide for human telomerase, Oligo 14ab #2.
XX
KW Human; telomerase; vaccine; antibody; cancer; EP2H;
KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH modified_base 1 /*tag= a
FH /mod_base= C
FH /note= "C is biotinylated"
XX
PN US6261556-B1.
XX
PD 17-JUL-2001.
XX
PP 18-OCT-1999; 99US-0420056.
XX
PR 04-APR-1997; 97US-0833377.
XX
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
XX
PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vaasero AP, Pruzan RA;
PI Kealey JT;
PI WPI; 2001-450477/48.
XX
DR Purified human telomerase, useful for inducing immune response in
PT animals, comprises several thousand folds increased purity compared
PT with cytoplasmic crude cell preparations
XX
PS Disclosure; Column 18; 29pp; English.
XX
CC The sequence represents a biotinylated antisense oligonucleotide
CC used in the purification of human telomerase. The invention
CC relates to a purified human telomerase core enzyme protein comprising
CC 2000-fold increased purity compared with a crude extract of cells from
CC adenovirus-transformed kidney cell line (293 cells) and when associated
CC with telomerase RNA component has DNA polymerase activity and a molecular
CC weight of 200-2000 kDa. The purified telomerase is useful
CC for inducing a humoral or cell-mediated immune response in an animal.
CC Purified telomerase or immunogenic fragments are useful as vaccines for
CC treating diseases associated with over-expression of telomerase, such as
CC cancer and for producing antibodies that recognize telomerase, which are
CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EP2H with
CC telomerase.
XX
SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.45; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
XX
DB 1 CGTTCCTTCTCTCGGCGCT 20
1 CGTTCCTTCTCTCGGCGCT 20

```

```

RESULT 7
ID AAV41169 standard; DNA; 30 BP.
XX
AC AAV41169;
XX
DT 08-OCT-1998 (first entry)
XX
DE RNA component of human telomerase (hTR) antisense oligo 14.
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; prostate cancer; cancer;
KW contraception; sterilization; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS Synthetic.
XX
FH Homo sapiens.
XX
FH WO9828442-A1.
XX
PN WO9828442-A1.
XX
PD 02-JUL-1998.
XX
PP 19-DEC-1997; 97WO-US23619.
XX
PR 20-DEC-1996; 96US-0770565.
XX
PR 20-DEC-1996; 96US-0770564.
XX
PA (GERO-) GERON CORP.
XX
PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
PI WPI; 1998-377670/32.
XX
DR New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
PS Claim 11; Page 65; 80pp; English.
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC assembly of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilization, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
SQ Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;
XX
Query Match 100.0%; Score 20; DB 19; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.44; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
XX
DB 1 CGTTCCTTCTCTCGGCGCT 20
1 CGTTCCTTCTCTCGGCGCT 20

```

```

RESULT 8
AA742916/c
ID   AAT42916 standard; DNA; 29 BP.
XX
XX
AC   AAT42916;
XX
XX
DT   16-JUN-1997 (first entry)
XX
DE   Primer 8201RN, amplifies TSP-1 and gene regulation sequences.
XX
XX   gene expression; regulation; plasmid; viral infection;
XX   human T-cell leukaemia; HIV; antiviral agent; detection; cancer;
XX   gene therapy; TSP; ss.
XX
OS   Synthetic.
XX
XX   WO9630522-A1.
XX
XX   03-OCT-1996.
XX
XX   19-MAR-1996; 96WO-JP00719.
XX
XX   27-APR-1995; 95JP-0104299.
XX   24-MAR-1995; 95JP-0065553.
XX
XX   (SHIO ) SHIONOGI & CO LTD.
XX
XX   Igatashi H, Okumura K, Orita S, Saiga A, Sakaguchi G;
XX   WPI; 1996-455367/45.
XX
XX   DNA molecule with gene expression regulation activity - for use in
XX   e.g. treatment of human T-cell leukemia and HIV, as antiviral agent
XX   and for detecting cancer
XX
XX   Example 1; Page 48; 77pp; Japanese.
XX
XX   The sequences given in AAT42904-16 are primers which were used in the
XX   construction of the plasmid of the invention. The plasmid contains a
XX   DNA sequence encoding the protein TSP-1 in conjunction with a DNA
XX   molecule with gene expression regulation activity. The plasmid is
XX   used for regulation of gene expression, and treatment of viral
XX   infection pref. human T-cell leukemia and HIV. The plasmid also encodes
XX   a protein which is used as an antiviral agent, and also in a method for
XX   detecting cancer. The DNA molecule and protein have potential uses in
XX   gene therapy, and the plasmid may also have potential use in the
XX   treatment of TSP.
XX
XX   Sequence 29 BP; 8 A; 5 C; 10 G; 6 T; 0 other;
XX
XX   Query Match      70.0%; Score 14; DB 17; Length 29;
XX   Best Local Similarity 100.0%; Pred. No. 4.2e+03;
XX   Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   6 CTCTTCTGCGGCC 19
XX   |||||
XX   19 CTCTTCTGCGGCC 6
XX
XX   RESULT 9
XX   AAT36484
XX   ID   AAT36484 standard; DNA; 21 BP.
XX
XX
XX   AAT36484;
XX
XX   09-OCT-1996 (first entry)
XX
XX   Upstream PCR primer for p53 gene region contg. Val 143 Ala mutation.
XX
XX   Primer; PCR; polymerase chain reaction; amplification; human;
XX   p53 gene; tumour; cancer; Cx3; mutation; Val 143 Ala; assay;
XX   HhaI cleavage site; detection; gel electrophoresis; diagnosis;
XX   radioactive probe hybridisation; nude mouse xenograft; ss.

```

```

XX
XX   Synthetic.
XX
XX   US5527676-A.
XX
XX   18-JUN-1996.
XX
XX   29-MAR-1989; 89US-0330566.
XX
XX   06-DEC-1989; 89US-0446584.
XX   29-MAR-1989; 89US-0330566.
XX   17-AUG-1992; 92US-0928661.
XX   22-MAR-1993; 93US-0047041.
XX
XX   (UYJO ) UNIV JOHNS HOPKINS.
XX
XX   Baker SJ, Fearon ER, Nigro JM, Vogelstein B;
XX   WPI; 1996-299851/30.
XX
XX   Nucleic acid assay for cancer detection - based on comparing
XX   neoplastic p53 gene with wild-type p53 gene
XX
XX   Example 4; Column 10; 38pp; English.
XX
XX   The primer pair AAT36484/85 was used for the PCR amplification of a
XX   111 bp fragment of the human p53 gene, which may contain the tumour
XX   nude mouse xenograft (Cx3) mutation. Val 143 Ala, where the wild
XX   type codon 143 GTG is substd. with GCG. This mutation also
XX   introduces a new HhaI site (GGC at nucleotides 427-430), so that
XX   HhaI cleavage of a PCR prod. amplified from a mutant template
XX   produces 68 and 43 nucleotide subfragments, which can be detected
XX   by gel electrophoresis separation, followed by radioactive probe
XX   hybridisation. This assay can be used to diagnose the presence of
XX   the Val 143 Ala mutation, and therefore the Cx3 tumour.
XX
XX   Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
XX
XX   Query Match      65.0%; Score 13; DB 17; Length 21;
XX   Best Local Similarity 100.0%; Pred. No. 1.3e+03;
XX   Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX   3 TTCTCTTCTGCG 15
XX   |||||
XX   1 TTCTCTTCTGCG 13
XX
XX   RESULT 10
XX   AAA72585
XX   ID   AAA72585 standard; DNA; 21 BP.
XX
XX
XX   AAA72585;
XX
XX   27-NOV-2000 (first entry)
XX
XX   Upstream PCR primer for mutant p53 gene fragment amplification.
XX
XX   Human; p53; chromosome 17p; neoplastic tissue detection; lung; breast;
XX   brain; colorectal; bladder; mesenchyme; prostate; stomach; cancer;
XX   tumour; leukemia; osteosarcoma; PCR primer; ss.
XX
XX   Homo sapiens.
XX
XX   US6090566-A.
XX
XX   18-JUL-2000.
XX
XX   02-JUN-1995; 95US-0459676.
XX
XX   22-MAR-1993; 93US-0047041.
XX   06-DEC-1989; 89US-0446584.
XX   17-AUG-1992; 92US-0928661.
XX   29-MAR-1989; 89US-0330566.

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```

RESULT 15
AAQ71941
ID AAQ71941 standard; DNA; 20 BP.
XX
XX
AC AAQ71941;
XX
XX
DT 03-MAY-1995 (first entry)
XX
DE Human IL-2R gamma gene exon 3 sense primer.
XX
KW IL2-R gamma gene; X-linked severe combined immunodeficiency;
XX XSCID; interleukin; ss.
XX
OS Homo sapiens.
XX
XX
Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "Biotin covalently bound to cytosine"
XX
XX
PN WO9420641-A.
XX
PD 15-SEP-1994.
XX
PF 10-MAR-1994; 94WO-US02891.
XX
PR 12-MAR-1993; 93US-0031143.
XX 14-SEP-1993; 93US-0121435.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Leonard WJ, McBride WO, Noguchi M;
XX
XX WPI; 1994-303046/37.
XX
XX
XX Diagnosis of X-linked severe combined immunodeficiency (XSCID) -
XX comprises detecting mutated IL-2R gamma gene, also vectors and
XX transgenic animals containing the mutated gene
XX
XX Claim 12; Page 88; 98pp; English.
XX
XX AAQ71941 to AAQ71975 are primers for the human IL-2R gamma gene, these
XX were used to amplify DNA from mutated and normal IL-2R gamma genes.
XX The mutated gene DNA was obtained either from female carriers or
XX male sufferers of X-linked severe combined immunodeficiency (XSCID).
XX The amplified DNA from normal and affected individuals was then
XX compared using a variety of methods including northern blotting and
XX dot and slot hybridisation. From this a claimed method for the
XX diagnosis of XSCID carriers and sufferers was developed.
XX
XX Sequence 20 BP; 2 A; 9 C; 1 G; 8 T; 0 other;
SQ
Query Match 60.0%; Score 12; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GTTCTCTTCT 13
|||
3 GTTCTCTTCT 14
Db

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Search completed: June 23, 2003, 05:43:34
 Job time : 134.216 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds

(without alignments)
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Title: US-08-770-564A-3

Perfect score: 20

Sequence: 1 CGTCCCTCTTCTGCGGCT 20

Scoring table:

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Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database :

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2: gb_hcg:*
3: gb_in:*
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29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rtd:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	A84604
2	20	100.0	20	6	AR063827
3	20	100.0	20	6	AR079894
4	20	100.0	30	6	AR063826
5	19	95.0	20	6	A84597
6	19	95.0	20	6	AR079898
7	14	70.0	29	6	AR146661
8	13	65.0	20	6	AR067594
9	13	65.0	31	6	AR092735
10	13	65.0	42	6	AR024197
11	13	65.0	45	6	AR024198
12	12	60.0	12	6	AR063828
13	12	60.0	19	6	A35686
14	12	60.0	20	6	I21035
15	12	60.0	20	6	I21062
16	12	60.0	25	6	AX196979
17	12	60.0	31	6	BD002728
18	12	60.0	33	6	AR162875
19	12	60.0	33	6	AR194025
20	12	60.0	37	6	AX283664
21	12	60.0	42	6	AX166899
22	11	55.0	11	6	AR051288
23	11	55.0	11	6	AR051324
24	11	55.0	11	6	I16936
25	11	55.0	11	6	I45730
26	11	55.0	11	6	AR051289
27	11	55.0	12	6	I16937
28	11	55.0	14	6	I45731
29	11	55.0	12	6	AR036791
30	11	55.0	18	6	AR166765
31	11	55.0	19	6	AX339205
32	11	55.0	20	6	AR086036
33	11	55.0	20	6	AR160506
34	11	55.0	20	6	I38898
35	11	55.0	20	6	I87929
36	11	55.0	22	6	AR017782
37	11	55.0	22	6	AR017783
38	11	55.0	22	6	AR017784
39	11	55.0	22	6	AR017785
40	11	55.0	22	6	AR017786
41	11	55.0	22	6	AR017787
42	11	55.0	22	6	AR077185
43	11	55.0	22	6	AR077186
44	11	55.0	22	6	AR077187
45	11	55.0	22	6	AR077188

ALIGNMENTS

RESULT 1
A84604
LOCUS A84604 20 bp DNA
DEFINITION Sequence 14 from Patent WO9845450.
ACCESSION A84604
VERSION A84604.1 GI:6733517
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PORIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 14 15-OCT-1998;
GERON CORP (US)

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                /organism="unidentified"
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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCTGCGGCT 20
Db 1 CGTTCCTCTTCTGCGGCT 20

RESULT 2
LOCUS      AR063827      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5846723.
ACCESSION  AR063827
VERSION     AR063827.1 GI:5993135
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Kim,N.Woo., Wu,P., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 3 08-DEC-1998;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCTGCGGCT 20
Db 1 CGTTCCTCTTCTGCGGCT 20

RESULT 3
LOCUS      AR079894      20 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5968506.
ACCESSION  AR079894
VERSION     AR079894.1 GI:10006647
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,
          Pruzan,R.A. and Kealey,J.T.
TITLE      Purified telomerase
JOURNAL    Patent: US 5968506-A 7 19-OCT-1999;
FEATURES
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                /organism="unknown"
BASE COUNT    0 a      9 c      4 g      7 t
ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCTGCGGCT 20
Db 1 CGTTCCTCTTCTGCGGCT 20

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RESULT 4
LOCUS      AR063826      30 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5846723.
ACCESSION  AR063826
VERSION     AR063826.1 GI:5993134
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unidentified.
REFERENCE   1 (bases 1 to 30)
AUTHORS    Kim,N.Woo., Wu,P., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE      Methods for detecting the RNA component of telomerase
JOURNAL    Patent: US 5846723-A 2 08-DEC-1998;
FEATURES
  source      1..30      Location/Qualifiers
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BASE COUNT    4 a      10 c      8 g      8 t
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Query Match      100.0%; Score 20; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTTCTGCGGCT 20
Db 1 CGTTCCTCTTCTGCGGCT 20

RESULT 5
LOCUS      AB4597      20 bp      DNA      linear      PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9845450.
ACCESSION  AB4597
VERSION     AB4597.1 GI:6733513
KEYWORDS
SOURCE      unidentified.
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Atkinson,E.M. and Kealey,J.T.
TITLE      PURIFIED TELOMERASE
JOURNAL    Patent: WO 9845450-A 7 15-OCT-1998;
          GERON CORP (US)
FEATURES
  source      1..20      Location/Qualifiers
                /organism="unidentified"
                /db_xref="taxon:32644"
                /note="N = BIOTINYLATED C"
                /mod_base=OTHER
BASE COUNT    0 a      8 c      4 g      7 t      1 others
ORIGIN
Query Match      95.0%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTTCTGCGGCT 20
Db 2 GTTCTCTTCTGCGGCT 20

RESULT 6
LOCUS      AR079898      20 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 14 from patent US 5968506.
ACCESSION  AR079898
VERSION     AR079898.1 GI:10006651
KEYWORDS
SOURCE      Unknown.

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ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
Weinrich, S.L., Atkinson, E.M. III, Lichtsteiner, S.P., Vassero, A.P.,
Pruzan, R.A. and Kealey, J.T.
TITLE Purified telomerase
JOURNAL Patent: US 5968506-A 14 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 0 a 8 c 4 g 7 t 1 others
ORIGIN

Query Match 95.0%; Score 19; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTCGCGGCT 20
Db 2 GTTCTCTCTCGCGGCT 20

RESULT 7
ARI46661/c
LOCUS ARI46661 29 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 14 from patent US 6218522.
ACCESSION ARI46661
VERSION ARI46661.1 GI:15109850
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Saiga, A., Orita, S., Igarashi, H., Okumura, K. and Sakaguchi, G.
TITLE DNA molecule relating to suppression of gene expression and novel
protein
JOURNAL Patent: US 6218522-A 14 17-APR-2001;
FEATURES Location/Qualifiers
source 1..29
/organism="unknown"

BASE COUNT 8 a 5 c 10 g 6 t
ORIGIN

Query Match 70.0%; Score 14; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCTCTCTCGCGGCT 19
Db 19 CTCTCTCTCGCGGCT 6

RESULT 8
AR067594
LOCUS AR067594 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5851769.
ACCESSION AR067594
VERSION AR067594.1 GI:5998816
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Gray, J.W. and Weier, H.-U.G.
TITLE Quantitative DNA fiber mapping
JOURNAL Patent: US 5851769-A 1 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 8 c 2 g 8 t
ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTCTCGGCT 15
Db 1 TTCCCTCTCGGCT 13

RESULT 9
AR092735/c
LOCUS AR092735 31 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 15 from patent US 5998194.
ACCESSION AR092735
VERSION AR092735.1 GI:10019487
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Summers, R.G. Jr., Katz, L., Donadio, S. and Staver, M.J.
TITLE Polyketide-associated sugar biosynthesis genes
JOURNAL Patent: US 5998194-A 15 07-DEC-1999;
FEATURES Location/Qualifiers
source 1..31
/organism="unknown"

BASE COUNT 10 a 8 c 11 g 2 t
ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTCTCTCGGCT 20
Db 19 CTCTCTCGGCT 7

RESULT 10
AR024197/c
LOCUS AR024197 42 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 8 from patent US 5795863.
ACCESSION AR024197
VERSION AR024197.1 GI:3977491
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Wolf, D.
TITLE Recombinant agents affecting thrombosis
JOURNAL Patent: US 5795863-A 8 18-AUG-1998;
FEATURES Location/Qualifiers
source 1..42
/organism="unknown"

BASE COUNT 12 a 9 c 17 g 4 t
ORIGIN

Query Match 65.0%; Score 13; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTCTCTCGGCT 16
Db 22 TTCTCTCTCGGCT 10

RESULT 11
AR024198/c
LOCUS AR024198 45 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5795863.
ACCESSION AR024198
VERSION AR024198.1 GI:3977492
KEYWORDS

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 45)
AUTHORS      Wolf, D.
TITLE        Recombinant agents affecting thrombosis
JOURNAL      Patent: US 575863-A 9 18-AUG-1998;
FEATURES     Location/Qualifiers
             source
             1..45
             /organism="unknown"
BASE COUNT   14 a 9 c 18 g 4 t
ORIGIN
Query Match 65.0%; Score 13; DB 6; Length 45;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          4 TCCTCTCTCTGCG 16
            |||||
            |||||
Db          22 TCCTCTCTCTGCG 10

RESULT 12
AR063828
LOCUS       AR063828
DEFINITION Sequence 4 from patent US 5846723.
ACCESSION  AR063828
VERSION     AR063828.1 GI:5993136
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Kim, N. Woc, Wu F., Kozley, J. T., Pruzan, R. and Weinrich, S. L.
TITLE        Methods for detecting the RNA component of telomerase
JOURNAL      Patent: US 5846723-A 4 08-DEC-1998;
FEATURES     Location/Qualifiers
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             /organism="unknown"
BASE COUNT   0 a 6 c 1 g 5 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 CGTCTCTCTCC 12
            |||||
            |||||
Db          1 CGTCTCTCTCC 12

RESULT 13
A35686/c
LOCUS       A35686/c
DEFINITION Synthetic human IFN-alpha 2 gene c1lgo.
ACCESSION  A35686
VERSION     A35686.1 GI:1927068
KEYWORDS
SOURCE      Synthetic construct.
ORGANISM     Synthetic construct.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Camble, R. and Edge, M. D.
TITLE        Analogous interleukin polypeptides, process for their preparation
JOURNAL      Patent: EP 0194006-A 131 10-SEP-1986;
FEATURES     Location/Qualifiers
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BASE COUNT   4 a 5 c 6 g 4 t
ORIGIN

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Query Match 60.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          6 CTCTCTCTGCG 17
            |||||
            |||||
Db          15 CTCTCTCTGCG 4

RESULT 14
I21035/c
LOCUS       I21035/c
DEFINITION Sequence 6 from patent US 5518880.
ACCESSION  I21035
VERSION     I21035.1 GI:1601389
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Leonard, W. J., Noguchi, M. and McBride, O. Wesley.
TITLE        Methods for diagnosis of XSCID and Kite thereof
JOURNAL      Patent: US 5518880-A 6 21-MAY-1996;
FEATURES     Location/Qualifiers
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             /organism="unknown"
BASE COUNT   8 a 1 c 9 g 2 t
ORIGIN
Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 GTTCTCTCTCT 13
            |||||
            |||||
Db          18 GTTCTCTCTCT 7

RESULT 15
I21062
LOCUS       I21062
DEFINITION Sequence 33 from patent US 5518880.
ACCESSION  I21062
VERSION     I21062.1 GI:1601416
KEYWORDS
SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 20)
AUTHORS      Leonard, W. J., Noguchi, M. and McBride, O. Wesley.
TITLE        Methods for diagnosis of XSCID and Kite thereof
JOURNAL      Patent: US 5518880-A 33 21-MAY-1996;
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ORIGIN
Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 GTTCTCTCTCT 13
            |||||
            |||||
Db          3 GTTCTCTCTCT 14

Search completed: June 23, 2003, 06:34:12
Job time : 234.051 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 286.661 Seconds

(Without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-4

Perfect score: 12 CGTTCCTCTCC 12

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7860393 seqs, 3496198572 residues

Total number of hits satisfying chosen parameters: 8677950

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
C 1	12	100.0	25	7	US-09-954-445A-45573
C 2	12	100.0	25	9	US-10-355-577-396546
C 3	12	100.0	25	12	US-10-355-577-396546
C 4	11	91.7	17	9	US-10-303-778-7608
C 5	11	91.7	18	9	US-10-303-778-7627
C 6	11	91.7	18	9	US-10-310-188-65996
C 7	11	91.7	20	9	US-10-315-474-66
C 8	11	91.7	20	9	US-10-315-474-137
C 9	11	91.7	25	6	US-09-660-222-124398
C 10	11	91.7	25	6	US-09-660-222-124402
C 11	11	91.7	25	6	US-09-660-222-124403
C 12	11	91.7	25	6	US-09-660-222-124417
C 13	11	91.7	25	6	US-09-660-222-124417
C 14	11	91.7	25	7	US-09-953-570-22842
C 15	11	91.7	25	7	US-09-953-570-131778
C 16	11	91.7	25	7	US-09-954-445A-7403
C 17	11	91.7	25	7	US-09-954-445A-21805
C 18	11	91.7	25	7	US-09-954-445A-31524
C 19	11	91.7	25	7	US-09-954-445A-79209
C 20	11	91.7	25	7	US-09-954-445A-79210
C 20	11	91.7	25	9	US-10-098-263B-24096

21	11	91.7	25	9	US-10-098-263B-81647	Sequence 81647, A
22	11	91.7	25	9	US-10-098-263B-81648	Sequence 81648, A
23	11	91.7	25	9	US-10-098-263B-96226	Sequence 96226, A
24	11	91.7	25	9	US-10-098-263B-114611	Sequence 114611, A
25	11	91.7	25	9	US-10-355-577-96775	Sequence 96775, A
26	11	91.7	25	9	US-10-355-577-101273	Sequence 101273, A
27	11	91.7	25	9	US-10-355-577-101274	Sequence 101274, A
28	11	91.7	25	9	US-10-355-577-164671	Sequence 164671, A
29	11	91.7	25	9	US-10-355-577-178073	Sequence 178073, A
30	11	91.7	25	9	US-10-355-577-198249	Sequence 198249, A
31	11	91.7	25	9	US-10-355-577-318084	Sequence 318084, A
32	11	91.7	25	9	US-10-355-577-394493	Sequence 394493, A
33	11	91.7	25	9	US-10-355-577-394494	Sequence 394494, A
34	11	91.7	25	9	US-10-355-577-396545	Sequence 396545, A
35	11	91.7	25	9	US-10-355-577-498091	Sequence 498091, A
36	11	91.7	25	9	US-10-355-577-581372	Sequence 581372, A
37	11	91.7	25	9	US-10-355-577-587426	Sequence 587426, A
38	11	91.7	25	9	US-10-355-577-650483	Sequence 650483, A
39	11	91.7	25	9	US-10-355-577-650484	Sequence 650484, A
40	11	91.7	25	9	US-10-355-577-653296	Sequence 653296, A
41	11	91.7	25	9	US-10-355-577-658872	Sequence 658872, A
42	11	91.7	25	9	US-10-355-577-667847	Sequence 667847, A
43	11	91.7	25	9	US-10-355-577-667848	Sequence 667848, A
44	11	91.7	25	9	US-10-355-577-730882	Sequence 730882, A
45	11	91.7	25	9	US-10-355-577-734855	Sequence 734855, A

ALIGNMENTS

```

RESULT 1
US-09-954-445A-45573/c
; Sequence 45573, Application US/09954445A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methode of Genetic Analysis of Arabidopsis Thaliana
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/09/954,445A
; PRIOR FILING DATE: 2000-09-17
; PRIOR APPLICATION NUMBER: 60/233,620
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 131820
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 45573
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-954-445A-45573

Query Match          100.0%; Score 12; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGTTCCTCTCC 12
Db      15 CGTTCCTCTCC 4

RESULT 2
US-10-355-577-396546/c
; Sequence 396546, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methode of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 396546
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

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US-10-355-577-396546

Query Match 100.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCCTCTCC 12
Db 24 GTTCCCTCTCC 13

RESULT 3

US-60-427-836-683575
Sequence 683575, Application US/60427836
GENERAL INFORMATION:
APPLICANT: Xue Wei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Rat.
FILE REFERENCE: 3527
CURRENT APPLICATION NUMBER: US/60/427,836
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 699466
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 683575
LENGTH: 25
TYPE: DNA
ORGANISM: Rattus norvegicus
US-60-427-836-683575

Query Match 100.0%; Score 12; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGTCCCTCTCC 12
Db 12 GTTCCCTCTCC 23

RESULT 4

US-10-303-778-7608
Sequence 7608, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7608
LENGTH: 17
TYPE: DNA
ORGANISM: Avian infectious bronchitis virus
US-10-303-778-7608

Query Match 91.7%; Score 11; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
Db 7 GTTCCCTCTCC 17

RESULT 5

US-10-303-778-7627
Sequence 7627, Application US/10303778
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
TITLE OF INVENTION: REGULATORY GENES AND USES THEREOF
FILE REFERENCE: 47416
CURRENT APPLICATION NUMBER: US/10/303,778

CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 17608
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7627
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-303-778-7627

Query Match 91.7%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
Db 7 GTTCCCTCTCC 17

RESULT 6

US-10-310-188-65996/c
Sequence 65996, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65996
LENGTH: 18
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-65996

Query Match 91.7%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
Db 12 GTTCCCTCTCC 2

RESULT 7

US-10-315-474-66/c
Sequence 66, Application US/10315474
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
FILE REFERENCE: RTS-0318
CURRENT APPLICATION NUMBER: US/10/315,474
CURRENT FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 156
SEQ ID NO 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-315-474-66

Query Match 91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCCCTCTCC 12
Db 12 GTTCCCTCTCC 2

```
RESULT 8
US-10-315-474-137
; Sequence 137, Application US/10315474
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Kenneth W. Doble
; TITLE OF INVENTION: MODULATION OF G PROTEIN-COUPLED RECEPTOR 3 EXPRESSION
; FILE REFERENCE: RTS-0338
; CURRENT APPLICATION NUMBER: US/10/315,474
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-315-474-137

Query Match          91.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CGTCTCTTCC 12
DB      9  GTTCTCTTCC 19

RESULT 9
US-09-660-222-124398
; Sequence 124398, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124398
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124398

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTTTC 11
DB     12  CGTCTCTTTC 22

RESULT 10
US-09-660-222-124402
; Sequence 124402, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124402
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; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124402

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTTTC 11
DB      6  CGTCTCTTTC 16

RESULT 11
US-09-660-222-124403
; Sequence 124403, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124403

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGTCTCTTTC 11
DB      4  CGTCTCTTTC 14

RESULT 12
US-09-660-222-124417
; Sequence 124417, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; PRIOR FILING DATE: 2000-09-12
; CURRENT APPLICATION NUMBER: 60/164,973
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124417
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank X76717
US-09-660-222-124417

Query Match          91.7%; Score 11; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGTCTCTCTTC 11
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 Db 3 GGTCTCTCTTC 13

RESULT 13
 US-09-953-570-22842/c
 ; Sequence 22842, Application US/09953570
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
 ; FILE REFERENCE: 3110.1
 ; CURRENT APPLICATION NUMBER: US/09/953,570
 ; CURRENT FILING DATE: 2001-09-13
 ; PRIOR APPLICATION NUMBER: 60/232,638
 ; PRIOR FILING DATE: 2000-09-14
 ; NUMBER OF SEQ ID NOS: 138410
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22842
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces Cerevisiae
 US-09-953-570-22842

Query Match 91.7%; Score 11; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTCTTC 12
 |||||
 Db 19 GTTCTCTCTTC 9

RESULT 14
 US-09-953-570-131778/c
 ; Sequence 131778, Application US/09953570
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
 ; FILE REFERENCE: 3110.1
 ; CURRENT APPLICATION NUMBER: US/09/953,570
 ; CURRENT FILING DATE: 2001-09-13
 ; PRIOR APPLICATION NUMBER: 60/232,638
 ; PRIOR FILING DATE: 2000-09-14
 ; NUMBER OF SEQ ID NOS: 138410
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 131778
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Saccharomyces Cerevisiae
 US-09-953-570-131778

Query Match 91.7%; Score 11; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTCTTC 12
 |||||
 Db 17 GTTCTCTCTTC 7

RESULT 15
 US-09-954-445A-7403/c
 ; Sequence 7403, Application US/09954445A
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
 ; FILE REFERENCE: 3116.1
 ; CURRENT APPLICATION NUMBER: US/09/954,445A
 ; CURRENT FILING DATE: 2000-09-17
 ; PRIOR APPLICATION NUMBER: 60/233,620
 ; PRIOR FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 131820

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 7403
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-954-445A-7403

Query Match 91.7%; Score 11; DB 7; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GTTCTCTCTTC 12
 |||||
 Db 12 GTTCTCTCTTC 2

Search completed: June 26, 2003, 04:15:11
 Job time : 289.969 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30
Sequence: 1 CGTTCCTCTCTCGCGCCTGAACGCTGA 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents, NA:*

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5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	66.7	20	2	US-08-770-565-3
3	20	66.7	20	2	US-08-770-565-12
4	20	66.7	20	2	US-08-833-377-7
5	19	63.3	20	2	US-08-833-377-14
6	14	46.7	29	3	US-09-121-321-14
7	14	46.7	29	4	US-08-933-803A-14
8	13	43.3	20	2	US-08-534-479-1
9	13	43.3	31	2	US-08-576-626A-15
10	13	43.3	42	1	US-08-487-037-8
11	13	43.3	45	1	US-08-487-037-9
12	12	40.0	12	2	US-08-770-565-4
13	12	40.0	20	1	US-08-031-143B-6
14	12	40.0	20	1	US-08-031-143B-33
15	12	40.0	20	4	US-09-851-896-86
16	12	40.0	20	5	PCT-US94-02891-6
17	12	40.0	20	5	PCT-US94-02891-33
18	12	40.0	33	4	US-08-090-369-15
19	12	40.0	33	4	US-09-482-971-15
20	12	40.0	36	1	US-09-384-372-15
21	12	40.0	36	2	US-08-458-372-15
22	12	40.0	36	2	US-08-956-047-19
23	12	40.0	36	6	5506118-6
24	12	40.0	38	4	US-09-638-202A-18
25	12	40.0	43	1	US-08-456-566-1
26	12	40.0	43	1	US-09-009-044-1
27	12	40.0	49	2	US-08-956-047-10

C 28	11	36.7	11	1	US-08-126-594-5	Sequence 5, Appl
C 29	11	36.7	11	1	US-08-465-811A-5	Sequence 5, Appl
C 30	11	36.7	11	2	US-08-619-542B-5	Sequence 5, Appl
C 31	11	36.7	11	2	US-08-619-542B-48	Sequence 48, Appl
C 32	11	36.7	12	1	US-08-126-594-6	Sequence 6, Appl
C 33	11	36.7	12	1	US-08-465-811A-6	Sequence 6, Appl
C 34	11	36.7	12	2	US-08-619-542B-6	Sequence 6, Appl
C 35	11	36.7	14	1	US-08-294-424-33	Sequence 33, Appl
C 36	11	36.7	17	4	US-09-277-457-28	Sequence 28, Appl
C 37	11	36.7	18	4	US-09-251-645-21	Sequence 21, Appl
C 38	11	36.7	19	4	US-09-442-143A-38	Sequence 38, Appl
C 39	11	36.7	19	4	US-09-442-143A-41	Sequence 41, Appl
C 40	11	36.7	20	1	US-08-068-945A-8	Sequence 8, Appl
C 41	11	36.7	20	1	US-08-442-806-8	Sequence 8, Appl
C 42	11	36.7	20	2	US-08-206-790A-18	Sequence 18, Appl
C 43	11	36.7	20	3	US-08-589-939-40	Sequence 40, Appl
C 44	11	36.7	20	4	US-09-288-377-30	Sequence 30, Appl
C 45	11	36.7	20	5	PCT-US95-02943-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-2
; Sequence 2, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinlich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-2
Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. NO. 1.4e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCTCGCGCCTGAACGCTGA 30

Db 1 CGTTCCTCTTCTGCGGCGCTGAACGGCTGA 30

RESULT 2

US-08-770-565-3

Sequence 3, Application US/08770565

Patent No. 5846723

GENERAL INFORMATION:

APPLICANT: Klm, Nam Woo

APPLICANT: Wu, Fred

APPLICANT: Kealey, James T.

APPLICANT: Pruzan, Ronald

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

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APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

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APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

APPLICANT: Weinrich, Scott L.

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770,565

FILING DATE: 20-DEC-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-12

Query Match 66.7%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 CGTGGCGGCTGAACGGCTGA 30

1 CGTGGCGGCTGAACGGCTGA 20

RESULT 4

US-08-833-377-7

Sequence 7, Application US/08833377

Patent No. 5968506

GENERAL INFORMATION:

APPLICANT: Weinrich, Scott L.

APPLICANT: Atkinson III, Edward M.

APPLICANT: Lichtenstein, Serge P.

APPLICANT: Vassero, Alain P.

APPLICANT: Pruzan, Ronald A.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

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APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,377

FILING DATE: 04-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-002300US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-770-565-12

Query Match 66.7%; Score 20; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.028;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 CGTGGCGGCTGAACGGCTGA 30

1 CGTGGCGGCTGAACGGCTGA 20

RESULT 4

US-08-833-377-7

Sequence 7, Application US/08833377

Patent No. 5968506

GENERAL INFORMATION:

APPLICANT: Weinrich, Scott L.

APPLICANT: Atkinson III, Edward M.

APPLICANT: Lichtenstein, Serge P.

APPLICANT: Vassero, Alain P.

APPLICANT: Pruzan, Ronald A.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

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APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

APPLICANT: Kealey, James T.

REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="Oligo 14ab"
US-08-833-377-7

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCGCGCCT 20
DB 1 CGTCTCTTCTCGCGCCT 20

RESULT 5
US-08-833-377-14
Sequence 14, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtesteiner, Serge P.
APPLICANT: Vaaserot, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note="N = 5' biotinylated cytidine"
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="biotinylated Oligo 14ab"
US-08-833-377-14

Query Match 63.3%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGCCT 20
DB 2 GTTCTCTTCTCGCGCCT 20

RESULT 6
US-09-121-321-14/C
Sequence 14, Application US/09121321
Patent No. 6090783
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igarashi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSES: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,321
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/933,803
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-09-121-321-14

Query Match 46.7%; Score 14; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTCTCTCTCGGCC 19
DB 19 CTCTCTCTCGGCC 6

RESULT 7

US-08-933-803A-14/C

Sequence 14, Application US/08933803A

Patent No. 6218522

GENERAL INFORMATION:

APPLICANT: Saiga, Akihiko

APPLICANT: Orita, Satoshi

APPLICANT: Igataashi, Hisanaga

APPLICANT: Okumura, Kouichi

APPLICANT: Sakaguchi, Gaku

TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSER: FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,803A

FILING DATE: 19-SEP-1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Haley, James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-12CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-596-9090

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-08-933-803A-14

Query Match 46.7%; Score 14; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 CTCTCTCTCGGCC 19
DB 19 CTCTCTCTCGGCC 6

RESULT 8

US-08-534-479-1

Sequence 1, Application US/08534479

Patent No. 5851769

GENERAL INFORMATION:

APPLICANT: GRAY, JOE M.

APPLICANT: MEYER, HEINZ-URICH G.

TITLE OF INVENTION: QUANTITATIVE FIBER MAPPING

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSER: MEDLEN & CARROLL

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/534,479

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MACKNIGHT, KAMRIN T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: LBL-01754

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-534-479-1

Query Match 43.3%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCTCTGC 15
DB 1 TTCTCTTCTCTGC 13

RESULT 9

US-08-576-626A-15/C

Sequence 15, Application US/08576626A

Patent No. 598194

GENERAL INFORMATION:

APPLICANT: Summers, R.G.

APPLICANT: Katz, L.

APPLICANT: Donadio, S.

APPLICANT: Staver, M.J.

TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSER: Abbott Laboratories

STREET: 100 Abbott Park Road

CITY: Abbott Park

STATE: Illinois

COUNTRY: USA

ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/576,626A

FILING DATE: 21-DEC-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Dianne Casulo

REGISTRATION NUMBER: P-40,943

REFERENCE/DOCKET NUMBER: 5857, US. 01

TELECOMMUNICATION INFORMATION:

TELEPHONE: (847) 938-3137
TELEFAX: (847) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-576-626A-15

Query Match 43.3%; Score 13; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TTCTCTGCGCGCT 20
DB 19 TTCTCTGCGCGCT 7

RESULT 10

US-08-487-037-8/c
Sequence 8, Application US/08487037
Patent No. 5795863
GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-037-8

Query Match 43.3%; Score 13; DB 1; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTCTTCTGCG 16
DB 22 TTCTCTTCTGCG 10

RESULT 11
US-08-487-037-9/c
Sequence 9, Application US/08487037
Patent No. 5795863

GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-037-9

Query Match 43.3%; Score 13; DB 1; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCTTTTCTGCG 16
DB 22 TTCTTTTCTGCG 10

RESULT 12
US-08-770-565-4
Sequence 4, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinlich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSES: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-4

Query Match 40.0%; Score 12; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTTCCTCTTCC 12
DB 1 GGTTCCTCTTCC 12

RESULT 13
US-08-031-143B-6/c
Sequence 6, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
APPLICANT: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,143B
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R

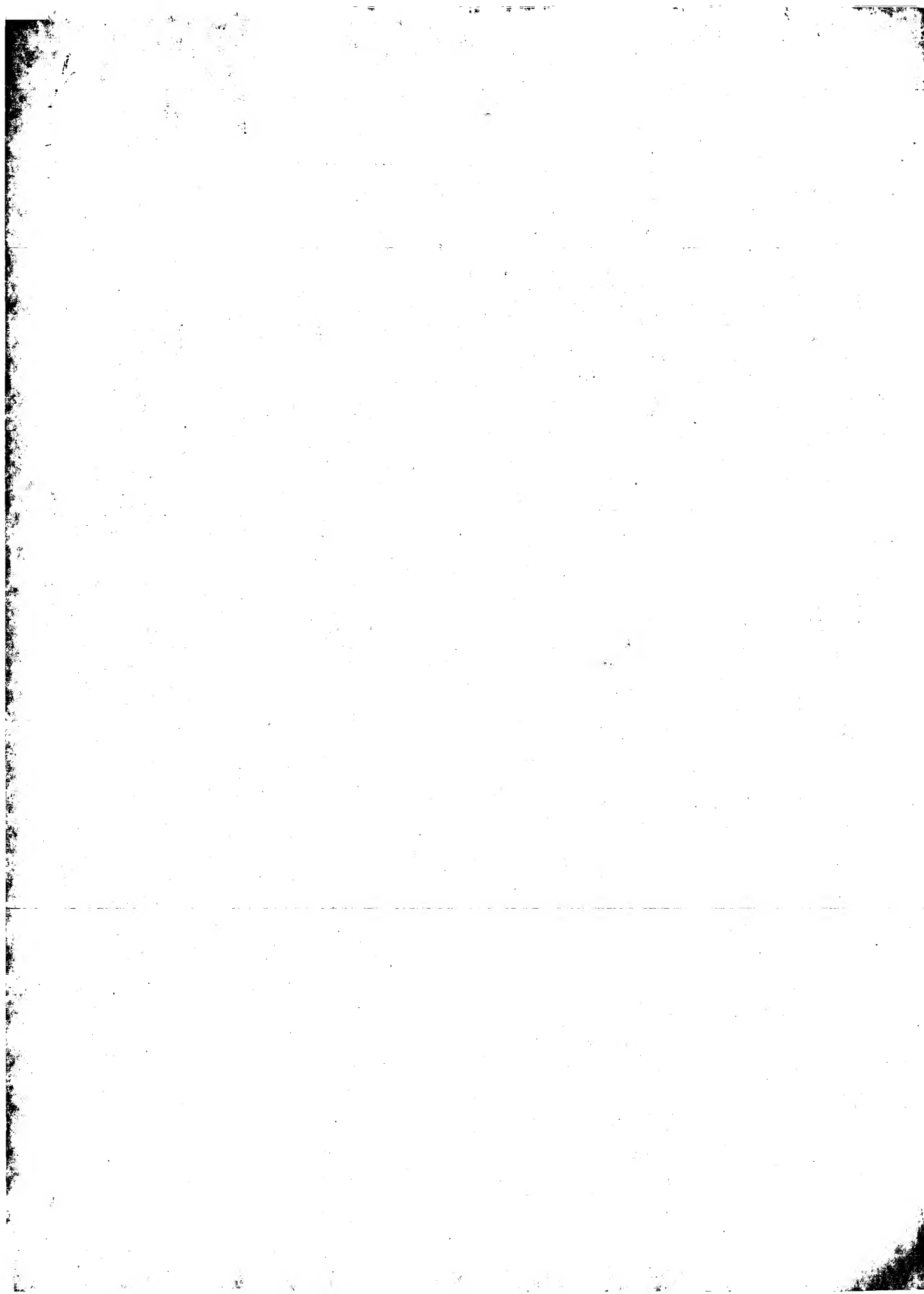
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCT 13
DB 18 GTTCCTCTTCT 7

RESULT 14
US-08-031-143B-33
Sequence 33, Application US/08031143B
Patent No. 5518880
GENERAL INFORMATION:
APPLICANT: LEONARD, WARREN J.; NOGUCHI, MASAYUKI;
APPLICANT: MCBRIDE, O. WESLEY
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND
TREATMENT OF XSCID
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,143B
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4061
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 20
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OLIGONUCLEOTIDE
DESCRIPTION: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HUMAN
INDIVIDUAL ISOLATE: IL-2R
US-08-031-143B-33
Query Match 40.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCT 13
DB 3 GTTCCTCTTCT 14

RESULT 15
US-09-851-896-86
Sequence 86, Application US/09851896
Patent No. 6410325



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 199.363 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30
Sequence: 1 CGTTCCTCTCTCGCGCCTGAACGCTGA 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N Geneseq_101002.*

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23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	100.0	30 19 AAV41169	RNA component of h
2	20	66.7	20 19 AAV71226	Antisense oligonuc
3	20	66.7	20 19 AAV41170	RNA component of h
4	20	66.7	20 20 AA223632	Human clone 28-1 t
5	20	66.7	20 20 AA223636	Human clone 28-1 t
6	20	66.7	20 22 AAS09477	Antisense oligonuc
7	20	66.7	20 22 AAS09480	Antisense oligonuc
8	14	46.7	29 17 AAT42916	Primer 8201RN, amp
9	13	43.3	21 17 AAT36484	Upstream PCR prime

10	13	43.3	21 21 AAT72585	Upstream PCR prime
11	13	43.3	21 22 AAT47842	Human p53 PCR prim
12	13	43.3	31 18 AAT72696	Sugar biosynthesis
13	13	43.3	50 22 AAT28060	Human SNP oligonuc
14	13	43.3	50 22 AAT34593	Human SNP oligonuc
15	12	40.0	12 19 AAV41171	RNA component of h
16	12	40.0	20 15 AAQ71941	Human IL-2R gamma
17	12	40.0	20 15 AAV45148	Homo sapiens P-TEN
18	12	40.0	20 19 AAV94325	PCR primer used to
19	12	40.0	20 20 AAH62356	RBSP2 polymorphism
20	12	40.0	21 22 AAH62356	Enzymatic RNA mole
21	12	40.0	24 15 AAQ57316	Oligonucleotide ad
22	12	40.0	24 24 ABQ01901	Oligonucleotide ad
23	12	40.0	24 24 ABQ07713	Oligonucleotide ad
24	12	40.0	24 24 ABQ07754	Oligonucleotide ad
25	12	40.0	25 22 AAT62055	Soybean 318013 reg
26	12	40.0	27 22 AAF87709	Human glutathione
27	12	40.0	30 22 AAH19632	Human t-PA primer
28	12	40.0	31 21 AAA79024	Human genomic DNA
29	12	40.0	33 14 AAQ49474	Primer "a332" to a
30	12	40.0	36 14 AAQ48727	Modified tissue pl
31	12	40.0	36 16 AAQ80463	Primer (PhoAUP2) c
32	12	40.0	36 20 AAQ03944	Oligodeoxyribonuc
33	12	40.0	36 21 AAH39099	Tissue plasminogen
34	12	40.0	36 22 AAB45119	Human tissue plas
35	12	40.0	37 24 ABA01509	EryCIII PCR primer
36	12	40.0	38 18 AAT95360	Mouse anti-Ptha MA
37	12	40.0	38 20 AAX05505	Synthetic Fn3 gene
38	12	40.0	38 24 ABL94482	Fibronectin 3 codi
39	12	40.0	40 17 AAT70784	Stenotic carotid a
40	12	40.0	40 17 AAT70788	Stenotic carotid a
41	12	40.0	40 17 AAT70789	Stenotic carotid a
42	12	40.0	41 24 ABA04329	Human tetrapeptide
43	12	40.0	41 24 ABA04330	Human tetrapeptide
44	12	40.0	43 17 AAT35002	Mutagenic oligonuc
45	12	40.0	49 16 AAQ80460	Primer (V110) for

ALIGNMENTS

RESULT 1	AAV41169	standard; DNA; 30 BP.
ID	AAV41169	
AC	AAV41169;	
DT	08-OCT-1998	(first entry)
DE	RNA component of human telomerase (htr) antisense oligo 14.	
KW	RNA component; human telomerase; antisense oligonucleotide; infection; neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer; contraseption; sterilisation; immunosuppression; therapeutic; htr; immune system down-regulation; anti-inflammatory therapy; ss.	
OS	Synthetic.	
XX	Homo sapiens.	
XX	WO9828442-A1.	
XX	02-JUL-1998.	
XX	19-DEC-1997;	97WO-US23619.
XX	20-DEC-1996;	96US-0770565.
XX	20-DEC-1996;	96US-0770564.
XX	(GERO-) GERON CORP.	
XX	Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F,	
PI	WPI, 1998-377670/32.	
XX		
DR		

XX New polynucleotide(s) antisense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 11; Page 65; 80pp; English.

XX Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridize to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridize to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting the
 CC assembly of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilization, for
 CC immunosuppression, and for selectively down-regulation, for
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX

SQ Sequence 30 BP; 4 A; 10 C; 8 G; 8 T; 0 other;

Query Match 100.0%; Score 30; DB 19; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.1e-06;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCTGAACGGTGA 30
 DB 1 CGTTCCTCTTCTCGGCGCTGAACGGTGA 30

RESULT 2

AAV71226
 ID AAV71226 standard; DNA; 20 BP.

XX AAV71226;

XX 15-FEB-1999 (first entry)

DE Antisense oligonucleotide 14ab for human telomerase RNA component.

XX Human; telomerase RNA component; anticancer therapy; purification;
 KM assay; vaccine; cancer; antisense oligonucleotide; ss.

XX Synthetic.

OS Homo sapiens.

XX Key modified_base 1 Location/Qualifiers

PT /*tag= a

PT /note= "biocliny1ated"

XX WO9845450-A1.

PN 15-OCT-1998.

XX 04-APR-1997; 97WO-US06012.

PR 04-APR-1997; 97WO-US06012.

XX (GERO-) GERON CORP.

PI Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA,
 Vassero AP, Weinrich SL;

XX WPI; 1998-594485/50.
 DR Purification of telomerase on affinity material - useful for, e.g.
 XX diagnosis and treatment of cancer
 PT
 XX
 PS Claim 6; Page 61; 76pp; English.

XX The present sequence represents an antisense oligonucleotide
 CC directed against the human telomerase RNA component gene sequences.
 CC The oligonucleotide can be used as an affinity agent in the methods of
 CC the invention, which are used to purify human telomerase. The methods
 CC involve the use of several sequential steps, including the use of two
 CC matrices that bind molecules bearing negative charges, a matrix that
 CC binds molecules bearing positive charges, an affinity purification step
 CC and a size separation. Telomerase is a particular target of anticancer
 CC therapies, and is useful in assays for characterizing (pre)cancerous
 CC cells. Telomerase can also be used to screen for specific modulators,
 CC for biochemical analysis of its activity, and in preparation of
 CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
 CC are used in vaccines, and for treating over expression of telomerase,
 CC particularly in cancer.
 XX

SQ Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCTCGGCGCT 20
 DB 1 CGTTCCTCTTCTCGGCGCT 20

RESULT 3

AAV41170
 ID AAV41170 standard; DNA; 20 BP.

XX AAV41170;

XX 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) antisense oligo 14ab.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
 KM neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KM contraception; sterilization; immunosuppression; therapeutic; hTR;
 KM immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9828442-A1.

PN 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

PR 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

XX Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F,

PI WPI; 1998-377670/32.

XX New polynucleotide(s) antisense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 11; Page 65; 80pp; English.

CC Sequences shown in AA41169 to AA41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridize to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridize to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting assembly
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilization, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCTGCGGCT 20
 |||||
 DB 1 CGTTCCTCTTCCTGCGGCT 20

RESULT 4

ID AA223632
 AA223632 standard; DNA; 20 BP.

AC AA223632;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 Vassero AP;

DR MPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases
 associated with overexpression of telomerase e.g. cancer -

XX Disclosure; Column 45-46; 34pp; English.

CC This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from
 CC adenovirus-transformed kidney cell line. The composition is useful for

CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used
 CC in the isolation of human clone 28-1 which contains a fragment of the
 CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCCTGCGGCT 20
 |||||
 DB 1 CGTTCCTCTTCCTGCGGCT 20

RESULT 5

ID AA223636
 AA223636 standard; DNA; 20 BP.

AC AA223636;

DT 07-JAN-2000 (first entry)

DE Human clone 28-1 telomerase oligonucleotide oligo 14ab.

KW Telomerase; human; immune response; cancer; vaccine; treatment;
 disease; primer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5968506-A.

PD 19-OCT-1999.

PF 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

PA (GERO-) GERON CORP.

PI Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 Vassero AP;

DR MPI; 1999-590379/50.

PT Compositions comprising human telomerase, useful for treating diseases
 associated with overexpression of telomerase e.g. cancer -

XX Disclosure; Column 49-50; 34pp; English.

CC This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 6000-fold) increased
 CC relative purity compared with crude extract of cells from
 CC adenovirus-transformed kidney cell line. The composition is useful for
 CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used
 CC in the isolation of human clone 28-1 which contains a fragment of the
 CC human telomerase described in the method of the invention.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGCCT 20
 DB 1 CGTTCCTCTCTCGGGCCT 20

RESULT 6

AAS09477 standard; DNA; 20 BP.

AC AAS09477;
 DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #1.

KM Human; Telomerase; vaccine; antibody; cancer; BP2H;
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

FN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.
 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

PI Weinlich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;
 PI Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations -

PS Disclosure; Column 2; 29pp; English.

XX The sequence represents an antisense oligonucleotide used in
 CC the purification of human telomerase. The invention relates
 CC to a purified human telomerase core enzyme protein comprising
 CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular
 CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.
 CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as
 CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the
 CC presence of proteins in a sample, such as cell or tissue. Identification
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
 CC Telomerase and/or telomerase associated proteins are also useful for
 CC screening compounds to identify agents that alter the association of
 CC telomerase-associated proteins, such as nucleolin or BP2H with
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGCCT 20
 DB 1 CGTTCCTCTCTCGGGCCT 20

RESULT 7
 AAS09480 standard; DNA; 20 BP.

XX AAS09480;

DT 24-OCT-2001 (first entry)

DE Antisense oligonucleotide for human telomerase, Oligo 14ab #2.

KM Human; Telomerase; vaccine; antibody; cancer; BP2H;
 KW nucleolin; antisense oligonucleotide; Oligo 14ab; ss.

OS Homo sapiens.

FN Key Location/Qualifiers

FT modified_base 1*tag= a
 FT /mod_base= C
 FT /note= "C is biotinylated"

FN US6261556-B1.

PD 17-JUL-2001.

PF 18-OCT-1999; 99US-0420056.

PR 04-APR-1997; 97US-0833377.
 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

PI Weinlich SL, Atkinson EM, Lichtsteiner SP, Vassero AP, Pruzan RA;
 PI Kealey JT;

DR WPI; 2001-450477/48.

PT Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations -

PS Disclosure; Column 16; 29pp; English.

XX The sequence represents a biotinylated antisense oligonucleotide
 CC used in the purification of human telomerase. The invention
 CC relates to a purified human telomerase core enzyme protein comprising
 CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular
 CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.
 CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as
 CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the
 CC presence of proteins in a sample, such as cell or tissue. Identification
 CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
 CC Telomerase and/or telomerase associated proteins are also useful for
 CC screening compounds to identify agents that alter the association of
 CC telomerase-associated proteins, such as nucleolin or BP2H with
 CC telomerase.

XX Sequence 20 BP; 0 A; 9 C; 4 G; 7 T; 0 other;

Query Match 66.7%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.49;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGCCT 20
 DB 1 CGTTCCTCTCTCGGGCCT 20

```

RESULT 8
AAAT42916/c
ID   AAT42916 standard; DNA; 29 BP.
XX
XX
AC   AAT42916;
XX
XX
DT   16-JUN-1997 (first entry)
XX
XX
DE   Primer 8201RN, amplifies TSP-1 and gene regulation sequences.
XX
XX
KW   gene expression; regulation; plasmid; viral infection;
KW   human T-cell leukaemia; HIV; antiviral agent; detection; cancer;
KW   gene therapy; TSP; ss.
XX
XX
OS   Synthetic.
XX
XX
PN   WO960522-A1.
XX
XX
PD   03-OCT-1996.
XX
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PF   19-MAR-1996; 96WO-JP00719.
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PR   27-APR-1995; 95JP-0104299.
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PR   24-MAR-1995; 95JP-0066559.
XX
XX
PA   (SHIO ) SHIONOGI & CO LTD.
XX
XX
PI   Igarashi H, Okumura K, Orita S, Saiga A, Sakaguchi G;
XX
XX
DR   WPI; 1996-455367/45.
XX
XX
PT   DNA molecule with gene expression regulation activity - for use in
XX
XX
PT   e.g. treatment of human T-cell leukaemia and HIV, as antiviral agent
XX
XX
PT   and for detecting cancer
XX
XX
PS   Example 1; Page 48; 77pp; Japanese.
XX
XX
SQ   The sequences given in AAT42904-16 are primers which were used in the
CC   construction of the plasmid of the invention. The plasmid contains a
CC   DNA sequence encoding the protein TSP-1 in conjunction with a DNA
CC   molecule with gene expression regulation activity. The plasmid is
CC   used for regulation of gene expression, and treatment of viral
CC   infection pref. human T-cell leukaemia and HIV. The plasmid also encodes
CC   a protein which is used as an antiviral agent, and also in a method for
CC   detecting cancer. The DNA molecule and protein have potential uses in
CC   gene therapy, and the plasmid may also have potential use in the
CC   treatment of TSP.
XX
XX
SQ   Sequence 29 BP; 8 A; 5 C; 10 G; 6 T; 0 other;
XX
XX
Query Match      46.7%; Score 14; DB 17; Length 29;
Best Local Similarity 100.0%; Pred.No.5.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 CTCCTTCCTGCGGC 19
      19 CTCCTTCCTGCGGC 6
DB

```

```

XX
XX
OS   Synthetic.
XX
XX
PN   US5527676-A.
XX
XX
PD   18-JUN-1996.
XX
XX
PF   29-MAR-1989; 89US-0330566.
XX
XX
PR   06-DEC-1989; 89US-0446584.
XX
XX
PR   29-MAR-1989; 89US-0330566.
XX
XX
PR   17-AUG-1992; 92US-0928661.
XX
XX
PR   22-MAR-1993; 93US-0047041.
XX
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
XX
PI   Baker SJ, Fearon ER, Nigro JM, Vogelstein B;
XX
XX
DR   WPI; 1996-299851/30.
XX
XX
PT   Nucleic acid assay for cancer detection - based on comparing
XX
XX
PT   neoplastic p53 gene with wild-type p53 gene
XX
XX
PS   Example 4; Column 10; 38pp; English.
XX
XX
SQ   The primer pair AAT36484/85 was used for the PCR amplification of a
CC   111 bp fragment of the human p53 gene, which may contain the tumour
CC   nude mouse xenograft (Cx3) mutation, Val 143 Ala, where the wild
CC   type codon 143 GTG is substd. with GCG. This mutation also
CC   introduces a new HhaI site (GCGC at nucleotides 427-430), so that
CC   HhaI cleavage of a PCR prod. amplified from a mutant template
CC   produces 68 and 43 nucleotide subfragments, which can be detected
CC   by gel electrophoresis separation, followed by radioactive probe
CC   hybridisation. This assay can be used to diagnose the presence of
CC   the Val 143 Ala mutation, and therefore the Cx3 tumour.
XX
XX
SQ   Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
XX
XX
Query Match      43.3%; Score 13; DB 17; Length 21;
Best Local Similarity 100.0%; Pred.No.1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      3 TTCCTTCCTTCGC 15
      1 TTCCTTCCTTCGC 13
DB

```

```

RESULT 9
AAT36484
ID   AAT36484 standard; DNA; 21 BP.
XX
XX
AC   AAT36484;
XX
XX
DT   09-OCT-1996 (first entry)
XX
XX
DE   Upstream PCR primer for p53 gene region contg. Val 143 Ala mutation.
XX
XX
KW   Primer; PCR; polymerase chain reaction; amplification; human;
KW   p53 gene; tumour; cancer; Cx3; mutation; Val 143 Ala; assay;
KW   HhaI cleavage site; detection; gel electrophoresis; diagnosis;
KW   radioactive probe hybridisation; nude mouse xenograft; ss.
XX
XX

```

```

RESULT 10
AAA72585
ID   AAA72585 standard; DNA; 21 BP.
XX
XX
AC   AAA72585;
XX
XX
DT   27-NOV-2000 (first entry)
XX
XX
DE   Upstream PCR primer for mutant p53 gene fragment amplification.
XX
XX
KW   Human; p53; chromosome 17p; neoplastic tissue detection; lung; breast;
KW   brain; colorectal; bladder; mesenchyme; prostate; stomach; cancer;
KW   tumour; leukaemia; osteosarcoma; PCR primer; ss.
XX
XX
OS   Homo sapiens.
XX
XX
PN   US6090566-A.
XX
XX
PD   18-JUL-2000.
XX
XX
PF   02-JUN-1995; 95US-0459676.
XX
XX
PR   22-MAR-1993; 93US-0047041.
XX
XX
PR   06-DEC-1989; 89US-0446584.
XX
XX
PR   17-AUG-1992; 92US-0928661.
XX
XX
PR   29-MAR-1989; 89US-0330566.
XX
XX

```

XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX
 PI Nigro JM, Fearon ER, Baker SJ, Vogelstein B;
 DR WPI; 2000-531419/48.
 XX
 PT Determining neoplastic tissue by detecting alteration in sequence of
 PT neoplastic p53 proteins and wild type p53, comparing antibody binding
 PT to p53 proteins or testing antigen complexing ability of p53 proteins
 PT
 XX
 PS Example 4; Column 10; 19pp; English.
 CC A method for determining whether a human tissue is neoplastic comprises
 CC detecting an alteration in the amino acid sequence of the p53 proteins in
 CC a neoplastic tissue and wild type tissue by comparing binding of a
 CC monoclonal antibody to the two p53 proteins and detecting loss of binding
 CC in the mutant compared to the wild type protein. Alternatively a mutation
 CC may be detected by testing the ability of the p53 proteins to bind an
 CC antigen. Several genetic alterations occur during colorectal tumour
 CC formation, the most common of which are deletions of the short arm of
 CC chromosome 17. Allelic deletions of chromosome 17p particularly in the
 CC p53 gene occur in a wide variety of cancers. The method of the invention
 CC is useful for the diagnosis of neoplastic tissues such as lung, breast,
 CC brain, colorectal, bladder, mesenchyme, prostate or stomach tumours and
 CC also in the diagnosis of leukaemia and osteosarcoma.
 CC The present sequence represents a PCR primer used to amplify a fragment
 CC of the human p53 gene from a tumour which has an allelic deletion of
 CC chromosome 17p, yet still expresses p53. The primer is used to determine
 CC that the tumour carries a point mutation at codon 143 of the p53 gene.
 CC
 SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
 Query Match 43.3%; Score 13; DB 21; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCTCTGC 15
 DB 1 TTCTCTTCTCTGC 13
 RESULT 11
 ID AAH47842 standard; DNA; 21 BP.
 AC AAH47842;
 XX
 DT 21-SEP-2001 (first entry)
 DE Human p53 PCR primer 1.
 DE Human p53; PCR primer; immunological detection; ss.
 KW Human; p53; PCR primer; immunological detection; ss.
 OS Homo sapiens.
 OS
 PN JP2001128685-A.
 PD 15-MAY-2001.
 PF 05-NOV-1999; 99JP-0315678.
 XX
 PR 05-NOV-1999; 99JP-0315678.
 PA (IATR) IATRON LAB INC.
 XX
 DR WPI; 2001-373029/39.
 PT A method for detection of variation of human p53 gene.
 PS Claim 2; Page 10; 12pp; Japanese.
 XX

CC The present sequence is that of a PCR primer for detection of variation
 CC in the human p53 gene useful to the invention. The invention relates to
 CC detection of variation in the human p53 gene with an antibody which
 CC specifically react with human p53 protein by steps of: immunological
 CC detection of a sample with immunological staining; separation of stained
 CC and un-stained cells; extraction of genome DNA from stained cells;
 CC PCR amplification of a p53 DNA fragment which may contain an area of
 CC variation of human p53 gene from the genome DNA obtained in the
 CC preceding extraction step; and analysis of the reaction product.
 CC
 SQ Sequence 21 BP; 2 A; 9 C; 2 G; 8 T; 0 other;
 Query Match 43.3%; Score 13; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTCTCTTCTCTGC 15
 DB 1 TTCTCTTCTCTGC 13

RESULT 12
 ID AAT72696/c standard; DNA; 31 BP.
 AC AAT72696;
 XX
 DT 18-SEP-1997 (first entry)
 DE Sugar biosynthesis gene eryBII PCR primer.
 DE
 XX
 KW Polyketide; glycosylation; eryBII; L-mycarose; antimicrobial;
 KW antibiotic; antifungal; fungicide; anticancer; cytostatic;
 KW anthelmintic; Saccharopolyspora erythraea; primer; PCR;
 KW polymerase chain reaction; px86; oleandomycin; ss.
 OS Synthetic.
 OS
 PN W09723630-A2.
 PD 03-JUL-1997.
 PF 23-DEC-1996; 96WO-US20238.
 XX
 PR 21-DEC-1995; 95US-0576626.
 PA (ABBO) ABBOTT LAB.
 XX
 PI Donadio S, Katz L, Staver MJ, Summers RG;
 DR WPI; 1997-351066/32.
 DE
 XX
 PT New genes involved in sugar biosynthesis and attachment - used to
 PT generate polyketide antimicrobials etc. with altered pattern of
 PT glycosylation
 PT
 PS Example 3; Page 25; 85pp; English.
 CC 2 PCR primers (AAT72696-97) were used to amplify a 1.0 kb DNA
 CC segment comprising nucleotides 2385-3410 of a Saccharopolyspora
 CC erythraea gene segment (AAT72684), covering the eryBII gene that
 CC encodes an enzyme (AAM1976) involved in L-mycarose biosynthesis.
 CC The amplified DNA was utilised in the construction of plasmid pXB4
 CC and hence of plasmid pXB6, which was used to transform Streptomyces
 CC antibioticus ATCC 11891, resulting in prodn. of the novel
 CC polyketide 3-dee-oleandomycin-3-mycarosyl oleandomycin.
 CC
 SQ Sequence 31 BP; 10 A; 8 C; 11 G; 2 T; 0 other;
 Query Match 43.3%; Score 13; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTTCTCGGGCCT 20
 |||||
 DB 19 CTTCTCGGGCCT 7

RESULT 13

ID AAL28060/c
 AAL28060 standard; DNA; 50 BP.

AC AAL28060;
 XX

DT 24-JAN-2002 (first entry)
 XX

DE Human SNP oligonucleotide #1268.
 XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

OS Homo sapiens.
 XX

PN WO200147944-A2.
 XX

PD 05-JUL-2001.
 XX

PF 28-DEC-2000; 2000WO-US35498.
 XX

PR 28-DEC-1999; 99US-0173419.
 XX

PR 27-DEC-2000; 2000US-0173419.
 XX

PA (CURA-) CURAGEN CORP.
 XX

PI Shimketa RA, Leach M;
 XX

DR WPI; 2001-465210/50.
 XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 1743; 4143pp; English.
 XX

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX

SO Sequence 50 BP; 11 A; 14 C; 8 G; 17 T; 0 other;
 XX

Query Match 43.3%; Score 13; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GGCCTGAACGGT 28
 |||||
 DB 21 GGCCTGAACGGT 9

RESULT 14
 AAL34593/c
 ID AAL34593 standard; DNA; 50 BP.
 XX

AC AAL34593;
 XX

DT 24-JAN-2002 (first entry)
 XX

DE Human SNP oligonucleotide #7801.
 XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

OS Homo sapiens.
 XX

PN WO200147944-A2.
 XX

PD 05-JUL-2001.
 XX

PF 28-DEC-2000; 2000WO-US35498.
 XX

PR 28-DEC-1999; 99US-0173419.
 XX

PR 27-DEC-2000; 2000US-0173419.
 XX

PA (CURA-) CURAGEN CORP.
 XX

PI Shimketa RA, Leach M;
 XX

DR WPI; 2001-465210/50.
 XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3646; 4143pp; English.
 XX

CC The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.
 XX

SO Sequence 50 BP; 17 A; 12 C; 15 G; 6 T; 0 other;
 XX

Query Match 43.3%; Score 13; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCTCGGGCC 19
 |||||
 DB 21 TCTTCTCGGGCC 9

RESULT 15

```

AAV41171
ID AAV41171 standard; DNA; 12 BP.
XX
XX
AC AAV41171:
XX
XX
DN 08-OCT-1998 (first entry)
XX
XX
DE RNA component of human telomerase (hTR) antisense oligo 14d.
XX
XX
KW RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX
XX
OS Synthetic.
XX
XX
OS Homo sapiens.
XX
XX
PN W09828442-A1.
XX
XX
PD 02-JUL-1998.
XX
XX
PF 19-DEC-1997; 97WO-US23619.
XX
XX
PR 20-DEC-1996; 96US-0770565.
XX
XX
PR 20-DEC-1996; 96US-0770564.
XX
XX
PA (GERO-) GERON CORP.
XX
XX
PI Kealey JT, Kim NM, Pruzan R, Weinrich SL, Wu F;
XX
XX
DR WPI; 1998-37670/32.
XX
XX
PT New polynucleotide(s) antisense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection
XX
XX
PS Claim 11; Page 65; 80pp; English.
XX
XX
CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting the
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.
XX
XX
SQ Sequence 12 BP; 0 A; 6 C; 1 G; 5 T; 0 other;

```

Query Match 40.0%; Score 12; DB 19; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5; 7e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 CGTCTCTCTCC 12
   |||||
DB 1 CGTCTCTCTCC 12

```

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

(without alignments)
2502.502 Million cell updates/sec

CGGTGA 30

residues

ameters: 841850

redicted by chance to have a

SUMMARIES

Description

1	30	100.0	30	6	AR063826	AR063826 Sequence
2	20	66.7	20	6	A84604	A84604 Sequence 14
3	20	66.7	20	6	AR063827	AR063827 Sequence
4	20	66.7	20	6	AR063836	AR063836 Sequence
5	20	66.7	20	6	AR079894	AR079894 Sequence
6	19	63.3	20	6	A84597	A84597 Sequence 7
7	19	63.3	20	6	AR079898	AR079898 Sequence
8	14	46.7	29	6	AR146661	AR146661 Sequence
9	13	43.3	20	6	AR067594	AR067594 Sequence
10	13	43.3	31	6	AR092733	AR092733 Sequence
11	13	43.3	42	6	AR024197	AR024197 Sequence
12	13	43.3	45	6	AR024198	AR024198 Sequence
13	12	40.0	12	6	AR063828	AR063828 Sequence
14	12	40.0	19	6	A35686	A35686 Synthetic h
15	12	40.0	20	6	I21035	I21035 Sequence 6
16	12	40.0	20	6	I21062	I21062 Sequence 33
17	12	40.0	24	6	AX445453	AX445453 Sequence
18	12	40.0	25	6	AX146979	AX146979 Sequence
19	12	40.0	31	6	BD002728	BD002728 Gene comp
20	12	40.0	33	6	AR162875	AR162875 Sequence
21	12	40.0	33	6	AR194025	AR194025 Sequence
22	12	40.0	36	6	A41698	A41698 Sequence 25
23	12	40.0	36	6	B59618	B59618 Human prote
24	12	40.0	36	6	I05106	I05106 Sequence 5
25	12	40.0	36	6	I07406	I07406 Sequence 18
26	12	40.0	36	6	I07637	I07637 Sequence 6
27	12	40.0	36	6	I71445	I71445 Sequence 15
28	12	40.0	37	6	AX283664	AX283664 Sequence
29	12	40.0	38	6	AX375329	AX375329 Sequence
30	12	40.0	38	6	BD006272	BD006272 Artificia
31	12	40.0	42	6	AX166899	AX166899 Sequence
32	12	40.0	43	6	A51765	A51765 Sequence 1
33	12	40.0	43	6	AR070601	AR070601 Sequence
34	12	40.0	43	6	I89763	I89763 Sequence 1
35	12	40.0	49	6	A41685	A41685 Sequence 12
36	11	36.7	11	6	AR051288	AR051288 Sequence
37	11	36.7	11	6	AR051324	AR051324 Sequence
38	11	36.7	11	6	I16936	I16936 Sequence 5
39	11	36.7	11	6	I45730	I45730 Sequence 5
40	11	36.7	12	6	AR051289	AR051289 Sequence
41	11	36.7	12	6	I16937	I16937 Sequence 6
42	11	36.7	12	6	I45731	I45731 Sequence 6
43	11	36.7	14	6	AR036791	AR036791 Sequence
44	11	36.7	17	6	AR199264	AR199264 Sequence
45	11	36.7	18	6	AR16765	AR16765 Sequence

ALIGNMENTS

RESULT 1			
AR063826			
LOCUS	AR063826	30 bp	DNA
DEFINITION	Sequence 2 from patent US 5846723.		linear
ACCESSION	AR063826		
VERSION	AR063826.1		
KEYWORDS	GI:593134		
SOURCE	.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 30)		
TITLE	Kim,N.Yoo., Wu,F., Kealey,J.T., Priznan,R. and Weinrich,S.L.		
JOURNAL	Methods for detecting the RNA component of telomerase		
FEATURES	Patent: US 5846723-A 2 08-DEC-1998;		
	Location/Qualifiers		

Source

1. 30
/organism="unknown"
BASE COUNT 4 a 10 c 8 g 8 t
ORIGIN

Query Match 100.0%; Score 30; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 8.9e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGCTGA 30
DB 1 CGTCTCTTCTCTGCGGCTGA 30

RESULT 2

LOCUS A84604 20 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 14 from Patent WO9845450.
ACCESSION A84604.1 GI:6733517
VERSION
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 14 15-OCT-1998;
GERON CORP (US)

FEATURES
Location/Qualifiers
source 1..20

BASE COUNT 0 a 9 c 4 g 7 t
ORIGIN /db_xref="taxon:32644"

Query Match 66.7%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGCT 20
DB 1 CGTCTCTTCTCTGCGGCT 20

RESULT 3

LOCUS AR063827 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5846723.
ACCESSION AR063827
VERSION AR063827.1 GI:5993135
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 3 08-DEC-1998;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 0 a 9 c 4 g 7 t
ORIGIN /organism="unknown"

Query Match 66.7%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGCT 20
DB 1 CGTCTCTTCTCTGCGGCT 20

RESULT 4

LOCUS AR063836 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5846723.
ACCESSION AR063836
VERSION AR063836.1 GI:5993144
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
TITLE Methods for detecting the RNA component of telomerase
JOURNAL Patent: US 5846723-A 12 08-DEC-1998;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 4 a 6 c 7 g 3 t
ORIGIN /organism="unknown"

Query Match 66.7%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGTGGCGGCTGAAACGGTGA 30
DB 1 CGTGGCGGCTGAAACGGTGA 20

RESULT 5

LOCUS AR079894 20 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5968506.
ACCESSION AR079894
VERSION AR079894.1 GI:10006647
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Weinrich,S.L., Atkinson,E.M. III, Lichtsreiner,S.P., Vaessero,A.P., Pruzan,R.A. and Kealey,J.T.
TITLE Purified telomerase
JOURNAL Patent: US 5968506-A 7 19-OCT-1999;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 0 a 9 c 4 g 7 t
ORIGIN /organism="unknown"

Query Match 66.7%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCTGCGGCT 20
DB 1 CGTCTCTTCTCTGCGGCT 20

RESULT 6

LOCUS A84597 20 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 7 from Patent WO9845450.
ACCESSION A84597
VERSION A84597.1 GI:6733513
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE

JOURNAL Patent: WO 9845450-A 7 15-OCT-1998;
 FEATURES GERON CORP (US)
 Location/Qualifiers
 source 1..20
 /organism="unidentified"
 /db_xref="taxon:32844"
 modified_base 1
 /note="N = BIOTINYLATED C"
 /mod_base=OTHER

BASE COUNT 0 a 8 c 4 g 7 t 1 others
 ORIGIN

Query Match 63.3%; Score 19; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTCGCGGCT 20
 Db 2 GTTCCCTTCTCGCGGCT 20

RESULT 7
 LOCUS AR079898 20 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 14 from patent US 5968506.
 ACCESSION AR079898
 VERSION AR079898.1 GI:10006651
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Weinrich,S.L., Atkinson,E.M. II, Lichtsteiner,S.P., Vassero,A.P.,
 Pruzan,R.A. and Kealey,J.T.
 TITLE Purified telomerase
 JOURNAL Patent: US 5968506-A 14 19-OCT-1999;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"

BASE COUNT 0 a 8 c 4 g 7 t 1 others
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Query Match 63.3%; Score 19; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTCGCGGCT 20
 Db 2 GTTCCCTTCTCGCGGCT 20

RESULT 8
 LOCUS ARI46661/c 29 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 14 from patent US 6218522.
 ACCESSION ARI46661
 VERSION ARI46661.1 GI:15109850
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 29)
 AUTHORS Saiga,A., Orita,S., Igarashi,H., Okumura,K. and Sakaguchi,G.
 TITLE DNA molecule relating to suppression of gene expression and novel
 JOURNAL Protein Patent: US 6218522-A 14 17-APR-2001;
 FEATURES Location/Qualifiers
 source 1..29
 /organism="unknown"

BASE COUNT 8 a 5 c 10 g 6 t
 ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CTCTCCGCGGCGC 19
 Db 19 CTCTCCGCGGCGC 6

RESULT 9
 LOCUS AR067594 20 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5851769.
 ACCESSION AR067594
 VERSION AR067594.1 GI:5998816
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Gray,J.W. and Weller,H.-U.G.
 TITLE Quantitative DNA fiber mapping
 JOURNAL Patent: US 5851769-A 1 22-DEC-1998;
 FEATURES Location/Qualifiers
 source 1..20
 /organism="unknown"

BASE COUNT 2 a 8 c 2 g 8 t
 ORIGIN

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTTCTCGC 15
 Db 1 TTCCCTTCTCGC 13

RESULT 10
 LOCUS AR092735/c 31 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 15 from patent US 5998194.
 ACCESSION AR092735
 VERSION AR092735.1 GI:10019487
 KEYWORDS

SOURCE Unknown.
 ORGANISM Unidentified.
 REFERENCE 1 (bases 1 to 31)
 AUTHORS Summers,R.G. Jr., Katz,L., Donadio,S. and Staver,M.J.
 TITLE Polyketide-associated sugar biosynthesis genes
 JOURNAL Patent: US 5998194-A 15 07-DEC-1999;
 FEATURES Location/Qualifiers
 source 1..31
 /organism="unknown"

BASE COUNT 10 a 8 c 11 g 2 t
 ORIGIN

Query Match 43.3%; Score 13; DB 6; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTTCCTGCGGCGCT 20
 Db 19 CTTCCTGCGGCGCT 7

RESULT 11
 LOCUS AR024197 42 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 8 from patent US 5795863.
 ACCESSION AR024197
 VERSION AR024197.1 GI:3977491
 KEYWORDS

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SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 42)
AUTHORS     Wolf, D.
TITLE       Recombinant agents affecting thrombosis
JOURNAL     Patent: US 5795863-A 8 18-AUG-1998;
FEATURES    Location/Qualifiers
            source          1..42
                        /organism="unknown"
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Query Match 43.3%; Score 13; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 TCCTCTCTCTCGG 16
Db          22 TCCTCTCTCTCGG 10

RESULT 12
LOCUS      AR024198      45 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 9 from patent US 5795863.
ACCESSION  AR024198
VERSION    AR024198.1 GI:3977492
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 45)
AUTHORS     Wolf, D.
TITLE       Recombinant agents affecting thrombosis
JOURNAL     Patent: US 5795863-A 9 18-AUG-1998;
FEATURES    Location/Qualifiers
            source          1..45
                        /organism="unknown"
BASE COUNT  14 a      9 c      18 g      4 t
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Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          4 TCCTCTCTCTCGG 16
Db          22 TCCTCTCTCTCGG 10

RESULT 13
LOCUS      AR063828      12 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5846723.
ACCESSION  AR063828
VERSION    AR063828.1 GI:5993136
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Kim, N. W., Wu, F., Keasley, J. T., Pruzan, R., and Weintrich, S. L.
TITLE       Methods for detecting the RNA component of telomerase
JOURNAL     Patent: US 5846723-A 4 08-DEC-1998;
FEATURES    Location/Qualifiers
            source          1..12
                        /organism="unknown"
BASE COUNT  0 a      6 c      1 g      5 t
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Query Match 40.0%; Score 12; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 CGTTCCTCTTCC 12
Db          1 CGTTCCTCTTCC 12

RESULT 14
LOCUS      A35686/C      19 bp      DNA      linear      PAT 02-DEC-1996
DEFINITION Synthetic human IFN-alpha 2 gene oligo.
ACCESSION  A35686
VERSION    A35686.1 GI:1927068
KEYWORDS
SOURCE     synthetic construct.
ORGANISM   artificial sequences.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Camde, R., and Edge, M. D.
TITLE       Analogous interferon polypeptides, process for their preparation
JOURNAL     Patent: EP 0194006-A 131 10-SEP-1986;
FEATURES    Location/Qualifiers
            source          1..19
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
BASE COUNT  4 a      5 c      6 g      4 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 CTCTCTCTCTCGG 17
Db          15 CTCTCTCTCTCGG 4

RESULT 15
LOCUS      I21035/C      20 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION Sequence 6 from patent US 5518880.
ACCESSION  I21035
VERSION    I21035.1 GI:1601389
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Leonard, W. J., Noguchi, M., and McBride, O. Wesley.
TITLE       Methods for diagnosis of XSCID and kits thereof
JOURNAL     Patent: US 5518880-A 6 21-MAY-1996;
FEATURES    Location/Qualifiers
            source          1..20
                        /organism="unknown"
BASE COUNT  8 a      1 c      9 g      2 t
ORIGIN
Query Match 40.0%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 GTTCCCTCTTCC 13
Db          18 GTTCCCTCTTCC 7

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
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Title: US-08-770-564a-3

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	72.0	25	12	US-60-427-808-363970 Sequence 363970,
2	14.4	72.0	25	12	US-60-427-808-469548 Sequence 469548,
3	14.2	71.0	22	9	US-10-310-188-18988 Sequence 18988, A
4	14.2	71.0	25	9	US-10-098-2638-114611 Sequence 114611,
5	14.2	71.0	25	9	US-10-355-577-421837 Sequence 421837,
6	14.2	71.0	25	12	US-60-427-808-324892 Sequence 324892,
7	14.2	71.0	25	12	US-60-427-808-504791 Sequence 504791,
8	14.2	71.0	25	12	US-60-427-836-347776 Sequence 347776,
9	14.2	71.0	50	5	US-09-749-2808-7801 Sequence 7801, Ap
10	14	70.0	19	1	PCT-US03-04088-26 Sequence 26, Appl
11	14	70.0	19	1	PCT-US03-04088-290 Sequence 290, Appl
12	13.8	69.0	18	9	US-10-310-188-1208 Sequence 1208, Ap
13	13.8	69.0	23	10	US-10-287-787-17323 Sequence 17323, A
14	13.8	69.0	24	10	US-10-287-787-17324 Sequence 17324, A
15	13.8	69.0	25	6	US-09-660-222-118104 Sequence 118104,
16	13.8	69.0	25	9	US-10-098-2638-23782 Sequence 23782, A
17	13.8	69.0	25	9	US-10-355-577-593121 Sequence 593121,
18	13.8	69.0	25	9	US-10-355-577-646261 Sequence 646261,
19	13.8	69.0	25	9	US-10-355-577-749521 Sequence 749521,
20	13.8	69.0	25	12	US-60-427-808-614542 Sequence 614542,

21	13.8	69.0	25	12	US-60-427-808-829890 Sequence 829890,
22	13.8	69.0	25	12	US-60-427-836-165430 Sequence 165430,
23	13.8	69.0	33	9	US-10-341-967-6 Sequence 6, Appl1
24	13.8	69.0	39	8	US-10-447-242-23365 Sequence 23365, A
25	13.8	69.0	47	9	US-10-349-143-3619 Sequence 3619, Ap
26	13.6	68.0	24	9	US-10-310-188-76918 Sequence 76918, A
27	13.6	68.0	25	7	US-09-953-570-107932 Sequence 107932,
28	13.6	68.0	25	7	US-09-954-4454-5462 Sequence 5462, Ap
29	13.6	68.0	25	9	US-10-098-2638-69585 Sequence 69585, A
30	13.6	68.0	25	12	US-60-427-808-194584 Sequence 194584,
31	13.6	68.0	25	12	US-60-427-808-636422 Sequence 636422,
32	13.6	68.0	25	12	US-60-427-808-636423 Sequence 636423,
33	13.6	68.0	25	12	US-60-427-808-636425 Sequence 636425,
34	13.6	68.0	25	12	US-60-427-836-427516 Sequence 427516,
35	13.4	67.0	50	9	US-10-325-899-38659 Sequence 3869, Ap
36	13.4	67.0	20	6	US-09-905-688-11 Sequence 11, Appl
37	13.4	67.0	21	4	US-08-825-746-11 Sequence 11, Appl
38	13.4	67.0	25	7	US-09-953-570-16633 Sequence 16633, A
39	13.4	67.0	25	7	US-09-953-570-16639 Sequence 16639, A
40	13.4	67.0	25	7	US-09-953-570-16672 Sequence 16672, A
41	13.4	67.0	25	9	US-09-953-570-16673 Sequence 16673, A
42	13.4	67.0	25	9	US-10-355-577-397620 Sequence 397620,
43	13.4	67.0	25	9	US-10-355-577-766703 Sequence 766703,
44	13.4	67.0	25	12	US-60-427-836-104000 Sequence 104000,
45	13.4	67.0	25	12	US-60-427-836-357087 Sequence 327087,
					Sequence 384194,

ALIGNMENTS

RESULT 1
US-60-427-808-363970
; Sequence 363970, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 363970
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-363970

Query Match 72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTCCTCTCTCTGCGGC 18
DB 5 TTCCTCTCTCTGCGGC 20

RESULT 2
US-60-427-808-469548
; Sequence 469548, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 469548
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-469548

Query Match 72.0%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCGCGC 17
DB 9 GTTCCTCTTCGCGC 24

RESULT 3
US-10-310-188-18988
; Sequence 18988, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18988
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-18988

Query Match 71.0%; Score 14.2; DB 9; Length 22;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGCC 19
DB 4 CTTTCCTCTTCGCGCC 22

RESULT 4
US-10-098-2638-114611
; Sequence 114611, Application US/100982638
; GENERAL INFORMATION:
; APPLICANT: Mitterman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3116.1
; CURRENT APPLICATION NUMBER: US/10/098,2638
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 114611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-098-2638-114611

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCGCGCCT 20
DB 6 GTTCCTCTTCGCGCCT 24

RESULT 5
US-10-355-577-421837/c
; Sequence 421837, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mitterman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31

; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 421837
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-355-577-421837

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGCC 19
DB 20 GTTCCTCTTCGCGCC 2

RESULT 6
US-60-427-808-324892
; Sequence 324892, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-324892

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCGCGCCT 20
DB 3 GTTCCTCTTCGCGCCT 21

RESULT 7
US-60-427-808-504791
; Sequence 504791, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 504791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-504791

Query Match 71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCCTCTTCGCGCCT 20
DB 6 GTTCCTCTTCGCGCCT 24

RESULT 8
US-60-427-836-347776/c
; Sequence 347776, Application US/60427836
; GENERAL INFORMATION:

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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 347776
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-347776

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Query Match          71.0%; Score 14.2; DB 12; Length 25;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 GTTCCTCTCTCGGCGCT 20
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DB      20 GGTCTCTCTGCTGCGGCT 2

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RESULT 9
US-09-749-2808-7801/c
; Sequence 7801, Application US/09749280B
; GENERAL INFORMATION:
; APPLICANT: Shimketers, Richard A.
; APPLICANT: Leach, Martin
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 15966-610
; CURRENT APPLICATION NUMBER: US/09/749,280B
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 7801
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43294227
US-09-749-2808-7801

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Query Match          71.0%; Score 14.2; DB 5; Length 50;
Best Local Similarity 84.2%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      1 GGTTCCTCTCTCGGCGCT 19
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DB      27 CATGCGCTCTCTGCGGCT 9

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RESULT 10
PCT-US03-04088-26/c
; Sequence 26, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

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; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
; OTHER INFORMATION: region
PCT-US03-04088-26

```

```

Query Match          70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 TCTTCTCTGCGGCT 20
        |||||
DB      19 TCTTCTCTGCGGCT 6

```

```

RESULT 11
PCT-US03-04088-290
; Sequence 290, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 290
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial

```

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-290

```

```

Query Match          70.0%; Score 14; DB 1; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.6e+04;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 TCTTCTGCGGCGCT 20
    |||||
DB 1 UCUUCUGGCGCCU 14

```

```

RESULT 12
US-10-310-188-1208/c
; Sequence 1208, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosestraGemonics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1208
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-1208

```

```

Query Match          69.0%; Score 13.8; DB 9; Length 18;
Best Local Similarity 88.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 4 TCCTCTGCGGCGCT 20
    |||||
DB 18 TCCTCTGCGGCGCT 2

```

```

RESULT 13
US-10-287-787-17323
; Sequence 17323, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J., Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 17323
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (2648691)...(2648713)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectronObjectNumber = 19213
US-10-287-787-17323

```

```

Query Match          69.0%; Score 13.8; DB 10; Length 23;
Best Local Similarity 88.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 GTTCTCTGCGGCGC 18
    |||||
DB 1 GTTCTCTGCGGCGC 17

```

```

RESULT 14
US-10-287-787-17324/c
; Sequence 17324, Application US/10287787

```

```

; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J., Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 17324
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.
; FEATURE:
; LOCATION: (2648691)...(2648713)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1921
US-10-287-787-17324

```

```

Query Match          69.0%; Score 13.8; DB 10; Length 24;
Best Local Similarity 88.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 2 GTTCTCTGCGGCGC 18
    |||||
DB 24 GTTCTCTGCGGCGC 8

```

```

RESULT 15
US-09-660-222-118104
; Sequence 118104, Application US/09660222
; GENERAL INFORMATION:
; APPLICANT: Miltmann et al.
; TITLE OF INVENTION: Methods of Genetic Analysis of Human
; FILE REFERENCE: 3102.1
; CURRENT APPLICATION NUMBER: US/09/660,222
; CURRENT FILING DATE: 2000-09-12
; PRIOR FILING DATE: 1999-11-11
; NUMBER OF SEQ ID NOS: 140981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118104
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank X56654
US-09-660-222-118104

```

```

Query Match          69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 1.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 CGTTCCTCTGCGG 17
    |||||
DB 2 CGTTCCTCTGCGG 18

```

```

Search completed: June 26, 2003, 04:15:08
Job time : 487.077 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 / Search time 2545.58 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30

Sequence: 1 CGTTCCTTCTTCGCGCGCTGAAACGTGA 30

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending Patents_MA Main:

1: /cgn2_6/ptodata/2/pna/PCTUS_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq:*
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Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	1 PCT-US97-23619-2	Sequence 2, Appl1
2	30	100.0	30	11 US-08-770-564A-2	Sequence 2, Appl1
3	30	100.0	31	9 US-08-521-634-17	Sequence 17, Appl1
4	20	66.7	20	1 PCT-US97-23619-3	Sequence 3, Appl1
5	20	66.7	20	1 PCT-US97-23619-27	Sequence 27, Appl1
6	20	66.7	20	11 US-08-770-564A-3	Sequence 3, Appl1
7	20	66.7	20	11 US-08-770-564A-15	Sequence 15, Appl1
8	16.6	55.3	50	1 PCT-US01-47856-304	Sequence 304, App
9	16.6	55.3	40	40 US-10-131-827-304	Sequence 304, App
10	16.6	55.3	50	40 US-10-131-831-304	Sequence 304, App
11	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, Appl1
12	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, Appl1
13	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, Appl1
14	16	53.3	25	36 US-09-956-604-116016	Sequence 116016, Appl1
15	15.8	52.7	25	67 US-60-234-049-104243	Sequence 104243, Appl1
16	15.8	52.7	20	41 US-10-174-020-71	Sequence 71, Appl1
17	15.8	52.7	40	1 PCT-US99-12295-97	Sequence 138, App
18	15.8	52.7	40	1 PCT-US99-12295-97	Sequence 97, Appl1
19	15.6	52.0	44	1 PCT-US02-16223-24	Sequence 24, Appl1
20	15.6	52.0	44	37 US-09-992-4308-55	Sequence 55, Appl1
21	15.6	52.0	44	41 US-10-154-460-24	Sequence 24, Appl1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 15.6 52.0 47 3 US-07-972-453-38 Sequence 38, Appl
23 15.6 52.0 49 3 US-07-972-453-40 Sequence 40, Appl
24 15.4 51.3 25 17 US-09-396-196F-14541 Sequence 14541, A
25 15.4 51.3 25 17 US-09-396-196F-71995 Sequence 71995, A
26 15.4 51.3 25 17 US-09-396-196G-14541 Sequence 14541, A
27 15.4 51.3 25 17 US-09-396-196G-71995 Sequence 71995, A
28 15.4 51.3 39 29 US-09-724-750-23365 Sequence 23365, A
29 15.4 51.3 39 61 PCT-US01-171-431-23365 Sequence 23365, A
30 15.2 50.7 24 1 PCT-US01-30828-5 Sequence 18, Appl
31 15.2 50.7 24 1 PCT-US01-42432-18 Sequence 413, App
32 15.2 50.7 32 16 US-09-225-201B-413 Sequence 413, App
33 15.2 50.7 50 1 PCT-US01-47856-4600 Sequence 4600, App
34 15.2 50.7 50 40 US-10-131-827-4600 Sequence 4600, App
35 15.2 50.7 50 40 US-10-131-831-4600 Sequence 4600, App
36 15.2 50.7 25 17 US-09-396-196F-18575 Sequence 18575, A
37 15.2 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A
38 15.2 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A
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44 15.2 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A
45 15.2 50.0 25 17 US-09-396-196F-18575 Sequence 18575, A

ALIGNMENTS

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTTCTCTTCTGCGGCGCTGAAACGCTGA 30
1 CGTTCTCTTCTGCGGCGCTGAAACGCTGA 30

LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 1..30
LOCATION: 1..30
OTHER INFORMATION: /note="oligo 14"

PCT-US97-23619-2

RESULT 1

PCT-US97-23619-2
Sequence 2, Application PC/TUS9723619

GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

RESULT 2

US-08-770-564A-2
Sequence 2, Application US/08770564A

GENERAL INFORMATION:

APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGTTCTCTTCTGCGGCGCTGAAACGCTGA 30
1 CGTTCTCTTCTGCGGCGCTGAAACGCTGA 30

RESULT 3

US-08-521-634-17/c

Sequence 17, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-17

Query Match 100.0%; Score 30; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCTGAACGGTGA 30
DB 31 CGTTCCTCTTCGCGGCTGAACGGTGA 2

RESULT 4
PCT-US97-23619-3
Sequence 3, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 14a"
PCT-US97-23619-3

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTTCGCGGCT 20
DB 1 CGTTCCTCTTCGCGGCT 20

RESULT 5
PCT-US97-23619-27
Sequence 27, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 14bc"
PCT-US97-23619-27

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGCCTGAACGGTGA 30
|||||
DB 1 CCTGGCGCCTGAACGGTGA 20

RESULT 6
US-08-770-564A-3
Sequence 3, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-15

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCTCTCTCTGGCGCT 20
|||||
DB 1 CATTCTCTCTCTGGCGCT 20

RESULT 7
US-08-770-564A-15
Sequence 15, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-15

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGCCTGAACGGTGA 30
|||||
DB 1 CCTGGCGCCTGAACGGTGA 20

RESULT 8

PCT-US01-47856-304/C
; Sequence 304, Application PC/TUS0147856
; GENERAL INFORMATION:
; APPLICANT: BIOCARDIA, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Queternous, Thomas
; APPLICANT: Johnson, Frances
; APPLICANT: Fry, Kirk
; APPLICANT: Matcuk, George
; APPLICANT: Prentice, James
; APPLICANT: Phillips, Julie
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Altman, Peter
; TITLE OF INVENTION: LEUKOCYTE EXPRESSION PROFILING
; FILE REFERENCE: 506612000140
; CURRENT APPLICATION NUMBER: PCT/US01/47856
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/241,994
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 8832
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47856-304

Query Match 55.3%; Score 16.6; DB 1; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCTTCCTGGCGCTGAACGCTG 29
DB 46 TCTTTTGTGGCTGAACGATG 24

RESULT 9
US-10-131-827-304/C
; Sequence 304, Application US/10131827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9030
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-304

Query Match 55.3%; Score 16.6; DB 40; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCTTCCTGGCGCTGAACGCTG 29
DB 46 TCTTTTGTGGCTGAACGATG 24

RESULT 10
US-10-131-831-304/C
; Sequence 304, Application US/10131831
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 304
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-304

Query Match 55.3%; Score 16.6; DB 40; Length 50;
Best Local Similarity 82.6%; Pred. No. 1.1e+04;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCTTCCTGGCGCTGAACGCTG 29
DB 46 TCTTTTGTGGCTGAACGATG 24

RESULT 11
US-09-956-604-116016/C
; Sequence 116016, Application US/09956604
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 141629
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116016
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-956-604-116016

Query Match 53.3%; Score 16; DB 36; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 CCTTTCTCTGGCGCTGAACGCT 28
DB 24 CCTATTCAGCGCGCTGAATGTT 1

RESULT 12
US-09-956-604A-116016/C
; Sequence 116016, Application US/09956604A
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
; FILE REFERENCE: 3117.1
; CURRENT APPLICATION NUMBER: US/09/956,604A
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,049
; PRIOR FILING DATE: 2000-09-19

Fri Jun 27 07:42:19 2003

us-08-770-564a-2.rnmp

Page 6

NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 116016
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
US-09-956-604A-116016

Query Match 53.3%; Score 16; DB 36; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGCT 28
DB 24 CCTATTCACGCGCGGTAAATGGT 1

RESULT 13
US-09-956-604B-116016/c
Sequence 116016, Application US/09956604B
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Escherichia coli
FILE REFERENCE: 3117.1
CURRENT APPLICATION NUMBER: US/09/956,604B
CURRENT FILING DATE: 2001-09-19
PRIOR APPLICATION NUMBER: 60/234,049
PRIOR FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 116016
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
US-09-956-604B-116016

Query Match 53.3%; Score 16; DB 36; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGCT 28
DB 24 CCTATTCACGCGCGGTAAATGGT 1

RESULT 14
US-60-234-049-104243/c
Sequence 104243, Application US/60234049
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of
FILE REFERENCE: 3117
CURRENT APPLICATION NUMBER: US/60/234,049
CURRENT FILING DATE: 2000-09-19
NUMBER OF SEQ ID NOS: 141629
SOFTWARE: Parseq for Windows Version 4.0
SEQ ID NO: 104243
LENGTH: 25
TYPE: DNA
ORGANISM: Escherichia coli
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank U00096
US-60-234-049-104243

Query Match 53.3%; Score 16; DB 67; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.7e+04;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 CCTCTTCTGCGGCGCTGAACGCT 28
DB 24 CCTATTCACGCGCGGTAAATGGT 1

RESULT 15
US-10-174-020-71
Sequence 71, Application US/10174020
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EX
FILE REFERENCE: RTS-0369
CURRENT APPLICATION NUMBER: US/10/174,020
CURRENT FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 149
SEQ ID NO: 71
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-020-71

Query Match 52.7%; Score 15.8; DB 41; Length 20;
Best Local Similarity 89.5%; Pred. No. 2e+04;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGTTCCTTCTGCGGCGC 19
DB 2 CGTTCCTTCTGCGGCGC 20

Search completed: June 25, 2003, 06:20:20
Job time : 2551.19 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 91.1952 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30
Sequence: 1 CGTTCCTCTTCTGCGGCGTGAACGCTGA 30

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCR_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCUTS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	50.0	25	9	US-10-098-263B-89577
2	15	50.0	25	9	US-10-098-263B-89578
3	14.6	48.7	39	9	US-09-832-355A-71
4	14.4	48.0	30	9	US-10-251-385-115
5	14.2	47.3	25	9	US-10-098-263B-114611
6	14	46.7	35	9	US-09-978-600-120
7	14	46.7	40	9	US-09-918-696-13
8	14	46.7	40	9	US-09-918-696-14
9	13.8	46.0	25	9	US-10-215-112-5699
10	13.8	46.0	25	9	US-10-098-263B-23782
11	13.8	46.0	25	9	US-10-098-263B-127465
12	13.8	46.0	25	9	US-10-098-263B-127466
13	13.8	46.0	36	9	US-10-023-096-3
14	13.6	45.3	25	9	US-10-098-263B-48187
15	13.6	45.3	25	9	US-10-098-263B-69585
16	13.6	45.3	25	9	US-10-098-263B-115381
17	13.6	45.3	25	9	US-10-098-263B-115382
18	13.6	45.3	28	10	US-09-225-201-40
19	13.6	45.3	45	9	US-09-995-847-26

20	13.6	45.3	46	9	US-09-995-847-25	Sequence 25, Appl
21	13.4	44.7	24	9	US-09-754-853A-683	Sequence 683, Appl
22	13.4	44.7	25	9	US-10-098-263B-61269	Sequence 61269, A
23	13.4	44.7	25	9	US-10-098-263B-62932	Sequence 62932, A
24	13.4	44.7	25	9	US-10-098-263B-96093	Sequence 96093, A
25	13.4	44.7	25	9	US-10-098-263B-96094	Sequence 96094, A
26	13.4	44.7	25	9	US-10-098-263B-106347	Sequence 106347, A
27	13.4	44.7	31	9	US-09-912-263-428	Sequence 428, Appl
28	13.2	44.0	23	9	US-09-439-429-17	Sequence 429, Appl
29	13.2	44.0	25	9	US-10-215-112-8421	Sequence 8421, Appl
30	13.2	44.0	25	9	US-10-098-263B-24011	Sequence 24011, A
31	13.2	44.0	25	9	US-10-098-263B-48100	Sequence 48100, A
32	13.2	44.0	25	9	US-09-866-108-5278	Sequence 5278, Ap
33	13.2	44.0	25	10	US-09-866-108-5279	Sequence 5279, Ap
34	13.2	44.0	25	10	US-09-866-108-5280	Sequence 5280, Ap
35	13.2	44.0	25	10	US-09-866-108-5281	Sequence 5281, Ap
36	13.2	44.0	25	10	US-09-866-108-5282	Sequence 5282, Ap
37	13.2	44.0	25	10	US-09-866-108-5283	Sequence 5283, Ap
38	13.2	44.0	25	10	US-09-866-108-5284	Sequence 5284, Ap
39	13.2	44.0	25	10	US-09-866-108-5285	Sequence 5285, Ap
40	13.2	44.0	31	9	US-09-836-705-39	Sequence 39, Appl
41	13.2	44.0	38	9	US-09-903-412-18	Sequence 18, Appl
42	13.2	44.0	38	9	US-09-780-533A-3230	Sequence 3230, Ap
43	13.2	44.0	38	9	US-09-930-423-1849	Sequence 1849, Ap
44	13.2	44.0	38	9	US-10-174-717A-18	Sequence 18, Appl
45	13.2	44.0	38	9	US-10-174-717A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-098-263B-89577
Sequence 89577, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276, 759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 89577
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-89577

Query Match 50.0%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 7 TCTTCCTGCGGCGCTGAACGCTG 29
3 TCTTCCTGCGGCGCTGAACGCTG 25

RESULT 2
US-10-098-263B-89578
Sequence 89578, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276, 759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 89578
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-89578

Query Match 50.0%; Score 15; DB 9; Length 25;
Best Local Similarity 78.3%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 TCTCTCGCGCGCTGAAACGCTG 29
DB 3 TCTCTCGCGCGCTGAAACGCTG 25

RESULT 3
US-09-832-355A-71/c
Sequence 71, Application US/09832355A
Publication No. US20030027751A1
GENERAL INFORMATION:
APPLICANT: Kovesdi, Imre
APPLICANT: Kovesdi, Paul
TITLE OF INVENTION: VEGF FUSION PROTEINS
FILE REFERENCE: 205654
CURRENT APPLICATION NUMBER: US/09/832,355A
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 126
SOFTWARE: Patentin version 3.0
SEQ ID NO 71
LENGTH: 39
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: misc feature
LOCATION: (1..71)
OTHER INFORMATION: Synthetic
US-09-832-355A-71

Query Match 48.7%; Score 14.6; DB 9; Length 39;
Best Local Similarity 81.0%; Pred. No. 2.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGCGGCTGA 22
DB 32 GTTCTCTTCTCTGCGGCTGA 12

RESULT 4
US-10-251-385-115/c
Sequence 115, Application US/10251385
Publication No. US20030105292A1
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/10/251,385
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US/09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 115
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: No. US20030105292A1e1 Sequence
US-10-251-385-115

Query Match 48.0%; Score 14.4; DB 9; Length 30;
Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGCGGCTGAAC 25
DB 28 GTTCCCATCTTGGGCTGAAGC 5

RESULT 5
US-10-098-263B-114611
Sequence 114611, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittern, Michael
APPLICANT: Mittern, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 114611
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-114611

Query Match 47.3%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 3.4e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGCGGCT 20
DB 6 GTTCTCTTCTCTGAGACT 24

RESULT 6
US-09-978-600-120/c
Sequence 120, Application US/09978600
Publication No. US20030087858A1
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, therapy and cellular and animal models for diseases associated with Mitochondrial Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESS: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/978,600
FILING DATE: 15-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 120:
US-09-978-600-120

Query Match 46.7%; Score 14; DB 9; Length 35;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 TTCTCTTCTCGGCGCTGAAC 25
DB 29 TTCTCTTCTCGGCGGACGAC 8

RESULT 7
US-09-918-696-13
Sequence 13, Application US/09918696
Publication No. US20030003076A1
GENERAL INFORMATION:
APPLICANT: Shen, Yuguao
APPLICANT: Nye, Julie
APPLICANT: Hermonston, Terry
TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE
FILE REFERENCE: ONYX1047-US
CURRENT APPLICATION NUMBER: US/09/918,696
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US 60/222,887
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ONYX-058
US-09-918-696-13

Query Match 46.7%; Score 14; DB 9; Length 40;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGGCGCTGAAC 23
DB 17 GTTCTTTTACTGCTGTGAAC 38

RESULT 8
US-09-918-696-14/c
Sequence 14, Application US/09918696
Publication No. US20030003076A1
GENERAL INFORMATION:
APPLICANT: Shen, Yuguao
APPLICANT: Nye, Julie
APPLICANT: Hermonston, Terry
TITLE OF INVENTION: ADENOVIRUS E1B-55K SINGLE AMINO ACID MUTANT AND METHODS OF USE
FILE REFERENCE: ONYX1047-US
CURRENT APPLICATION NUMBER: US/09/918,696
CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US 60/222,887
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ONYX-058; A284A MUTATION
US-09-918-696-14

Query Match 46.7%; Score 14; DB 9; Length 40;
Best Local Similarity 77.3%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGGCGCTGAAC 23
DB 24 GTTCTTTTACTGCTGTGAAC 3

RESULT 9
US-10-215-112-5699/c
Sequence 5699, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5699
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-5699

Query Match 46.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 TTCTCGGCGCTGAAC 25
DB 24 TTCTCGGCGCTGTAC 8

RESULT 10
US-10-098-263B-23782/c
Sequence 23782, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 23782
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-23782

Query Match 46.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 88.2%; Pred. No. 5.2e+03;

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Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CGTTCCTCTCTCTGGG 17
20 CGTCCCTCTCTCTGGG 4
Db

RESULT 11
US-10-098-263B-127465/C
Sequence 127465, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION: Michael
APPLICANT: Miltman; Human Microarray
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 127465
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-127465

Query Match Similarity 46.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 72.0%; Pred. No. 5.2e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 7;
QY 6 CTCTCTCTCTCTCTCTGAAACGCTGA 30
25 CTCTCTCTCTCTCTCTGAAACGCTGA 1
Db

RESULT 12
US-10-098-263B-127466/C
Sequence 127466, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION: Michael
APPLICANT: Miltman; Human Microarray
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 127466
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-127466

Query Match Similarity 46.0%; Score 13.8; DB 9; Length 25;
Best Local Similarity 72.0%; Pred. No. 5.2e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 7;
QY 6 CTCTCTCTCTCTCTCTGAAACGCTGA 30
25 CTCTCTCTCTCTCTCTGAAACGCTGA 1
Db

RESULT 13
US-10-023-096-3/C
Sequence 3, Application US/10023096
Publication No. US20020160941A1
GENERAL INFORMATION: Kruse, Marian L.
APPLICANT: Kruse, Marian L.
APPLICANT: Kureck, Tomasz
APPLICANT: Golinski, Paul D

APPLICANT: Doyle, Darrell J. Expression, and Uses of Human
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS: Price, Holman & Stern
ADDRESS: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE: 2003-01-08

CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/724,586
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
APPLICATION NUMBER: 60/276,759
FILING DATE: 2001-03-16
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C

TELEPHONE: (202) 393-5350
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NOS: 3;
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-10-023-096-3

Query Match Similarity 46.0%; Score 13.8; DB 9; Length 36;
Best Local Similarity 72.0%; Pred. No. 5.2e+03; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 7;
QY 4 TCCTCTCTCTCTCTCTGAAACGCT 28
25 TCCTCTCTCTCTCTCTGAAACGCT 1
Db

RESULT 14
US-10-098-263B-48187
Sequence 48187, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION: Michael
APPLICANT: Miltman; Human Microarray
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO: 48187
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-48187

Query Match Similarity 45.3%; Score 13.6; DB 9; Length 25;
Best Local Similarity 80.0%; Pred. No. 6.4e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

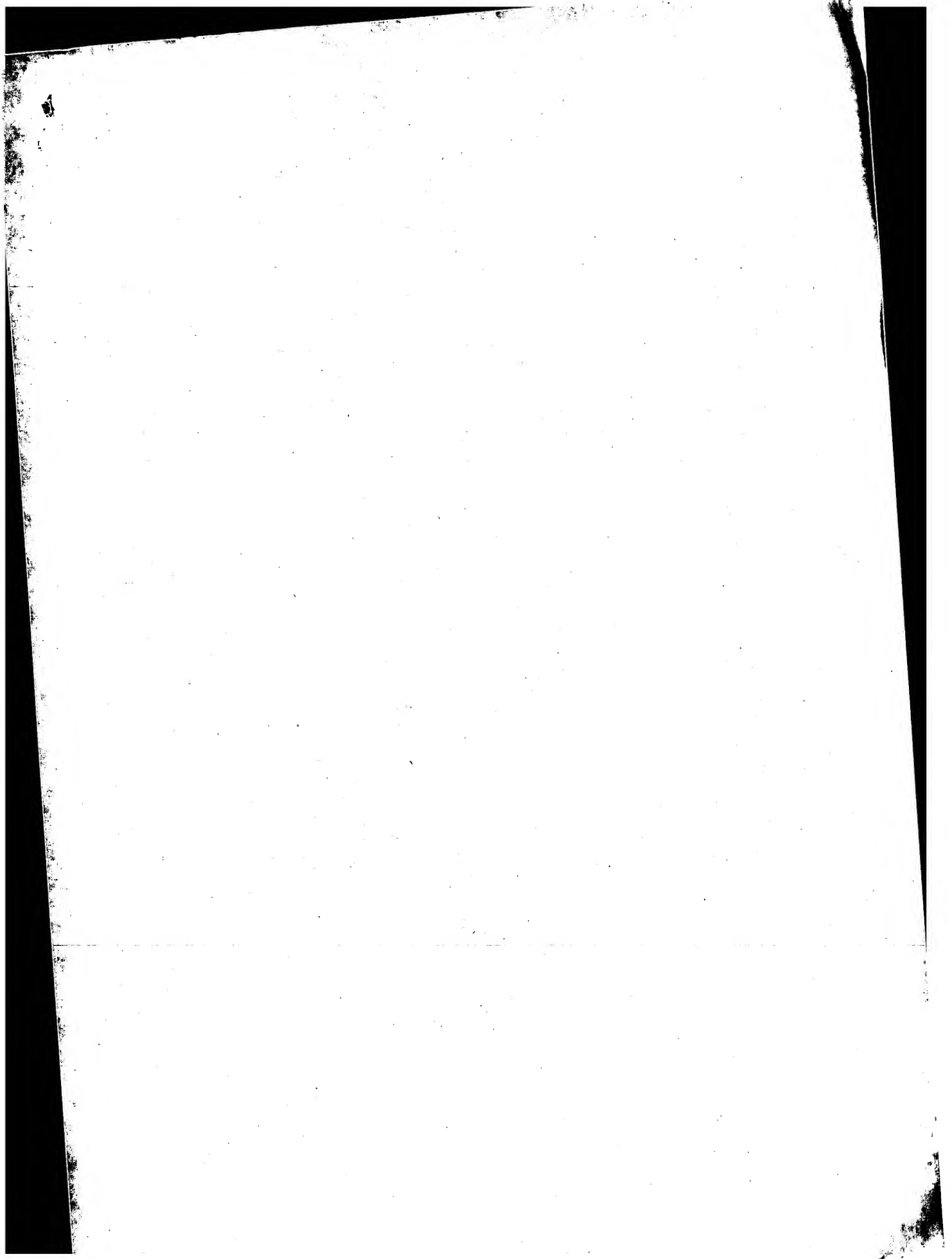
Qy 10 TCCTGCGGCTGAAACGGTG 29
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 Db 1 TCCTGCGGCTGAAACGGTTG 20

RESULT 15
 US-10-098-263B-69585/c
 ; Sequence 69585, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; PRIOR FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 69585
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-69585

Query Match 45.3%; Score 13.6; DB 9; Length 25;
 Best Local Similarity 80.0%; Pred. No. 6.4e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGTTCCTCTCTCGGCGCT 20
 |||||
 Db 21 CGTTCCTCTCTCGGCGACT 2

Search completed: June 25, 2003, 22:25:00
 Job time : 95.1952 secs



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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 45.5378 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30
Sequence: 1 CGTTCCTCTCTCTCGCGCGCTGAACGCTGA 30

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/1na/5A.COMB.seq: *
2: /cgn2_6/prodata/2/1na/5B.COMB.seq: *
3: /cgn2_6/prodata/2/1na/5A.COMB.seq: *
4: /cgn2_6/prodata/2/1na/5B.COMB.seq: *
5: /cgn2_6/prodata/2/1na/5A.COMB.seq: *
6: /cgn2_6/prodata/2/1na/5B.COMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	2	US-08-770-565-2
2	20	66.7	20	2	US-08-770-565-3
3	20	66.7	20	2	US-08-770-565-12
4	20	66.7	20	2	US-08-833-377-7
5	19	63.3	20	2	US-08-833-377-14
6	15.2	50.7	32	2	US-08-859-998-413
7	15.2	50.7	32	2	US-09-125-928-413
8	14.6	48.7	29	3	US-09-121-321-14
9	14.6	48.7	29	3	US-08-933-803A-14
10	14.6	48.7	43	2	US-08-456-566-1
11	14.6	48.7	43	2	US-09-009-044-1
12	14.4	48.0	38	1	US-08-463-115-85
13	14.4	48.0	38	1	US-08-465-388-85
14	14.4	48.0	42	1	US-08-487-037-8
15	14.2	47.3	47	4	US-09-641-638-840
16	14.2	47.3	35	4	US-08-413-740A-110
17	14.2	47.3	35	5	PCT-US95-04063-120
18	13.8	46.0	20	3	US-09-418-641-38
19	13.8	46.0	20	3	US-09-418-641-39
20	13.8	46.0	31	2	US-08-576-626A-15
21	13.8	46.0	33	4	US-08-672-213-8
22	13.8	46.0	33	4	US-08-672-213-49
23	13.8	46.0	33	4	US-08-973-131-38
24	13.8	46.0	36	3	US-08-724-586-3
25	13.8	46.0	36	4	US-09-421-632-3
26	13.8	46.0	36	4	US-09-932-190-3
27	13.8	46.0	38	1	US-08-435-350-102

28	13.8	46.0	41	1	US-08-656-716-51	Sequence 51, Appl
29	13.8	46.0	41	3	US-08-835-728D-211	Sequence 211, App
30	13.8	46.0	41	4	US-09-123-951-51	Sequence 51, Appl
31	13.8	46.0	41	4	US-09-490-558-211	Sequence 211, App
32	13.6	45.3	28	2	US-08-859-998-40	Sequence 40, Appl
33	13.6	45.3	28	4	US-09-225-928-40	Sequence 40, Appl
34	13.4	44.7	20	2	US-08-534-479-1	Sequence 1, Appl
35	13.4	44.7	31	1	US-08-039-137-22	Sequence 22, Appl
36	13.4	44.7	32	4	US-09-233-478-13	Sequence 13, Appl
37	13.2	44.0	20	3	US-09-009-913-173	Sequence 173, App
38	13.2	44.0	20	4	US-09-851-886-86	Sequence 86, Appl
39	13.2	44.0	22	1	US-08-538-875-55	Sequence 55, Appl
40	13.2	44.0	22	1	US-08-538-875-55	Sequence 59, Appl
41	13.2	44.0	23	3	US-09-176-862-17	Sequence 17, Appl
42	13.2	44.0	36	1	US-09-384-327-15	Sequence 15, Appl
43	13.2	44.0	36	1	US-08-427-097-6	Sequence 6, Appl
44	13.2	44.0	36	1	US-08-458-372-15	Sequence 15, Appl
45	13.2	44.0	36	2	US-08-878-957-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-2
; Sequence 2, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Kuzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-2
Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTTCCTCTCTCTCGCGCGCTGAACGCTGA 30

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Page 2

Db 1 CGTTCCTCTCTGCGGCTGGAACGGTGA 30

RESULT 2
US-08-770-565-3
Sequence 3, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770.565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-3
Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGTTCCTCTCTGCGGCTG 20
Db 1 CGTTCCTCTCTGCGGCTG 20
RESULT 3
US-08-770-565-12
Sequence 12, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESS: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770.565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-12
Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 CCTGCGGCTCTGGAACGGTGA 30
Db 1 CCTGCGGCTCTGGAACGGTGA 20
RESULT 4
US-08-833-377-7
Sequence 7, Application US/08833377
Patent No. 5988506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtsteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESS: TOWNSEND and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833.377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510.736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="Oligo 14ab"
US-08-833-377-7

Query Match 66.7%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTTCTCGCGCCT 20
DB 1 CGTCTCTTCTCGCGCCT 20

RESULT 5
US-08-833-377-14
Sequence 14, Application US/08833377
Patent No. 5968506
GENERAL INFORMATION:
APPLICANT: Weinrich, Scott L.
APPLICANT: Atkinson III, Edward M.
APPLICANT: Lichtesteiner, Serge P.
APPLICANT: Vassero, Alain P.
APPLICANT: Pruzan, Ronald A.
APPLICANT: Kealey, James T.
TITLE OF INVENTION: Purified Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,377
FILING DATE: 04-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/510,736
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note="N = 5' biotinylated cytidine"
FEATURE:
NAME/KEY: -
LOCATION: 1..20
OTHER INFORMATION: /note="Biotinylated Oligo 14ab"
US-08-833-377-14

Query Match 63.3%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCGCGCCT 20
DB 2 GTTCTCTTCTCGCGCCT 20

RESULT 6
US-08-859-998-413
Sequence 413, Application US/0885998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fieh & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 413:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-413

Query Match 50.7%; Score 15.2; DB 2; Length 32;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGCGCGCTGAACGCTGA 30

Db 1 TTCTGTTACTGAGAACTCAAGGCTTA 28

RESULT 7
US-09-225-928-413
Sequence 413, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
TELEPHONE/DOCKET NUMBER: 09096/002001
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 413:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 413:
US-09-225-928-413

Query Match 50.7%; Score 15.2; DB 4; Length 32;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 20; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 3 TTCTCTCTCTGCGGCTGAAGCGTGA 30
Db 1 TTCTGTTACTGAGAACTCAAGGCTTA 28

RESULT 8
US-09-121-321-14/c
Sequence 14, Application US/09121321
Patent No. 6090783
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
Orlita, Satoshi
APPLICANT: Igarashi, Hisanaga
Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF

TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,321
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/933,803
FILING DATE: 19-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"

US-09-121-321-14

Query Match 48.7%; Score 14.6; DB 3; Length 29;
Best Local Similarity 81.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 TCCTCTCTCTGCGGCTGAAG 24
Db 21 TACTCTCTCTGCGGCGCATTA 1

RESULT 9
US-08-933-803A-14/c
Sequence 14, Application US/08933803A
Patent No. 6218522
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
Orlita, Satoshi
APPLICANT: Igarashi, Hisanaga
Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,803A
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-933-803A-14

Query Match 48.7%; Score 14.6; DB 4; Length 29;
Best Local Similarity 81.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCCTCTCTCGCGCCTGAAA 24
Db 21 TACTCTCTCGCGCGCCGATA 1

RESULT 10
US-08-456-566-1
Sequence 1, Application US/08456566
Patent No. 5723122
GENERAL INFORMATION:
APPLICANT: Kohnert, Ulrich; Stern, Anne; Martin, Ulrich;
APPLICANT: Fischer, Stephan
TITLE OF INVENTION: Use Of The Protease Domain Of Human
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,566
FILING DATE: 1-JUNE-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5723122man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-456-566-1

Query Match 48.7%; Score 14.6; DB 1; Length 43;
Best Local Similarity 81.0%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCCTCTCTCGCGCCTGAAACG 27
Db 23 TCACCTCTCGCGCCTGAGACAG 43

RESULT 11
US-09-009-044-1
Sequence 1, Application US/0909044
Patent No. 5908625
GENERAL INFORMATION:
APPLICANT: Kohnert, Ulrich; Stern, Anne; Martin, Ulrich;
APPLICANT: Fischer, Stephan
TITLE OF INVENTION: Use Of The Protease Domain Of Human
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,044
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/456,566
FILING DATE: 1-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5908625man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1049
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-009-044-1

Query Match 48.7%; Score 14.6; DB 2; Length 43;
Best Local Similarity 81.0%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 TCCTCTCTCGCGCCTGAAACG 27
Db 23 TCACCTCTCGCGCCTGAGACAG 43

RESULT 12
US-08-463-115-85
Sequence 85, Application US/08463115
Patent No. 5703221
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles

STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5703221 September 23, 1993
APPLICATION NUMBER: 07/687,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-115-85

Query Match 48.0%; Score 14.4; DB 1; Length 38;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTCTTCTGCGCCCTGAACGGTG 29
DB 11 CTCTTCTGAGCAGATACGGTG 34

RESULT 13
US-08-465-388-85
Sequence 85, Application US/08465388
Patent No. 5753488
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,388
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 5753488 September 23, 1993
APPLICATION NUMBER: 07/687,502
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-388-85

Query Match 48.0%; Score 14.4; DB 1; Length 38;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 CTCTTCTGCGCCCTGAACGGTG 29
DB 11 CTCTTCTGAGCAGATACGGTG 34

RESULT 14
US-08-487-037-8/c
Sequence 8, Application US/08487037
Patent No. 5795863
GENERAL INFORMATION:
APPLICANT: Wolf, David L.
TITLE OF INVENTION: RECOMBINANT AGENTS AFFECTING THROMBOSIS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,037
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: 2803-0002.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-487-037-8

Query Match 48.0%; Score 14.4; DB 1; Length 42;
 Best Local Similarity 93.8%; Pred. No. 1e+03;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CGTTCCTCTCTGCG 16
 |||||
 DB 25 CGATCCTCTCTGCG 10

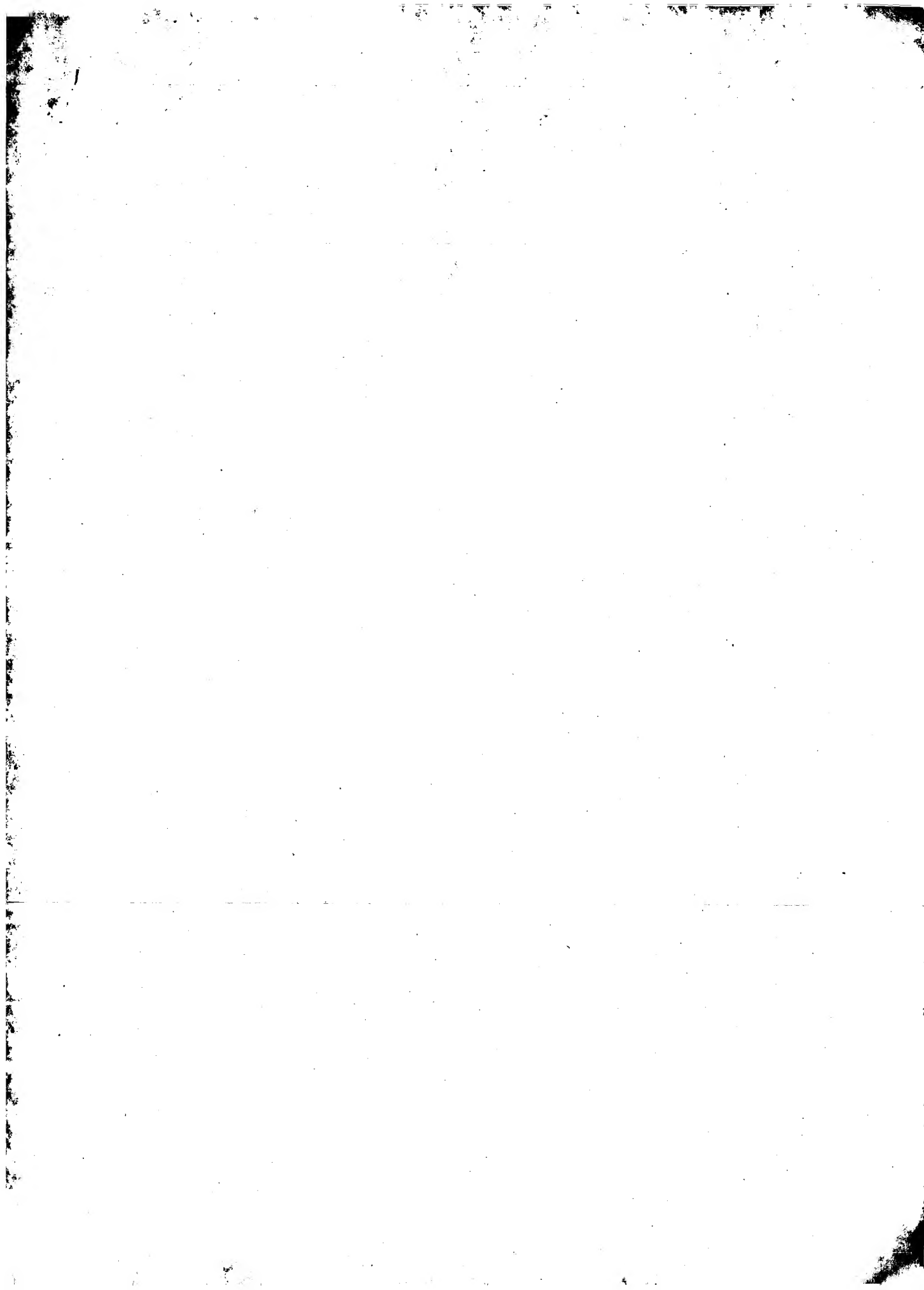
RESULT 15

US-09-641-638-840/C
 ; Sequence 840, Application US/09641638
 ; Patent No. 6432648
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumenfeld, Marta
 ; APPLICANT: Bouguetelret, Lydie
 ; APPLICANT: Chumakov, Ilya
 ; APPLICANT: Cohen, Amick
 ; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
 ; FILE REFERENCE: GENSET.051CP1
 ; CURRENT APPLICATION NUMBER: US/09/641,638
 ; PRIOR FILING DATE: 2000-08-16
 ; PRIOR APPLICATION NUMBER: US 09/502,330
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: US 60/133,200
 ; PRIOR FILING DATE: 1999-05-07
 ; PRIOR APPLICATION NUMBER: US 09/275,267
 ; PRIOR FILING DATE: 1999-03-23
 ; PRIOR APPLICATION NUMBER: US 60/119,917
 ; PRIOR FILING DATE: 1999-02-12
 ; NUMBER OF SEQ ID NOS: 1304
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 840
 ; LENGTH: 47
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: allele
 ; LOCATION: 24
 ; OTHER INFORMATION: 10-375-136 : polymorphic base C or T
 ; US-09-641-638-840

Query Match 47.3%; Score 14.2; DB 4; Length 47;
 Best Local Similarity 76.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 TCTTCTCGGCGCTGAACGG 27
 |||||
 DB 38 TGTTCGCGCGCCTRAAAGG 18

Search completed: June 25, 2003, 00:24:34
 Job time : 46.5378 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1546.73 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30
Sequence: 1 GCTTCCTCTCTCGCGCCGTGAACGTGA 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
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9: gb_est1:*
10: gb_est2:*
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13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_ges:*
18: em_ges_hum:*
19: em_ges_inv:*
20: em_ges_pln:*
21: em_ges_vrt:*
22: em_ges_fun:*
23: em_ges_mam:*
24: em_ges_mus:*
25: em_ges_other:*
26: em_ges_pro:*
27: em_ges_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
C 1	12	40.0	38 17	AZ974736 2M0249A03
C 2	12	40.0	43 17	AZ830358 2M0109M04
C 3	12	40.0	46 17	AL767395 Arabidops
C 4	11	36.7	26 17	AZ942099 2M0202C09
C 5	11	36.7	33 17	BH850686 SALK 0716
C 6	11	36.7	37 17	AZ392980 1M0155P13

Result No.	Score	Query Match length	ID	Description
C 7	11	36.7	40 17	AZ627381 1M0469H09
C 8	11	36.7	43 17	AZ419099 1M0195N23
C 9	11	36.7	45 17	AZ423992 1M0203A16
C 10	11	36.7	46 17	BT488502 603021011
C 11	11	36.7	50 9	AT102629
C 12	11	36.7	50 13	BT685073
C 13	10	33.3	21 17	AZ474246
C 14	10	33.3	27 17	AZ630179
C 15	10	33.3	28 14	N92455
C 16	10	33.3	29 17	AZ794049
C 17	10	33.3	31 14	T96040
C 18	10	33.3	32 17	AZ587757
C 19	10	33.3	32 17	AZ792853
C 20	10	33.3	32 17	BH847691
C 21	10	33.3	35 17	AZ391153
C 22	10	33.3	35 17	AZ581591
C 23	10	33.3	37 17	AZ625706
C 24	10	33.3	37 17	AZ761912
C 25	10	33.3	41 17	AZ608460
C 26	10	33.3	42 17	BH625029
C 27	10	33.3	42 17	BH640418
C 28	10	33.3	43 14	H41505
C 29	10	33.3	43 14	T77849
C 30	10	33.3	44 17	AZ761199
C 31	10	33.3	45 17	AZ657409
C 32	10	33.3	45 17	AZ843544
C 33	10	33.3	45 17	AL754108
C 34	10	33.3	46 9	AA052407
C 35	10	33.3	46 9	AT003193
C 36	10	33.3	46 14	R87862
C 37	10	33.3	47 14	H80650
C 38	10	33.3	47 17	AZ784478
C 39	10	33.3	47 17	AZ845343
C 40	10	33.3	48 17	AZ443723
C 41	10	33.3	48 17	BH840628
C 42	10	33.3	49 9	AA902962
C 43	10	33.3	50 9	AI252059
C 44	10	33.3	50 9	AU102657
C 45	10	33.3	50 9	AU102702

ALIGNMENTS

RESULT 1
LOCUS AZ974736 38 bp DNA linear GSS 27-APR-2001
DEFINITION 2M0249A03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
ACCESSION AZ974736
VERSION AZ974736.1 GI:13845963
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 38)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0249 row: A column: 03
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 38.
 Location/Qualifiers

FEATURES

source

1. 38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0249A03"
 /clone_1lb="Mouse 10kb plasmid UUGC2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

14 a 8 c 9 g 7 t

Query Match Best Local Similarity 100.0%; Score 12; DB 17; Length 38;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTTCTCG 14
 19 TTCCCTTCTCG 8

RESULT 2
 LOCUS

DEFINITION 2M0109M04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC2M0109M04 R. DNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00

Plate: 0109 row: M column: 04
 Seq primer: CACACGAGAAACGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 43.
 Location/Qualifiers

FEATURES

source

1. 43
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0109M04"
 /clone_1lb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN

7 a 10 c 8 g 18 t

Query Match Best Local Similarity 100.0%; Score 12; DB 17; Length 43;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCCTTCTCG 14
 23 TTCCCTTCTCG 34

RESULT 3
 LOCUS

DEFINITION AL767395 Arabidopsis thaliana T-DNA flanking sequence GK-219A03-014202,
 genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished
 Contact: Robert B. Weiss
 University of Utah
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

COMMENT

Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone fsk7. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1. 46
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-219A03-014202"
/clone_1ib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thaliana nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"

BASE COUNT

7 a 19 c 2 g 18 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 12; DB 17; Length 46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 GTTCTCTTCTCT 13
|||||||
29 GTTCTCTTCTCT 40

Db

RESULT 4

AZ942099 26 bp DNA linear GSS 26-APR-2001

LOCUS

AZ942099.1 26 bp DNA linear GSS 26-APR-2001

DEFINITION

2M0202C09F Mouse 10kb plasmid UUGCM library Mus musculus genomic
clone UUGCM20202C09 F, DNA sequence.

ACCESSION

AZ942099.1 GI:13805115

VERSION

KEYWORDS

SOURCE

house mouse.

ORGANISM

Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.
and Wright, D., Weis, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

Unpublished (2000)

TITLE

University of Utah Genome Center

JOURNAL

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0202 row: C column: 09

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1. 26
/organism="Mus musculus"
/strain="C57BL/6J"

BASE COUNT

10 a 0 c 16 g 0 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 11; DB 17; Length 26;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

3 TTCTCTTCTCT 13
|||||||
12 TTCTCTTCTCT 2

Db

RESULT 5

BH850686 33 bp DNA linear GSS 13-JUN-2002

LOCUS

BH850686 33 bp DNA linear GSS 13-JUN-2002

DEFINITION

SAK_071692.32.90.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SAK_071692.32.90.x, DNA
sequence.

ACCESSION

BH850686.1 GI:21421557

VERSION

KEYWORDS

SOURCE

GSS.

ORGANISM

thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; euroside II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 33)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab,
C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J., and Ecker, J.R.
A sequence-indexed library of Insertion Mutations in the
Arabidopsis Genome

Unpublished (2001)

TITLE

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (Signal)

JOURNAL

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 33
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SAK_071692.32.90.x"

/clone.lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/dna_protocols.html"

BASE COUNT
ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.8e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCCT 13
|||||
Db 19 TTCTCTTCCT 29

RESULT 6
AZ392980 37 bp DNA linear GSS 03-OCT-2000
LOCUS AZ392980/c
DEFINITION 1M0155P13 Mouse 10kb plasmid UUGCIM library Mus. musculus genomic
clone UUGCIM0155P13 R, DNA sequence.

ACCESSION AZ392980
VERSION AZ392980.1 GI:10508052
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 37)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0155 row: F column: 13
Seq primer: CACACAGGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 37.
Location/Qualifiers

FEATURES
source

1. 37
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0155P13"
/clone.lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of PMD42 (gi|4732114|gb|AF29072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match 36.7%; Score 11; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCTCTTCCT 13
|||||
Db 16 TTCTCTTCCT 6

RESULT 7
AZ627381 40 bp DNA linear GSS 13-DEC-2000
LOCUS AZ627381
DEFINITION 1M0469H09F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0469H09 F, DNA sequence.

ACCESSION AZ627381
VERSION AZ627381.1 GI:11749571
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamli,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weis
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0469 row: H column: 09
Seq primer: CGTGTAAACGACGCCACT
Class: plasmid ends
High quality sequence stop: 40.
Location/Qualifiers

FEATURES
source

1. 40
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0469H09"
/clone.lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 16 c 3 g 13 t

Query Match 36.7%; Score 11; DB 17; Length 40;
Best Local Similarity 100.0%; Pred.No. 4e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTCTCG 14
|||||
9 TCCTCTCTCG 19

RESULT 8
AZ419099/c 43 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0195N23F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION Clone UUGCIM0195N23 F, DNA sequence.
ACCESSION AZ419099
VERSION AZ419099.1 GI:10543112
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Haml,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0195 row: N column: 23
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 43.
Location/Qualifiers
1. .43

FEATURES

source

/organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0195N23"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 21 a 0 c 22 g 0 t

Query Match 36.7%; Score 11; DB 17; Length 43;
Best Local Similarity 100.0%; Pred.No. 4.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTCTTCT 13
|||||
33 TTCCTCTTCT 23

RESULT 9
AZ423992 45 bp DNA linear GSS 03-OCT-2000
LOCUS 1M0203A16F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION Clone UUGCIM0203A16 F, DNA sequence.
ACCESSION AZ423992
VERSION AZ423992.1 GI:10548005
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Haml,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausen,A. and Wright,D., Weis,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0203 row: A column: 16
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 45.
Location/Qualifiers
1. .45

FEATURES

source

/organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0203A16"
/clone_1lb="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

of pMD2 (g1473214|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 8 a 11 c 6 g 20 t
 Query Match 36.7%; Score 11; DB 17; Length 45;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 BI48502/c 46 bp mRNA linear EST 28-AUG-2001
 LOCUS 603021011f1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191659 5',
 DEFINITION mRNA sequence.
 ACCESSION BI48502
 VERSION BI48502.1 GI:15327730
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 46)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rt@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at:
 http://image.llnl.gov
 Plate: L14M11479 row: e column: 04
 High quality sequence stop: 46.
 Location/Qualifiers

FEATURES
 source 1..46
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5191659"
 /clone_id="NIH_MGC_114"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-Sport6; Site 1: NciI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Incyte Genomics). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

BASE COUNT 9 a 8 c 25 g 4 t

Query Match 36.7%; Score 11; DB 13; Length 46;
 Best Local Similarity 100.0%; Pred. No. 4.2e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTTCC 12
 DB 12 GTTCTCTTCC 2

RESULT 11
 AU102629/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AU102629 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION CA504232, mRNA sequence.
 ACCESSION AU102629
 VERSION AU102629.1 GI:13552150
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 H., Ota, T., Ito, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
 Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 EMBO Rep. 2 (5), 388-393 (2001)
 21270072
 CONTACT: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CA504232"
 /clone_id="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and
 dimethylformate treated U937 cells"

BASE COUNT 13 a 10 c 18 g 9 t

Query Match 36.7%; Score 11; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 4.3e+04;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTG 14
 DB 19 TCCTCTTCTG 9

RESULT 12
 BI685073 50 bp mRNA linear EST 18-SEP-2001
 LOCUS 603310058f1 NCI_GCAP_Mam6 Mus musculus cDNA clone IMAGE:5345990 5',
 DEFINITION mRNA sequence.
 ACCESSION BI685073
 VERSION BI685073.1 GI:15647701
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 50)
 NIH-MGC http://mgc.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rt@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNI at:

found through the I.M.A.G.E. Consortium/BLNI at:

http://image.llnl.gov
Plate: LLAM1879 row: c column: 15
High quality sequence stop: 50.
Location/Qualifiers

FEATURES
source
1. 50

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:534590"
/clone_1lb="NCI CGAP Mam6"
/sex="Female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, W.D., NIH"

BASE COUNT
ORIGIN
3 a 20 c 17 g 10 t

Query Match 36.7%; Score 11; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 TCCTGCGGCT 20
Db 6 TCCTGCGGCT 16

RESULT 13
AZ474246 21 bp DNA linear GSS 04-OCT-2000
LOCUS 1M0290L08R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0290L08 R, DNA sequence.
ACCESSION AZ474246 GI:10632371
VERSION AZ474246.1
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0290 row: L column: 08
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers

FEATURES
source
1. 21

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0290L08"
/clone_1lb="Mouse 10kb plasmid UGCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (GI:473214|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT
ORIGIN
9 a 5 c 4 g 3 t

Query Match 33.3%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 GGCTGGAAC 25
Db 4 GGCTGGAAC 13

RESULT 14
AZ630179 27 bp DNA linear GSS 13-DEC-2000
LOCUS 1M0483B10R Mouse 10kb plasmid UGCGM library Mus musculus genomic
DEFINITION clone UGCGM0483B10 R, DNA sequence.
ACCESSION AZ630179 GI:11752369
VERSION AZ630179.1
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0483 row: B column: 10
Seq primer: CACACAGAAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source
1. 27

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGM0483B10"
/clone_1lb="Mouse 10kb plasmid UGCGM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/nbases/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (914732114[SP|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 18 c 0 g 9 t

ORIGIN

Query Match 33.3%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 TTCTCTTCC 12
|||||||
Db 4 TTCTCTTCC 13

RESULT 15
N92455 28 bp mRNA linear EST 20-AUG-1996
LOCUS Zb63h01.s1 Soares fetal lung NBHL19W Homo sapiens cDNA clone
DEFINITION IMAGE:308305.3, similar to SB:X06323 cds1 MITOCHONDRIAL 60S
RIBOSOMAL PROTEIN L3 (HUMAN);, mRNA sequence.

ACCESSION N92455
VERSION N92455.1 GI:1264764
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 28)

AUTHORS

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Scheilberg, K., Soares, M. B., Tan, F., Thierry-Mieg, J., Trevas, B., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Warr, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

SOURCE

1
28
Location/Qualifiers
1
28
/organism="Homo sapiens"
/db_xref="GDB:125178"
/db_xref="taxon:9606"
/clone="IMAGE:308305"
/clone_lib="Soares_fetal_lung_NBHL19W"
/dev_stage="19 weeks"

/lab_host="DH10B (ampicillin resistant)"
/note="Organ: lung; Vector: pT73D (Pharmacia) with a modified polylinker; Site-1: Not I; Site-2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5'-TGTTACCAATCTGAGTGGAGCGCCGCAATTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Patricia Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

BASE COUNT 7 a 9 c 4 g 8 t

ORIGIN

Query Match 33.3%; Score 10; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GTTCTCTTC 11
|||||||
Db 3 GTTCTCTTC 12

Search completed: June 23, 2003, 10:10:14
Job time: 1554.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comphen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 / Search time 1316.89 seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30

Sequence: 1 CTTCTCTCTCTCGCGCCTGAACGTGA 30

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending_Patents_NA_New:*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	60.0	19	1	PCT-US03-04088-26
2	18	60.0	19	1	PCT-US03-04088-290
3	13	43.3	20	6	US-09-905-688-11
4	13	43.3	20	6	US-10-310-188-34029
5	13	43.3	21	4	US-08-825-746-11
6	13	43.3	25	7	US-09-954-445A-45573
7	13	43.3	25	9	US-10-355-577-198249
8	13	43.3	25	9	US-10-355-577-198680
9	13	43.3	25	9	US-10-355-577-223567
10	13	43.3	25	9	US-10-355-577-364423
11	13	43.3	25	9	US-10-355-577-422449
12	13	43.3	25	9	US-10-355-577-498091
13	13	43.3	25	12	US-60-417-190-11946
14	13	43.3	25	12	US-60-417-190-11947
15	13	43.3	25	12	US-60-417-190-48932
16	13	43.3	25	12	US-60-417-190-48933
17	13	43.3	25	12	US-60-417-190-48939
18	13	43.3	25	12	US-60-417-190-48940
19	13	43.3	25	12	US-60-427-808-112959
20	13	43.3	25	12	US-60-427-808-218754

21	13	43.3	25	12	US-60-427-808-275929	Sequence 275929,
22	13	43.3	25	12	US-60-427-808-469548	Sequence 469548,
23	13	43.3	25	12	US-60-427-808-564830	Sequence 564830,
24	13	43.3	25	12	US-60-427-836-440978	Sequence 440978,
25	13	43.3	25	12	US-60-427-836-455883	Sequence 455883,
26	13	43.3	25	12	US-60-427-836-459003	Sequence 549003,
27	13	43.3	25	12	US-60-427-836-599225	Sequence 599225,
28	13	43.3	25	12	US-60-427-836-683575	Sequence 683575,
29	13	43.3	25	13	US-60-470-475-51737	Sequence 51737, A
30	13	43.3	25	13	US-60-470-475-51738	Sequence 51738, A
31	13	43.3	25	13	US-60-470-475-55703	Sequence 55703, A
32	13	43.3	25	13	US-60-470-475-57853	Sequence 57853, A
33	13	43.3	25	13	US-60-470-475-61267	Sequence 61267, A
34	13	43.3	25	13	US-60-470-475-61272	Sequence 61272, A
35	13	43.3	25	13	US-60-470-475-73706	Sequence 73706, A
36	13	43.3	25	13	US-60-470-475-89881	Sequence 98881, A
37	13	43.3	29	9	US-10-294-719-499	Sequence 499, App
38	13	43.3	50	5	US-09-749-280B-1268	Sequence 1268, Ap
39	13	43.3	50	5	US-09-749-280B-7801	Sequence 7801, Ap
40	13	43.3	50	9	US-10-325-899-3869	Sequence 3869, Ap
41	12	40.0	15	10	US-10-367-892-6314	Sequence 6314, Ap
42	12	40.0	15	10	US-10-367-892-19280	Sequence 19280, A
43	12	40.0	19	9	US-10-293-338-4597	Sequence 4597, Ap
44	12	40.0	20	1	PCT-US02-24310-154	Sequence 154, App
45	12	40.0	20	9	US-10-303-778-15311	Sequence 15311, A

ALIGNMENTS

RESULT 1
PCT-US03-04088-26/c

Sequence 26, Application PC/TUS0304088

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, James

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

FILE REFERENCE: 02-708-A (400/080)

CURRENT APPLICATION NUMBER: PCT/US03/04088

CURRENT FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: US 60/396,600

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

NUMBER OF SEQ ID NOS: 626

SOFTWARE: PatentIn version 3.2

SEQ ID NO 26

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/sRNA sense

PCT-US03-04088-26

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 8.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TCTTCTGCGGCTGAAA 24
Db 19 TCTTCTGCGGCTGAAA 2

RESULT 2
PCT-US03-04088-290
Sequence 290, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: McSwigen, James
APPLICANT: Beigelman, Leonid
TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT FILING DATE: 2003-04-28
PCT/US03/04088
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 290
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: sRNA antisense
PCT-US03-04088-290

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 8.7;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 7 TCTTCTGCGGCTGAAA 24
Db 1 UCUCUCGCGGCTGAAA 18

RESULT 3
US-09-905-688-11
Sequence 11, Application US/0905688
GENERAL INFORMATION:
APPLICANT: CZERWIAK, BOGDAN
TITLE OF INVENTION: METHODS OF DETECTING AND DIAGNOSING BLADDER CANCER AND
IDENTIFYING NEOPLASTIC PROGRESSION
FILE REFERENCE: UTSC:663US
CURRENT APPLICATION NUMBER: US/09/905,688
CURRENT FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-905-688-11

Query Match 43.3%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTCTGC 15
Db 1 TTCTCTTCTCTGC 13

RESULT 4
US-10-310-188-34029/c
Sequence 34029, Application US/10310188
GENERAL INFORMATION:
APPLICANT: RosettaGenomics
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
FILE REFERENCE: 47487
CURRENT APPLICATION NUMBER: US/10/310,188
CURRENT FILING DATE: 2002-12-19
NUMBER OF SEQ ID NOS: 86841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34029
LENGTH: 20
TYPE: DNA
ORGANISM: Homo sapiens
US-10-310-188-34029

Query Match 43.3%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 TTCTCTTCTCTGC 15
Db 19 TTCTCTTCTCTGC 7

RESULT 5
US-08-825-746-11
Sequence 11, Application US/08825746
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne
APPLICANT: Pearson, Eric
APPLICANT: Nigro, J. A. M.
TITLE OF INVENTION: Methods for Restoring Wild-Type p53 Gene Function
FILE REFERENCE: 001107.05677
CURRENT APPLICATION NUMBER: US/08/825,746
CURRENT FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 08/035,366
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/860,758
PRIOR FILING DATE: 1992-03-21
PRIOR APPLICATION NUMBER: 07/715,182
PRIOR FILING DATE: 1991-06-14
PRIOR APPLICATION NUMBER: 07/928,661
PRIOR FILING DATE: 1992-08-17
PRIOR APPLICATION NUMBER: 07/446,584
PRIOR FILING DATE: 1989-12-06
PRIOR APPLICATION NUMBER: 07/330,566
PRIOR FILING DATE: 1989-03-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-08-825-746-11

Query Match 43.3%; Score 13; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTCCTTCTCTGC 15
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 DB 1 TTCCTTCTCTGC 13

RESULT 6
 US-09-954-445A-45573/c
 ; Sequence 45573, Application US/09954445A
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Arabidopsis Thaliana
 ; FILE REFERENCE: 3116.1
 ; CURRENT APPLICATION NUMBER: US/09/954,445A
 ; CURRENT FILING DATE: 2000-09-17
 ; PRIOR APPLICATION NUMBER: 60/233,620
 ; PRIOR FILING DATE: 2000-09-18
 ; NUMBER OF SEQ ID NOS: 131820
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 45573
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-954-445A-45573

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 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTCTCTCTCT 13
 |||||
 DB 15 CGTCTCTCTCT 3

RESULT 7
 US-10-355-577-198249
 ; Sequence 198249, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 198249
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-355-577-198249

Query Match 43.3%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTTCTCTCTCTG 14
 |||||
 DB 9 GTTCTCTCTCTG 21

RESULT 8
 US-10-355-577-198680
 ; Sequence 198680, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 198680
 ; LENGTH: 25
 ; TYPE: DNA

; ORGANISM: Homo sapien
 US-10-355-577-198680

Query Match 43.3%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAACG 26
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 DB 13 GCGGCGCTGAACG 25

RESULT 9
 US-10-355-577-223567/c
 ; Sequence 223567, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 223567
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-355-577-223567

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 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCTCTTCTCTCGG 17
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 DB 25 CCTCTTCTCTCGG 13

RESULT 10
 US-10-355-577-364423
 ; Sequence 364423, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31
 ; NUMBER OF SEQ ID NOS: 997516
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO: 364423
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-355-577-364423

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 Best Local Similarity 100.0%; Pred. No. 3.9e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 GCCTGAACGGTG 29
 |||||
 DB 7 GCCTGAACGGTG 19

RESULT 11
 US-10-355-577-422449
 ; Sequence 422449, Application US/10355577
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltmann, Michael
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
 ; FILE REFERENCE: 3121
 ; CURRENT APPLICATION NUMBER: US/10/355,577
 ; CURRENT FILING DATE: 2003-01-31

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; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422449
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-422449

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Query Match      43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      14 GCGGCTGAAACG 26
DB      3 GCGGCTGAAACG 15

```

```

RESULT 12
US-10-355-577-498091
; Sequence 498091, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittern, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 498091
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-498091

```

```

Query Match      43.3%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 GTTCCTCTCCTG 14
DB      3 GTTCCTCTCCTG 15

```

```

RESULT 13
US-60-417-190-13946
; Sequence 13946, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13946
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-13946

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```

Query Match      43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCCTCTTCTGCG 16
DB      2 TCCTCTTCTGCG 14

```

```

RESULT 14
US-60-417-190-13947

```

```

; Sequence 13947, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 13947
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-13947

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```

Query Match      43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      4 TCCTCTTCTGCG 16
DB      1 TCCTCTTCTGCG 13

```

```

RESULT 15
US-60-417-190-48932
; Sequence 48932, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 48932
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-417-190-48932

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```

Query Match      43.3%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 TTCTCTTCTGCG 15
DB      13 TTCTCTTCTGCG 25

```

```

Search completed: June 23, 2003, 19:12:10
Job time : 1319.89 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comogen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 2516.18 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564a-2

Perfect score: 30
Sequence: 1 CGTTCCTCTTCCCTGCGGCGCTGAACGGTGA 30

Scoring table: OLIGO NUC
Gapex 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending_Patents_NA_Main:*

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Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	PCT-US97-23619-2	Sequence 2, Appl 1
2	30	100.0	30	US-08-770-564a-2	Sequence 2, Appl 1
3	30	100.0	31	US-08-521-634-17	Sequence 17, Appl 1
4	20	66.7	20	PCT-US97-23619-3	Sequence 3, Appl 1
5	20	66.7	20	PCT-US97-23619-7	Sequence 27, Appl 1
6	20	66.7	20	US-08-770-564a-3	Sequence 3, Appl 1
7	20	66.7	20	US-08-770-564a-15	Sequence 15, Appl 1
8	14	46.7	25	US-09-396-196F-119937	Sequence 119937, A
9	14	46.7	25	US-09-396-196G-119937	Sequence 119937, A
10	14	46.7	25	US-09-956-584-18655	Sequence 18655, A
11	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
12	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
13	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
14	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
15	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
16	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
17	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
18	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
19	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
20	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
21	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
22	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
23	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
24	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
25	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
26	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
27	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
28	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
29	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
30	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
31	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
32	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
33	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
34	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
35	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
36	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
37	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
38	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
39	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
40	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
41	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
42	14	46.7	25	US-09-956-584-237631	Sequence 237631, A
43	14	46.7	25	US-09-956-584-237631	Sequence 237631, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 13 43.3 25 79 US-60-353-987-223567 Sequence 223567,
23 13 43.3 25 79 US-60-353-987-364423 Sequence 364423,
24 13 43.3 25 79 US-60-353-987-422449 Sequence 422449,
25 13 43.3 25 79 US-60-353-987-498091 Sequence 498091,
26 13 43.3 31 18 US-09-454-623-15 Sequence 15, Appl
27 13 43.3 42 26 US-09-671-346-8 Sequence 8, Appl
28 13 43.3 45 26 US-09-671-346-9 Sequence 9, Appl
29 13 43.3 50 40 PCT-US01-47856-3869 Sequence 3869, Ap
30 13 43.3 50 40 US-10-131-827-3869 Sequence 3869, Ap
31 13 43.3 50 40 US-10-131-827-3869 Sequence 3869, Ap
32 12 40.0 12 11 PCT-US97-23619-4 Sequence 4, Appl
33 12 40.0 12 11 US-08-770-564A-4 Sequence 4, Appl
34 12 40.0 15 1 PCT-US01-06051-14 Sequence 14, Appl
35 12 40.0 15 1 PCT-US02-25940-6314 Sequence 6314, Ap
36 12 40.0 15 1 PCT-US02-25940-19280 Sequence 19280, A
37 12 40.0 15 1 PCT-US02-25942-1021 Sequence 1021, Ap
38 12 40.0 15 1 PCT-US02-25942-1585 Sequence 1585, Ap
39 12 40.0 15 42 US-10-227-583-6318 Sequence 6318, Ap
40 12 40.0 15 42 US-10-227-583-19280 Sequence 19280, A
41 12 40.0 15 42 US-10-227-587-1021 Sequence 1021, Ap
42 12 40.0 15 42 US-10-227-587-1585 Sequence 1585, Ap
43 12 40.0 20 1 PCT-US02-14110-86 Sequence 86, Appl
44 12 40.0 20 15 US-09-198-452A-3651 Sequence 3651, Ap
45 12 40.0 20 17 US-09-366-483B-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
PCT-US97-23619-2
Sequence 2, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
TITLE OF INVENTION: RNA Component of Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PCT-US97-23619-2 /note="oligo 14"

QY 1 CGTTCCTCTTCCTGCGGCTGAACGGTGA 30
DB 1 CGTTCCTCTTCCTGCGGCTGAACGGTGA 30

RESULT 2
US-08-770-564A-2
Sequence 2, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-00220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-2

Query Match 100.0%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGTTCCTCTTCCTGCGGCTGAACGGTGA 30
DB 1 CGTTCCTCTTCCTGCGGCTGAACGGTGA 30

RESULT 3
US-08-521-634-17/c


```
/ Sequence 17, Application US/08521634
/ GENERAL INFORMATION:
/ APPLICANT: Villeponteau, Bryant
/ APPLICANT: Peng, Junli
/ APPLICANT: Funk, Walter
/ APPLICANT: Andrews, William
/ TITLE OF INVENTION: Mammalian Telomerase
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew
/ STREET: One Market Plaza, Steuart Tower, Suite 2000
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/521,634
/ FILING DATE: 31-AUG-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/482,115
/ FILING DATE: 7-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/472,802
/ FILING DATE: 7-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 7-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dunn, Tracy J.
/ REGISTRATION NUMBER: 34,587
/ REFERENCE/DOCKET NUMBER: 15389-000850
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (oligonucleotide)
/ US-08-521-634-17

Query Match      100.0%; Score 30; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      31 CGTTCCTCTTCGCGGCGCTGAAGGTGA 2
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RESULT 4

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PCT-US97-23619-3
/ Sequence 3, Application PC/TUS9723619
/ GENERAL INFORMATION:
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/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ TITLE OF INVENTION: Methods for Detecting and Inhibiting the
/ TITLE OF INVENTION: RNA Component of Telomerase
```

```
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/23619
/ FILING DATE: Not yet assigned
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/770,564
/ FILING DATE: 20-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/770,565
/ FILING DATE: 20-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 15389-27PC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..20
/ OTHER INFORMATION: /note="oligo 14ab"
/ PCT-US97-23619-3

Query Match      66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB      1 CGTTCCTCTTCGCGGCGCT 20
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RESULT 5

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PCT-US97-23619-27
/ Sequence 27, Application PC/TUS9723619
/ GENERAL INFORMATION:
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/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ APPLICANT:
/ TITLE OF INVENTION: Methods for Detecting and Inhibiting the
/ TITLE OF INVENTION: RNA Component of Telomerase
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: 1..20
LOCATION: 1..20
OTHER INFORMATION: /note="oligo 14pc"
PCT-US97-23619-27

Query Match 66.7%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGCGGCTGAACGGTGA 30
DB 1 CCTGCGGCTGAACGGTGA 20

RESULT 6
US-08-770-564A-3
Sequence 3, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-564A-3

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGTTCCTCTCTCGGGCCT 20
DB 1 CGTTCCTCTCTCGGGCCT 20

RESULT 7
US-08-770-564A-15
Sequence 15, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-15

Query Match 66.7%; Score 20; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGCGGCTGAACGGTGA 30
DB 1 CCTGCGGCTGAACGGTGA 20

RESULT 8

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US-09-396-196F-119937/C
; Sequence 119937, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-119937

```

```

Query Match          46.7%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 GTTCCCTCTCTGTC 15
    |||||
DB 25 GTTCCCTCTCTGTC 12

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RESULT 9
US-09-396-196G-119937/C
; Sequence 119937, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-119937

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Query Match          46.7%; Score 14; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 GTTCCCTCTCTGTC 15
    |||||
DB 25 GTTCCCTCTCTGTC 12

```

```

RESULT 10
US-09-956-584-18655/C
; Sequence 18655, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887

```

```

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 18655
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-18655

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```

Query Match          46.7%; Score 14; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGTTCCTCTCTG 14
    |||||
DB 18 CGTTCCTCTCTG 5

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RESULT 11
US-09-956-584-237631/C
; Sequence 237631, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 237631
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-237631

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```

Query Match          46.7%; Score 14; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 17 GCCTGAACGGTGA 30
    |||||
DB 24 GCCTGAACGGTGA 11

```

```

RESULT 12
US-60-234-017-52883/C
; Sequence 52883, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank U41285
US-60-234-017-52883

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```

Query Match          46.7%; Score 14; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 CGTTCCTCTCTG 14
    |||||
DB 18 CGTTCCTCTCTG 5

```

RESULT 13
US-60-234-017-208542/c
Sequence 208542, Application US/60234017
GENERAL INFORMATION:
APPLICANT: Miltmann, M
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis of Mus
FILE REFERENCE: 3115
CURRENT APPLICATION NUMBER: US/60/234.017
CURRENT FILING DATE: 2000-09-20
NUMBER OF SEQ ID NOS: 605887
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 208542
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank A1465630
US-60-234-017-208542

Query Match 46.7%; Score 14; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 GCCTGAACGGTGA 30
Db 24 GCCTGAACGGTGA 11

RESULT 14
US-08-913-665-14/c
Sequence 14, Application US/08913665
GENERAL INFORMATION:
APPLICANT: Saiga, Akihiko
APPLICANT: Orita, Satoshi
APPLICANT: Igatahshi, Hisanaga
APPLICANT: Okumura, Kouichi
APPLICANT: Sakaguchi, Gaku
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & BEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913.665
FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"
US-08-913-665-14

Query Match 46.7%; Score 14; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CTCCTCCTCGGCC 19
Db 19 CTCCTCCTCGGCC 6

RESULT 15
PCT-US02-18427-11
Sequence 11, Application PC/TUS0218427
GENERAL INFORMATION:
APPLICANT: JOHNSTON, DENNIS
APPLICANT: CZERWIAK, BOGDAN
TITLE OF INVENTION: METHODS OF DETECTING, DIAGNOSING AND TREATING CANCER
TITLE OF INVENTION: AND IDENTIFYING NEOPLASTIC PROGRESSION
FILE REFERENCE: UTFC-712-MO
CURRENT APPLICATION NUMBER: PCT/US02/18427
CURRENT FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: 60/297,813
PRIOR FILING DATE: 2001-06-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
PCT-US02-18427-11

Query Match 43.3%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTCCTCTCTCTCC 15
Db 1 TTCCTCTCTCTCC 13

Search completed: June 23, 2003, 16:08:16
Job time : 2520.25 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 241.076 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-2

Perfect score: 30
Sequence: 1 CGTTCCTCTCTCGCGCCTGAAACGTGA 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PTCTUS_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	40.0	20	US-10-139-496-25	Sequence 25, Appl
C 2	12	40.0	24	US-09-940-185-1908	Sequence 1908, Ap
C 3	12	40.0	25	US-09-754-853A-686	Sequence 686, App
C 4	12	40.0	25	US-10-098-263B-49318	Sequence 49318, A
C 5	12	40.0	25	US-10-098-263B-114611	Sequence 114611,
C 6	12	40.0	38	US-09-903-412-18	Sequence 18, Appl
C 7	12	40.0	38	US-09-930-423-2074	Sequence 2074, Ap
C 8	12	40.0	38	US-10-174-171A-18	Sequence 18, Appl
C 9	12	40.0	38	US-09-096-749A-18	Sequence 18, Appl
C 10	11	36.7	12	US-09-938-744-2	Sequence 2, Appl
C 11	11	36.7	18	US-09-969-373-1923	Sequence 1923, Ap
C 12	11	36.7	19	US-09-879-389B-4	Sequence 4, Appl
C 13	11	36.7	19	US-09-902-563-38	Sequence 38, Appl
C 14	11	36.7	19	US-09-902-563-41	Sequence 41, Appl
C 15	11	36.7	19	US-10-096-255-38	Sequence 38, Appl
C 16	11	36.7	19	US-10-096-255-41	Sequence 41, Appl
C 17	11	36.7	19	US-09-947-770-26	Sequence 26, Appl
C 18	11	36.7	20	US-09-919-197-23	Sequence 23, Appl
C 19	11	36.7	24	US-10-101-487-12	Sequence 12, Appl

20	11	36.7	24	9	US-10-101-487-13	Sequence 13, Appl
21	11	36.7	24	10	US-09-818-954A-4	Sequence 4, Appl
22	11	36.7	25	9	US-09-943-388-16	Sequence 16, Appl
23	11	36.7	25	9	US-09-990-940-48	Sequence 48, Appl
C 24	11	36.7	25	9	US-10-215-112-2042	Sequence 2042, Ap
C 25	11	36.7	25	9	US-10-215-112-5699	Sequence 5699, Ap
C 26	11	36.7	25	9	US-10-215-112-10249	Sequence 10249, A
C 27	11	36.7	25	9	US-10-215-112-10695	Sequence 10695, A
C 28	11	36.7	25	9	US-10-215-112-12736	Sequence 12736, A
C 29	11	36.7	25	9	US-10-098-263B-9249	Sequence 9249, Ap
C 30	11	36.7	25	9	US-10-098-263B-17568	Sequence 17568, A
C 31	11	36.7	25	9	US-10-098-263B-24096	Sequence 24096, A
C 32	11	36.7	25	9	US-10-098-263B-48100	Sequence 48100, A
C 33	11	36.7	25	9	US-10-098-263B-38102	Sequence 38102, A
C 34	11	36.7	25	9	US-10-098-263B-38729	Sequence 38729, A
C 35	11	36.7	25	9	US-10-098-263B-48043	Sequence 48043, A
C 36	11	36.7	25	9	US-10-098-263B-48044	Sequence 48044, A
C 37	11	36.7	25	9	US-10-098-263B-48100	Sequence 48100, A
C 38	11	36.7	25	9	US-10-098-263B-50057	Sequence 50057, A
C 39	11	36.7	25	9	US-10-098-263B-50058	Sequence 50058, A
C 40	11	36.7	25	9	US-10-098-263B-56723	Sequence 56723, A
C 41	11	36.7	25	9	US-10-098-263B-56724	Sequence 56724, A
C 42	11	36.7	25	9	US-10-098-263B-67054	Sequence 67054, A
C 43	11	36.7	25	9	US-10-098-263B-81647	Sequence 81647, A
C 44	11	36.7	25	9	US-10-098-263B-81648	Sequence 81648, A
C 45	11	36.7	25	9	US-10-098-263B-96226	Sequence 96226, A

ALIGNMENTS

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RESULT 1
US-10-139-496-25/c
; Sequence 25, Application US/10139496
; Publication No. US20030082646A1
; GENERAL INFORMATION:
; APPLICANT: Carey, Thomas E.
; APPLICANT: Naif, Thankam S.
; APPLICANT: Gray, Jennifer P.
; TITLE OF INVENTION: Antigenic Targets of Autoimmune Sensorineural Hearing Loss (AISHL)
; FILE REFERENCE: UM-6982
; CURRENT APPLICATION NUMBER: US/10/139,496
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/222,179
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-139-496-25

Query Match          40.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTCCCTCTCTCG 14
Db      17 TTCCCTCTCTCG 6

RESULT 2
US-09-940-185-1908/c
; Sequence 1908, Application US/09940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides

```

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/ FILE REFERENCE: A-69605-1
/ CURRENT APPLICATION NUMBER: US/09/940.185
/ CURRENT FILING DATE: 2001-08-27
/ PRIOR APPLICATION NUMBER: US 60/227,948
/ PRIOR FILING DATE: 2000-08-25
/ PRIOR APPLICATION NUMBER: US 60/228,854
/ PRIOR FILING DATE: 2000-08-29
/ NUMBER OF SEQ ID NOS: 4768
/ SOFTWARE: Patent version 3.1
/ SEQ ID NO 1908
/ LENGTH: 24
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-1908

Query Match      40.0%; Score 12; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      17 GCCTGAACCGT 28
DB      20 GCCTGAACCGT 9

RESULT 3
US-09-754-853a-686/c
/ Sequence 686, Application US/09754853a
/ Publication No. US20030005491A1
/ GENERAL INFORMATION:
/ APPLICANT: Hauge, Brian M.
/ APPLICANT: Patnell, Laurence D.
/ APPLICANT: Parsons, Jeremy D.
/ APPLICANT: Wang, Ming Li
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Soybean Cyst Nematode Resistance
/ FILE REFERENCE: 38-10(15810)B
/ CURRENT APPLICATION NUMBER: US/09/754.853a
/ CURRENT FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: US 60/174,880
/ PRIOR FILING DATE: 2000-01-07
/ NUMBER OF SEQ ID NOS: 1119
/ SEQ ID NO 686
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 318013_region_A3_151839_17_reverse_Primer_Seq
US-09-754-853a-686

Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 TTCCTCTCTCTG 14
DB      12 TTCCTCTCTCTG 1

RESULT 4
US-10-098-263b-49318/c
/ Sequence 49318, Application US/10098263b
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ APPLICANT: Human Microarray
/ TITLE OF INVENTION: 3118.1
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098.263b
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
```

```
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 49318
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263b-49318

Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 CTCTCTCTGCGG 17
DB      14 CTCTCTCTGCGG 3

RESULT 5
US-10-098-263b-114611
/ Sequence 114611, Application US/10098263b
/ Publication No. US20030104410A1
/ GENERAL INFORMATION:
/ APPLICANT: Miltman, Michael
/ APPLICANT: Human Microarray
/ TITLE OF INVENTION: 3118.1
/ FILE REFERENCE: 3118.1
/ CURRENT APPLICATION NUMBER: US/10/098.263b
/ CURRENT FILING DATE: 2003-01-08
/ PRIOR APPLICATION NUMBER: 60/276,759
/ PRIOR FILING DATE: 2001-03-16
/ NUMBER OF SEQ ID NOS: 131066
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 114611
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-098-263b-114611

Query Match      40.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 GTTCTCTTCTCT 13
DB      6 GTTCTCTTCTCT 17

RESULT 6
US-09-903-412-18/c
/ Sequence 18, Application US/09903412
/ Publication No. US20030027319A1
/ GENERAL INFORMATION:
/ APPLICANT: Koide, Shohel
/ TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
/ FILE REFERENCE: 109.050US1
/ CURRENT APPLICATION NUMBER: US/09/903.412
/ CURRENT FILING DATE: 2001-07-11
/ PRIOR APPLICATION NUMBER: US 60/217,474
/ PRIOR FILING DATE: 2000-07-11
/ NUMBER OF SEQ ID NOS: 121
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 18
/ LENGTH: 38
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Oligonucleotide FN3R.
US-09-903-412-18

Query Match      40.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      14 GCGGCTGAAC 25
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Db 28 GCGGCGCTGAAC 17

RESULT 7

US-09-930-423-2074
Sequence 2074, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blatt, Larry
APPLICANT: McSwigen, Jim
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MBH00,918-A 400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 2074
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc.feature
LOCATION: (31)-(31)
OTHER INFORMATION: n stands for inosine
US-09-930-423-2074

Query Match

40.0%; Score 12; DB 9; Length 38;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCTGGCGGCTGA 22
|||
Db 1 CCTGGCGGCTGA 12

RESULT 8

US-10-174-717A-18/c
Sequence 18, Application US/10174717A
Publication No. US20030108948A1
APPLICANT: Koide, Shohel
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSeq Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikens
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:

LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-174-717A-18

Query Match

40.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAAC 25
|||||
Db 28 GCGGCGCTGAAC 17

RESULT 9

US-09-096-749A-18/c
Sequence 18, Application US/09096749A
Patent No. US20020019517A1
GENERAL INFORMATION:
APPLICANT: Koide, Shohel
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749A
FILING DATE: June 12, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikens
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-09-096-749A-18

Query Match

40.0%; Score 12; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GCGGCGCTGAAC 25
|||||

Db 28 GCGGCTGAAAC 17

RESULT 10
US-09-938-744-2/c
; Sequence 2, Application US/09938744
; Patent No. US20020172954A1
; GENERAL INFORMATION:
; APPLICANT: Mao, Yumin
; APPLICANT: Xie, Yi
; TITLE OF INVENTION: METHOD FOR LARGE SCALE CDNA CLONING AND
; TITLE OF INVENTION: SEQUENCING BY CIRCUITATING SUBTRACTION
; FILE REFERENCE: A34606-PCF-USA-A 072975.0111
; CURRENT APPLICATION NUMBER: US/09/938,744
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/CN00/00036
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: CN 99102450.8
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-938-744-2

Query Match 36.7%; Score 11; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TTCTCTCGGCC 19
Db 11 TTCTCTCGGCC 1

RESULT 11
US-09-969-373-1923/c
; Sequence 1923, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Haugse, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 1923
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-1923

Query Match 36.7%; Score 11; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCTCTCTCTGC 15
Db 14 CCTCTCTCTGC 4

RESULT 12
US-09-879-389B-4/c

Sequence 4, Application US/09879389B

Publication No. US20030032165A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030032165A1
; APPLICANT: Wu, Wendeng
; APPLICANT: Ostergaard, Peter Rahbek
; APPLICANT: Kauppinen, Markus Sakari
; TITLE OF INVENTION: ASPARTIC ACID PROTEASES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 6123.200-US
; CURRENT APPLICATION NUMBER: US/09/879,389B
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-879-389B-4

Query Match 36.7%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 TTCTCTCGGCC 19
Db 11 TTCTCTCGGCC 1

RESULT 13
US-09-902-563-38/c
; Sequence 38, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-902-563-38

Query Match 36.7%; Score 11; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCTCTCTCTG 14
Db 17 TTCTCTCTCTG 7

RESULT 14
US-09-902-563-41
; Sequence 41, Application US/09902563
; Publication No. US20030099654A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Gary
; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
; FILE REFERENCE: 9579-37
; CURRENT APPLICATION NUMBER: US/09/902,563
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 09/442,143
; PRIOR FILING DATE: 1999-11-15

; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 41
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-09-902-563-41

Query Match 36.7%; Score 11; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred.No.Se+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCG 14
 |||||
 DB 8 TCCTCTTCTCG 18

RESULT 15
 US-10-096-255-38/c
 ; Sequence 38, Application US/10096255
 ; Publication No. US20030103974A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Levy, Gary
 ; APPLICANT: Clark, David A.
 ; TITLE OF INVENTION: Methods of Modulating Immune Coagulation
 ; FILE REFERENCE: 9579-52
 ; CURRENT APPLICATION NUMBER: US/10/096,255
 ; CURRENT FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: US 60/046,537
 ; PRIOR FILING DATE: 1997-05-17
 ; PRIOR APPLICATION NUMBER: US 60/061,684
 ; PRIOR FILING DATE: 1997-10-10
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 38
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 US-10-096-255-38

Query Match 36.7%; Score 11; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred.No.Se+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCTCTTCTCG 14
 |||||
 DB 17 TCCTCTTCTCG 7

Search completed: June 23, 2003, 20:01:28
 Job time : 244.076 secs

Query Match 51.3%; Score 15.4; DB 8; Length 39;
 Best Local Similarity 76.0%; Pred. No. 9.5e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 TCCTCTTCTGCGGCTGAACGCT 28
 DB 15 TCCTCTTCTGCGGCTGAACGCT 39

RESULT 12
 US-10-287-787-22949/c
 ; Sequence 22949, Application US/10287787

; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Caulobacter crescentus complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/287,787
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 27958
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 22949
 ; LENGTH: 48
 ; TYPE: DNA
 ; ORGANISM: Caulobacter crescentus complete genome.
 ; FEATURE:
 ; LOCATION: (3315887)...(3315934)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 25340
 US-10-287-787-22949

Query Match 51.3%; Score 15.4; DB 10; Length 48;
 Best Local Similarity 76.0%; Pred. No. 9.7e+03;
 Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCCCTTCTGCGGCTGAACG 26
 DB 48 GTTCCCTTCTGCGGCTGAACG 24

RESULT 13
 US-60-427-808-174226/c
 ; Sequence 174226, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 174226
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-174226

Query Match 50.7%; Score 15.2; DB 12; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 CTTCCTGCGGCTGAACG 27
 DB 22 CTTCCTGCGGCTGAACG 3

RESULT 14
 US-60-427-808-358682
 ; Sequence 358682, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808

; CURRENT FILING DATE: 2002-11-20

; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 358682
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-358682

Query Match 50.7%; Score 15.2; DB 12; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11 CTTCGCGGCTGAACGCTGA 30
 DB 2 CTTCGCGGCTGAACGCTGA 21

RESULT 15
 US-60-427-808-829890
 ; Sequence 829890, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 829890
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-829890

Query Match 50.7%; Score 15.2; DB 12; Length 25;
 Best Local Similarity 85.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCTCTTCTGCGGCTGA 23
 DB 3 TCCTCTTCTGCGGCTGA 22

Search completed: June 26, 2003, 04:14:59
 Job time : 757.961 secs

RESULT 8
US-60-427-808-739619, Application US/60/427.836
; Sequence 739619, Application US/60/427.836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 549003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

Query Match 52.7%; Score 15.8; DB 12; Length 25;
Best Local Similarity 89.5%; Pred. No. 6.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CTCTCTCTGCGGCGCTGAAA 24
DB 6 CTCTCTCTGCGGCGCAAGAA 24

RESULT 7
US-60-427-808-551160/C
; Sequence 551160, Application US/60/427.808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427.808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 551160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

Query Match 52.0%; Score 15.6; DB 12; Length 25;
Best Local Similarity 81.8%; Pred. No. 7.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 CTCTCTCTGCGGCGCTGAAA 27
DB 24 CTCTCTCTGCGGCGCTGAAA 3

RESULT 8
US-60-427-808-739619
; Sequence 739619, Application US/60/427.808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427.808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 739619
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus

Query Match 51.3%; Score 15.4; DB 12; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTCTGCGGCGCTGAAA 26
DB 1 GTTCTCTTCTCTGCGGCGCTGAAA 25

RESULT 9
US-60-427-836-669241, Application US/60/427.836
; Sequence 669241, Application US/60/427.836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427.836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 669241
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

Query Match 51.3%; Score 15.4; DB 12; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGCGGCGCTGAAA 27
DB 1 TTCTCTTCTCTGCGGCGGAACTGAAA 25

RESULT 10
US-60-427-836-669242
; Sequence 669242, Application US/60/427.836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427.836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 669242
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus

Query Match 51.3%; Score 15.4; DB 12; Length 25;
Best Local Similarity 76.0%; Pred. No. 9.1e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTCTCTTCTCTGCGGCGCTGAAA 27
DB 1 TTCTCTTCTCTGCGGCGGAACTGAAA 25

RESULT 11
US-10-447-242-23365
; Sequence 23365, Application US/10/447.242
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Polynucleotide, Materials Incorporating
; FILE REFERENCE: 11000.1049AU.c1
; CURRENT APPLICATION NUMBER: US/10/447.242
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: 09/724,750
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/171,431
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 25203
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 23365
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Pinus radiata

US-10-447-242-23365

QY 7 TCTTCCTGGGCGCTGAAA 24
Db 19 TCTTCCTGGGCGCTGAAA 2

RESULT 2

PCT-US03-04088-290
; Sequence 290, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 290
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-290

Query Match 60.0%; Score 18; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 6.6e+02;
Matches 13; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 7 TCTTCCTGGGCGCTGAAA 24
Db 1 UCUUCCUGCGGCGGAAA 18

RESULT 3

US-60-427-808-174225/c
; Sequence 174225, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 174225
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-174225

Query Match 56.0%; Score 16.8; DB 12; Length 25;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CTTCCTGGGCGCTGAAACGG 27
Db 22 CTTCCTGGGCGGACGAAACGG 3

RESULT 4

US-10-325-899-304/c
; Sequence 304, Application US/10325899
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Ly, Ngoc
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING TRANSPLANT
; TITLE OF INVENTION: REJECTION
; FILE REFERENCE: 50661200122
; CURRENT APPLICATION NUMBER: US/10/325,899
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 9966
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 304
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-325-899-304

Query Match 55.3%; Score 16.6; DB 9; Length 50;
Best Local Similarity 82.6%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 TCTTCCTGGGCGCTGAAACGG 29
Db 46 TCTTTTGTGGCTGAAACGATG 24

RESULT 5

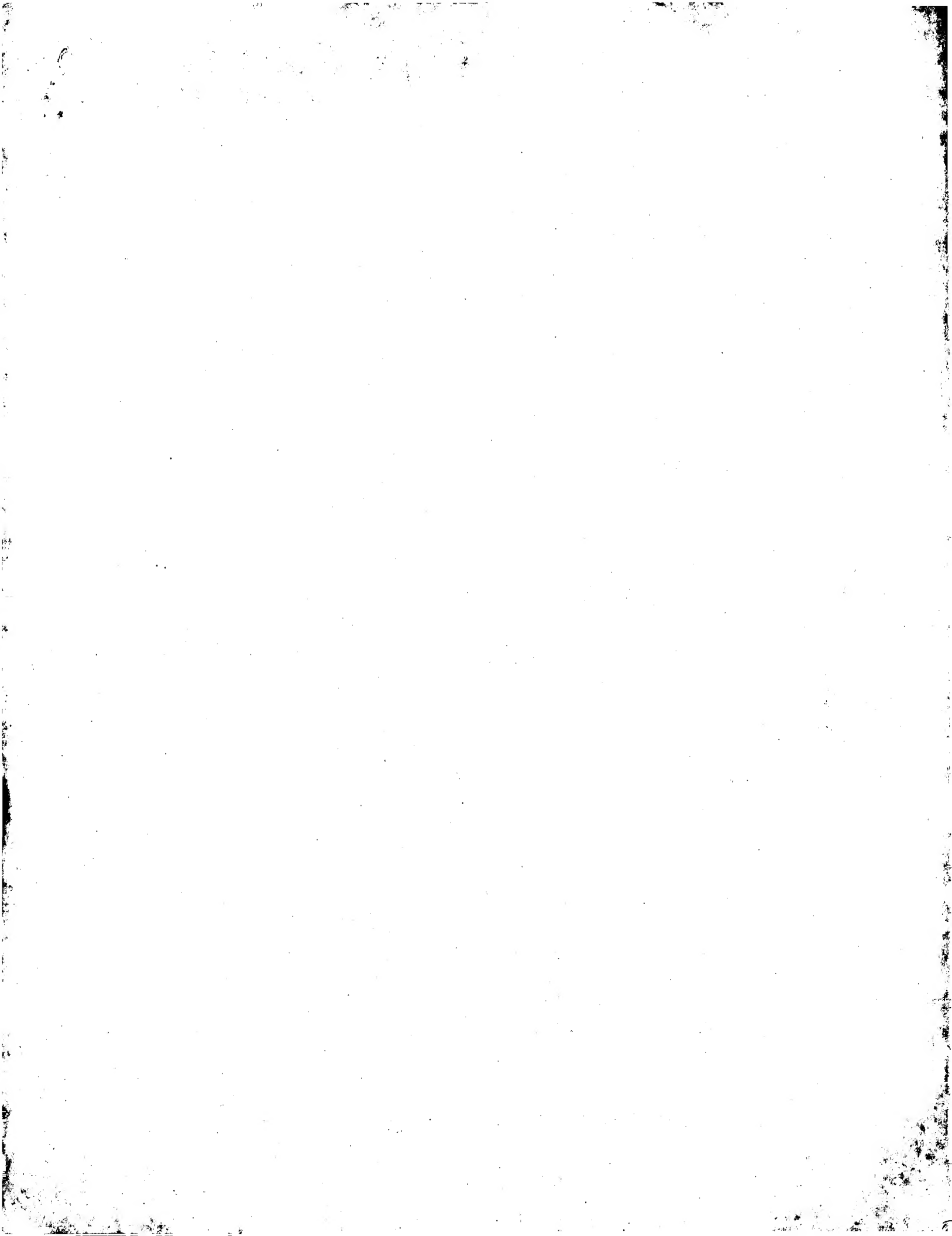
US-60-427-808-324892
; Sequence 324892, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 324892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-60-427-808-324892

Query Match 54.0%; Score 16.2; DB 12; Length 25;
Best Local Similarity 85.7%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GTTCTCTTCTGCGGCGCTGA 22
Db 3 GTTCATCTTCGACGAGCCTGA 23

RESULT 6

US-60-427-836-549003
; Sequence 549003, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou



Fri Jun 27 07:41:44 2003

us-08-770-564a-1_copy_137_196.01go.rge

Page 5

FEATURES
source location/Qualifiers
1..16
/organism="unknown"
BASE COUNT 5 a 5 c 3 g 3 t
ORIGIN

Query Match 20.0%; Score 12; DB 6; Length 16;
Best Local Similarity 100.0%; Fred.No. 3.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGAAGCTCT 45
|||||
Db 16 GAGAGTGAAGCTCT 5

RESULT 15
AR009327/c 17 bp DNA linear PAT 04-DEC-1998
LOCUS AR009327
DEFINITION Sequence 95 from patent US 5756291.
ACCESSION AR009327
VERSION AR009327.1 GI:3968132
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
Griffin,L., Albrecht,G., Latham,J., Leung,L., Vermaas,E. and
Toole,J.J.
TITLE Apatemers specific for biomolecules and methods of making
JOURNAL Patent: US 5756291-A 95 26-MAY-1998;
FEATURES location/Qualifiers
source 1..17
/organism="unknown"

BASE COUNT 1 a 1 c 10 g 5 t
ORIGIN

Query Match 20.0%; Score 12; DB 6; Length 17;
Best Local Similarity 100.0%; Fred.No. 3.1e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACGAGCCC 27
|||||
Db 17 CCCAACGAGCCC 6

Search completed: June 23, 2003, 20:29:39
Job time : 601.016 secs


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source      1. .31
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BASE COUNT      6 a      9 c      11 g      5 t
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Query Match      21.7%; Score 13; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 7.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      48 CGAGAGCCCGCAG 60
        |||||
        14 CGAGAGCCCGCAG 26

Db
19 AATTCCCGTTC 7

RESULT 11
AR043925/c      40 bp      DNA      linear      PAT 29-SEP-1999
LOCUS
DEFINITION      Sequence 1 from patent US 5817310.
ACCESSION      AR043925
VERSION      AR043925.1 GI:5965390
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unidentified.
REFERENCE      1 (bases 1 to 40)
AUTHORS      Ramakrishnan,V., Escobedo,M,Amelia., Pretto,L.J. and Lokker,N.
TITLE      Inhibitory immunoglobulin polypeptides to human PDGF beta receptor
JOURNAL      Patent: US 5817310-A 1 06-OCT-1998;
FEATURES
    source      1. .40
                /organism="unknown"
BASE COUNT      12 a      10 c      12 g      6 t
ORIGIN
Query Match      21.7%; Score 13; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AATTCCCGTTC 14
        |||||
        19 AATTCCCGTTC 7

Db
19 AATTCCCGTTC 7

RESULT 12
BD000714/c      40 bp      DNA      linear      PAT 31-JAN-2002
LOCUS
DEFINITION      Drug composition for inhibiting hyperplasia of inner membrane in
                mammal vasculature.
ACCESSION      BD000714
VERSION      BD000714.1 GI:18623827
KEYWORDS      JP 2000355548-A/1.
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 40)
AUTHORS      Ramakrishnan,V., Escobedo,M.A. and Pret,R.J.
TITLE      Drug composition for inhibiting hyperplasia of inner membrane in
                mammal vasculature
JOURNAL      Patent: JP 2000355548-A 1 26-DEC-2000;
COMMENT
    OS      Unidentified
    PN      JP 2000355548-A/1
    PD      26-DEC-2000
    PF      26-APR-2000 JP 2000126131
    PR      02-DEC-1991 US 07/801795
    PI      VANITA RAMAKRISHNAN,MARIA A ESCOBED,RALY J FRET PC
    AG1K39/395,A61K39/395,A61P9/00,A61P43/00,G01N33/53, PC
    G01N33/566,
    PC      G01N33/577//C07K16/28,C12N15/09,C12P21/08,C12N15/00 CC
    FH      key
    FT      source      1. .40
                Location/Qualifiers
FEATURES
    source      Location/Qualifiers

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source      1. .40
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            /db_xref="taxon:32644"
BASE COUNT      12 a      10 c      12 g      6 t
ORIGIN
Query Match      21.7%; Score 13; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AATTCCCGTTC 14
        |||||
        19 AATTCCCGTTC 7

Db
19 AATTCCCGTTC 7

RESULT 13
BD000716/c      40 bp      DNA      linear      PAT 31-JAN-2002
LOCUS
DEFINITION      Inhibitory immunoglobulin polypeptide against human PDGF
                beta-receptor.
ACCESSION      BD000716
VERSION      BD000716.1 GI:18623829
KEYWORDS      JP 2000355600-A/1.
SOURCE      unidentified.
ORGANISM      unidentified.
REFERENCE      1 (bases 1 to 40)
AUTHORS      Ramakrishnan,V., Escobedo,M.A. and Pret,R.J.
TITLE      Inhibitory immunoglobulin polypeptide against human PDGF
JOURNAL      Patent: JP 2000355600-A 1 26-DEC-2000;
COMMENT
    OS      Unidentified
    PN      JP 2000355600-A/1
    PD      26-DEC-2000
    PF      26-APR-2000 JP 2000126152
    PR      02-DEC-1991 US 07/801795
    PI      VANITA RAMAKRISHNAN,MARIA A ESCOBED,RALY J FRET PC
    C07K16/28,A61K9/20,A61K39/395,A61K48/00,A61P9/00, PC
    A61P9/08,
    PC      A61P35/00,G01N33/531//C12N15/09,C12P21/08,C12N15/00 CC
    FH      key
    FT      source      1. .40
                Location/Qualifiers
FEATURES
    source      Location/Qualifiers
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            /organism="unidentified"
            /db_xref="taxon:32644"
BASE COUNT      12 a      10 c      12 g      6 t
ORIGIN
Query Match      21.7%; Score 13; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AATTCCCGTTC 14
        |||||
        19 AATTCCCGTTC 7

Db
19 AATTCCCGTTC 7

RESULT 14
I34311/c      16 bp      DNA      linear      PAT 06-FEB-1997
LOCUS
DEFINITION      Sequence 10 from patent US 5597710.
ACCESSION      I34311
VERSION      I34311.1 GI:1825102
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unidentified.
REFERENCE      1 (bases 1 to 16)
AUTHORS      Dalle,B., Miller,K., Murgolo,N. and Tindall,S.
TITLE      Humanized monoclonal antibodies against human interleukin-4
JOURNAL      Patent: US 5597710-A 10 28-JAN-1997;

```

Db 18 AGAGAGTGACTCT 6

RESULT 6
LOCUS AX038445/c
DEFINITION Sequence 202 from Patent WO0061795.
ACCESSION AX038445
VERSION AX038445.1 GI:11227793
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 202 19-OCT-2000;
CANCER IL28 DB (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEILIES (BE)
FEATURES
source Location/Qualifiers
1..24
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 8 c 4 g 6 t
ORIGIN

Query Match 21.7%; Score 13; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AGAGAGTGACTCT 45
19 AGAGAGTGACTCT 7

RESULT 7
LOCUS AX038446/c
DEFINITION Sequence 203 from Patent WO0061795.
ACCESSION AX038446
VERSION AX038446.1 GI:11227794
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 203 19-OCT-2000;
CANCER IL28 DB (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEILIES (BE)
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 6 a 8 c 5 g 6 t
ORIGIN

Query Match 21.7%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 33 AGAGAGTGACTCT 45
20 AGAGAGTGACTCT 8

RESULT 8
LOCUS AX428325/c
25 bp DNA 11near PAT 20-JUN-2002

DEFINITION Sequence 37 from Patent EP1199356.
ACCESSION AX428325
VERSION AX428325.1 GI:21538283
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE
AUTHORS Araki, H.C., Hagihara, H.C., Hayashi, Y.C., Endo, K.C., Igarashi, K.C.
TITLE Highly productive alpha-amylases
JOURNAL Patent: EP 1199356-A 37 24-APR-2002;
Kao Corporation (JP)
FEATURES
source Location/Qualifiers
1..25
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 6 a 2 c 10 g 7 t
ORIGIN

Query Match 21.7%; Score 13; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 TTCCCCCACA 23
15 TTCCCCCACA 3

RESULT 9
LOCUS AR088753/c
DEFINITION Sequence 8 from patent US 5990092.
ACCESSION AR088753
VERSION AR088753.1 GI:10015516
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Walsh, K.
TITLE GATA-6 transcription factor: compositions and methods
JOURNAL Patent: US 5990092-A 8 23-NOV-1999;
FEATURES
source Location/Qualifiers
1..27
/organism="unknown"

BASE COUNT 2 a 11 c 8 g 6 t
ORIGIN

Query Match 21.7%; Score 13; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 CGAGAGCCGCGAG 60
15 CGAGAGCCGCGAG 3

RESULT 10
LOCUS AR088752
DEFINITION Sequence 7 from patent US 5990092.
ACCESSION AR088752
VERSION AR088752.1 GI:10015515
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Walsh, K.
TITLE GATA-6 transcription factor: compositions and methods
JOURNAL Patent: US 5990092-A 7 23-NOV-1999;
FEATURES
source Location/Qualifiers
1 (bases 1 to 31)
Unclassified.

RESULT 10
LOCUS AR088752
DEFINITION Sequence 7 from patent US 5990092.
ACCESSION AR088752
VERSION AR088752.1 GI:10015515
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS Walsh, K.
TITLE GATA-6 transcription factor: compositions and methods
JOURNAL Patent: US 5990092-A 7 23-NOV-1999;
FEATURES
source Location/Qualifiers
1 (bases 1 to 31)
Unclassified.

KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT
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Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCAGCCCCCGAGAGAGT 39
1 ACCAGCCCCCGAGAGAGT 20

RESULT 2

AX038441/c 20 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 198 from Patent WO0061795.
ACCESSION AX038441.
VERSION AX038441.1 GI:11227789

KEYWORDS
SOURCE
ORGANISM
human.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 20)

De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 198 19-OCT-2000;
CANCK IISE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEELIES (BE)

FEATURES
source
Location/Qualifiers
1. .20
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT
4 a 6 c 4 g 6 t

Query Match 21.7%; Score 13; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45
15 AGAGAGTGACTCT 3

RESULT 3
AX038442/c 21 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 199 from Patent WO0061795.
ACCESSION AX038442
VERSION AX038442.1 GI:11227790

KEYWORDS
SOURCE
ORGANISM
human.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 21)

De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 199 19-OCT-2000;
CANCK IISE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEELIES (BE)

FEATURES
source
Location/Qualifiers
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/db_xref="taxon:9606"

BASE COUNT
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45
16 AGAGAGTGACTCT 4

RESULT 4
AX038443/c 22 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 200 from Patent WO0061795.
ACCESSION AX038443
VERSION AX038443.1 GI:11227791

KEYWORDS
SOURCE
ORGANISM
human.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 22)

De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 200 19-OCT-2000;
CANCK IISE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEELIES (BE)

FEATURES
source
Location/Qualifiers
1. .22
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/db_xref="taxon:9606"

BASE COUNT
4 a 8 c 4 g 6 t

Query Match 21.7%; Score 13; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45
17 AGAGAGTGACTCT 5

RESULT 5
AX038444/c 23 bp DNA linear PAT 16-NOV-2000
LOCUS
DEFINITION Sequence 201 from Patent WO0061795.
ACCESSION AX038444
VERSION AX038444.1 GI:11227792

KEYWORDS
SOURCE
ORGANISM
human.

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL 1 (bases 1 to 23)

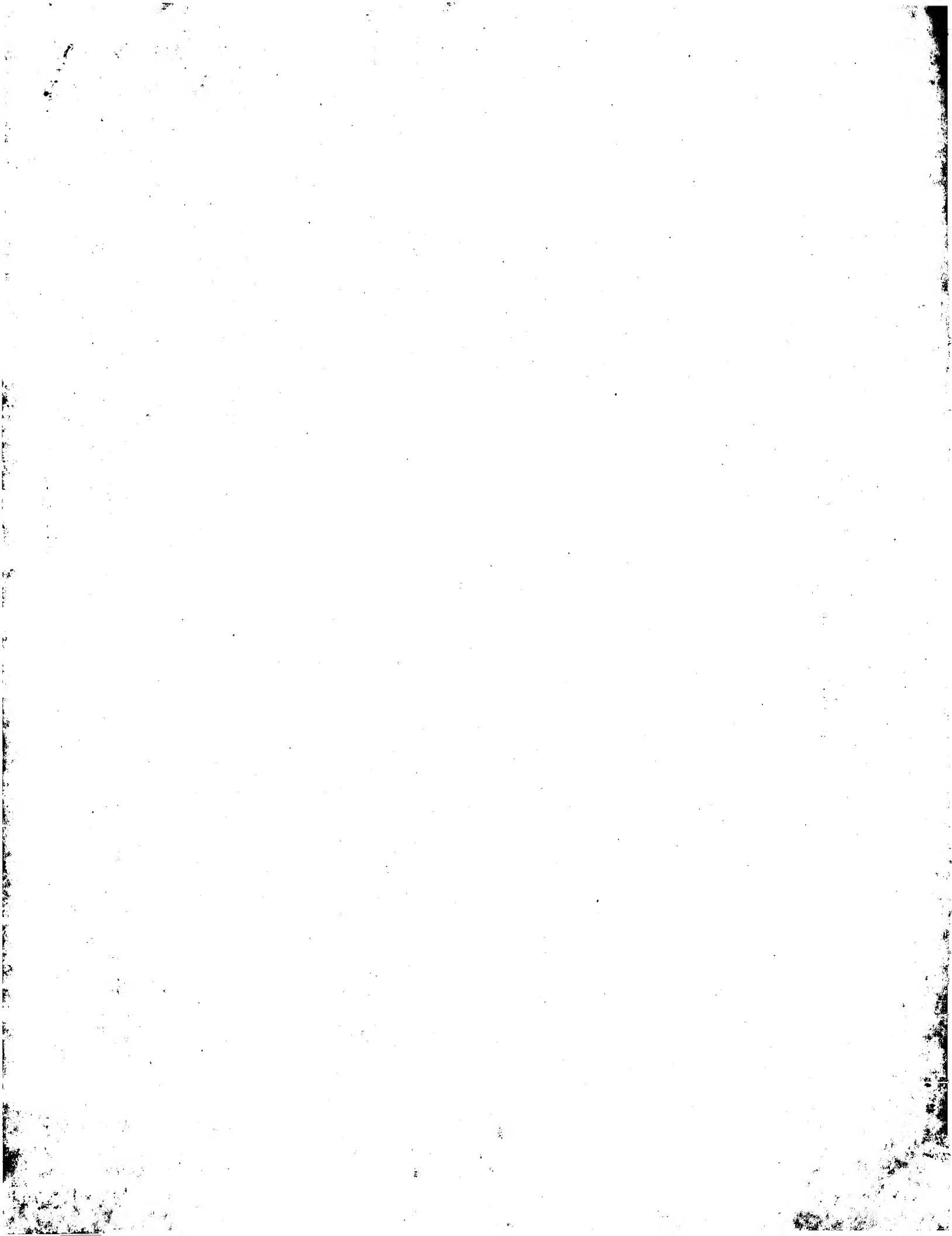
De Canck, I.D., Rossau, R. and Rombout, A.
Method for the amplification of hla class I alleles
Patent: WO 0061795-A 201 19-OCT-2000;
CANCK IISE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
ROMBOUT ANNEELIES (BE)

FEATURES
source
Location/Qualifiers
1. .23
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT
5 a 8 c 4 g 6 t

Query Match 21.7%; Score 13; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTGACTCT 45



PI De Canck I, Rombout A, Rousseau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
 PT defined primer sets, useful for subtyping or typing of HLA Class I
 PT alleles -
 XX
 PS Claim 4; Page 40; 128bp; English.
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method.
 XX
 SQ Sequence 22 BP; 4 A; 8 C; 4 G; 6 T; 0 other;
 Query Match 21.7%; Score 13; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 AGAGAGTACTCT 45
 DB 17 AGAGAGTACTCT 5
 RESULT 14
 AAC80283/C
 ID AAC80283 standard; DNA; 23 BP.
 XX
 AC AAC80283;
 XX
 DT 03-MAY-2001 (first entry)
 DE Reverse primer #11 used for amplification of HLA-A exon 3.
 XX
 KM HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200061795-A2.
 PS 19-OCT-2000.
 PF 05-APR-2000; 2000WO-EP02998.
 PR 09-APR-1999; 99EP-0870068.
 PR 11-JUN-1999; 99US-0138614.
 XX
 PA (INNO-) INNOGENETICS NV.
 PI De Canck I, Rombout A, Rousseau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
 PT defined primer sets, useful for subtyping or typing of HLA Class I
 PT alleles -
 XX
 PS Claim 4; Page 40; 128bp; English.
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method.
 XX
 SQ Sequence 23 BP; 5 A; 8 C; 4 G; 6 T; 0 other;

Query Match 21.7%; Score 13; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 AGAGAGTACTCT 45
 DB 18 AGAGAGTACTCT 6
 RESULT 15
 AAC80284/C
 ID AAC80284 standard; DNA; 24 BP.
 XX
 AC AAC80284;
 XX
 DT 03-MAY-2001 (first entry)
 DE Reverse primer #12 used for amplification of HLA-A exon 3.
 XX
 KM HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 OS Homo sapiens.
 OS Synthetic.
 PN WO200061795-A2.
 PS 19-OCT-2000.
 PF 05-APR-2000; 2000WO-EP02998.
 PR 09-APR-1999; 99EP-0870068.
 PR 11-JUN-1999; 99US-0138614.
 XX
 PA (INNO-) INNOGENETICS NV.
 PI De Canck I, Rombout A, Rousseau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
 PT defined primer sets, useful for subtyping or typing of HLA Class I
 PT alleles -
 XX
 PS Claim 4; Page 40; 128bp; English.
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method.
 XX
 SQ Sequence 24 BP; 6 A; 8 C; 4 G; 6 T; 0 other;
 Query Match 21.7%; Score 13; DB 21; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 33 AGAGAGTACTCT 45
 DB 19 AGAGAGTACTCT 7
 Search completed: June 23, 2003, 20:09:18
 Job time : 229.107 secs

Db 14 AGAGAGTACTCT 2

RESULT 11
AAK38046/c
ID AAK38046 standard; DNA; 21 BP.
XX
XX
AC AAK38046;
XX
DT 04-JUN-1999 (first entry)
XX
DE HLA-A untranslated region primer SEQ ID NO:202.
XX
KM Human; histocompatibility locus antigen; HLA; determination; allele;
XX HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN WO907883-A1.
XX
PD 18-FEB-1999.
XX
XX 11-AUG-1998; 98WO-CA00768.
XX
PR 11-AUG-1997; 97US-0909290.
XX
PA (BLAS/) BLASZKY R H.
XX (VISI-) VISIBLE GENETICS INC.
XX
PI Blaszyk RH, Leushner J;
XX
DR WPI; 1999-167446/14.
XX
PT Determination of HLA class I group type of a subject - using group
XX specific untranslated region primer pair
XX
PS Disclosure; Page 19; 195pp; English.

CC The present invention describes a method using novel primers involving
CC the PCR-based determination of histocompatibility locus antigen B
CC (HLA-B) Class I group type. Determining the HLA-B Class I group type of
CC a subject comprises: (i) combining a group-specific untranslated region
CC primer pair with a target DNA sample from the subject under conditions
CC such that primer-based amplification of the target DNA may occur; and
CC (ii) determining whether a nucleic acid product is produced by the
CC amplification; where the ability of the primer pair to produce a nucleic
CC acid product is associated with a particular HLA group type. The method
CC can be used for HLA-B typing. In the method, the initial group specific
CC amplification allows a PCR based separation of haplotypes in 95% of
CC patient samples. It permits the resolution of cis/trans linkages of
CC heterozygote sequencing results which cannot be achieved with other
CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the
CC exemplification of the present invention.
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 other;

Query Match 21.7%; Score 13; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
DB 13 AGAGAGTACTCT 1

RESULT 12
AAC80281/c
ID AAC80281 standard; DNA; 21 BP.
XX
XX AAC80281;
XX
DT 03-MAY-2001 (first entry)

XX
XX Reverse primer #109 used for amplification of HLA-A exon 3.
DE
XX
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
KM
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
PN WO200061795-A2.
XX
XX 19-OCT-2000.
PD
XX
XX 05-APR-2000; 2000WO-EP02998.
XX
XX 09-APR-1999; 99EP-0870068.
PR 11-JUN-1999; 99US-0138614.
XX
XX (INNO-) INNOGENETICS NV.
XX
PI De Canck I, Rombout A, Rossau R;
XX
XX WPI; 2000-647426/62.
DR
XX
XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
XX of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
XX defined primer sets, useful for subtyping or typing of HLA Class I
XX alleles -
XX
PS Claim 4; Page 40; 128pp; English.
XX
XX The present invention relates to a method for the locus-specific,
XX separate amplification of exon 2, exon 3, and/or exon 4 of human
XX leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
XX for subtyping or typing of HLA class I alleles. The present sequence is
XX an amplification primer used in the method.
XX
SQ Sequence 21 BP; 4 A; 7 C; 4 G; 6 T; 0 other;

Query Match 21.7%; Score 13; DB 21; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
DB 16 AGAGAGTACTCT 4

RESULT 13
AAC80282/c
ID AAC80282 standard; DNA; 22 BP.
XX
XX AAC80282;
XX
DT 03-MAY-2001 (first entry)
XX
XX Reverse primer #110 used for amplification of HLA-A exon 3.
DE
XX
XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
KM
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
PN WO200061795-A2.
XX
XX 19-OCT-2000.
PD
XX
XX 05-APR-2000; 2000WO-EP02998.
XX
XX 09-APR-1999; 99EP-0870068.
PR 11-JUN-1999; 99US-0138614.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX

XX AAV46054 and AAV46200-V46264 are primers used in isolating human
 CC histocompatibility locus antigen (HLA-A) Class I alleles which are used
 CC in a novel method of HLA Class I typing. The method involves combining
 CC a group-specific untranslated region primer pair with a target DNA to
 CC allow primer-based amplification of the DNA, and determining whether a
 CC nucleic acid product is produced by the amplification. The ability of
 CC the primer pair to produce a product is associated with a particular
 CC HLA group type. The methods can be used for typing with a particular
 CC Class I genes (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g.
 CC donors and hosts for tissue transplantation. The initial group specific
 CC amplification allows a PCR based separation of haplotypes in 95% of
 CC patient samples. The subsequent sequencing can provide for
 CC high-resolution typing.

XX Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 other;
 SQ

Query Match 21.7%; Score 13; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
 |||||
 DB 14 AGAGAGTACTCT 2

RESULT 9
 AAV46221/c
 ID AAV46221 standard; DNA; 21 BP.
 XX
 AC AAV46221;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human HLA-A primer 13-282.
 XX
 KW Histocompatibility locus antigen; HLA-A class I; human; class typing;
 XX donor; host; tissue transplantation; primer; ss.
 XX
 OS Synthetic.
 XX Homo sapiens.
 XX
 PI WO9826091-A2.
 XX
 PD 18-JUN-1998.
 XX
 PF 12-DEC-1997; 97WO-CA00955.
 XX
 PR 12-DEC-1996; 96US-0766189.
 XX
 PA (VISI-) VISIBLE GENETICS INC.
 XX
 PI Blaszczk RH, Leushner J;
 XX
 WPI; 1998-348544/30.
 XX
 PT HLA Class I typing - by primer-based amplification of target DNA.
 PT using group-specific untranslated region primer pair
 XX
 PS Claim 4; Page 128; 185pp; English.
 XX
 CC AAV46054 and AAV46200-V46264 are primers used in isolating human
 CC histocompatibility locus antigen (HLA-A) Class I alleles which are used
 CC in a novel method of HLA Class I typing. The method involves combining
 CC a group-specific untranslated region primer pair with a target DNA to
 CC allow primer-based amplification of the DNA, and determining whether a
 CC nucleic acid product is produced by the amplification. The ability of
 CC the primer pair to produce a product is associated with a particular
 CC HLA group type. The methods can be used for typing with a particular
 CC Class I genes (comprising the loci HLA-A, HLA-B, and HLA-C) in e.g.
 CC donors and hosts for tissue transplantation. The initial group specific
 CC amplification allows a PCR based separation of haplotypes in 95% of
 CC patient samples. The subsequent sequencing can provide for

CC high-resolution typing.
 XX
 SQ Sequence 21 BP; 6 A; 5 C; 5 G; 5 T; 0 other;
 XX

Query Match 21.7%; Score 13; DB 19; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
 |||||
 DB 13 AGAGAGTACTCT 1

RESULT 10
 AAX38044/c
 ID AAX38044 standard; DNA; 21 BP.
 XX
 AC AAX38044;
 XX
 DT 04-JUN-1999 (first entry)
 XX
 DE HLA-A untranslated region primer SEQ ID NO:200.
 XX
 DE Human; histocompatibility locus antigen; HLA; determination; allele;
 KW HLA-B typing; PCR; HLA class I; cis/trans linkage resolution; ss.
 XX
 OS Synthetic.
 XX Homo sapiens.
 XX
 PI WO9907683-A1.
 XX
 PD 18-FEB-1999.
 XX
 PF 11-AUG-1998; 98WO-CA00768.
 XX
 PR 11-AUG-1997; 97US-0909290.
 XX
 PA (BLAS/) BLASZCZYK R H.
 XX (VISI-) VISIBLE GENETICS INC.
 XX
 PI Blaszczk RH, Leushner J;
 XX
 WPI; 1999-167446/14.
 XX
 PD Determination of HLA class I group type of a subject - using group
 PT specific untranslated region primer pair
 XX
 PS Disclosure; Page 19; 195pp; English.
 XX
 CC The present invention describes a method using novel primers involving
 CC the PCR-based determination of histocompatibility locus antigen B
 CC (HLA-B) Class I group type. Determining the HLA-B class I group type of
 CC a subject comprises: (i) combining a group-specific untranslated region
 CC primer pair with a target DNA sample from the subject under conditions
 CC such that primer-based amplification of the target DNA may occur; and
 CC (ii) determining whether a nucleic acid product is produced by the
 CC amplification; where the ability of the primer pair to produce a nucleic
 CC acid product is associated with a particular HLA group type. The method
 CC can be used for HLA-B typing. In the method, the initial group specific
 CC amplification allows a PCR based separation of cis/trans linkages of
 CC patient samples. It permits the resolution of cis/trans linkages of
 CC heterozygote sequencing results which cannot be achieved with other
 CC protocols. AAX37845 to AAX38286 represent DNA sequence used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 other;
 XX

Query Match 21.7%; Score 13; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
 |||||

DT 09-MAR-1999 (first entry)
 XX Antisense primer for intron boundary mapping of DNA Metase exon 38-39.
 DE
 XX DNA methyltransferase; DNA Metase; antisense oligonucleotide; human;
 KW cellular growth; tumour growth inhibition; silenced gene activation;
 KM beta thalassemia; sickle cell anemia; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9854313-A2.
 XX
 PD 03-DEC-1998.
 XX
 XX 29-MAY-1998; 98WO-1801107.
 XX
 XX 17-DEC-1997; 97US-0069865.
 PR 30-MAY-1997; 97US-0866340.
 XX
 XX (UYMC-) UNIV MCGILL.
 XX
 XX Bigey P, Ramchandani S, Szyf M;
 DR WPI; 1999-059833/05.
 XX
 XX New DNA methyltransferase nucleotide sequences - used particularly
 PT to develop antisense oligonucleotides for diagnostic and therapeutic
 PT purposes, particularly for inhibiting tumour growth
 XX
 PS Example 8; Page 32; 108pp; English.
 XX
 CC PCR primers AAV99163-220 were used to map the intron boundaries of
 CC the exons of DNA methyltransferase (DNA Metase) genomic sequence.
 CC Antisense oligonucleotides which inhibit DNA Metase expression
 CC can be derived from the genomic DNA Metase sequence. The antisense
 CC oligonucleotides can be used in investigating the role of DNA Metase
 CC in cellular growth. They can be administered at different points in
 CC the cell cycle, or in conjunction with promoters or inhibitors of cell
 CC growth to determine the role of DNA Metase in the growth of the cell
 CC type of interest. The antisense oligonucleotides can also be used for
 CC inhibiting tumour growth in a mammal, or to activate silenced genes to
 CC provide a missing gene function. This ameliorates disease symptoms,
 CC e.g. in beta thalassemia and sickle cell anemia. The antisense
 CC oligonucleotides can also be used as analytical and diagnostic tools
 CC and a potentiators of transgenic plant and animal studies.
 CC
 XX
 SQ Sequence 20 BP; 1 A; 6 C; 7 G; 6 T; 0 other;
 XX
 Query Match 21.7%; Score 13; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 28 GCCCGAGAGAGTG 40
 |||||
 Db 15 GCCCGAGAGAGTG 3
 |||||
 RESULT 7
 AAC80280/c
 ID AAC80280 standard; DNA; 20 BP.
 XX
 AC AAC80280;
 XX
 DT 03-MAY-2001 (first entry)
 XX
 XX Reverse primer #108 used for amplification of HLA-A exon 3.
 DE
 XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200061795-A2.
 XX
 PD 19-OCT-2000.
 XX
 XX 05-APR-2000; 2000WO-EP02998.
 PF
 XX 09-APR-1999; 99EP-0870068.
 PR 11-JUN-1999; 99US-0138614.
 XX
 XX (INNO-) INNOGENETICS NV.
 PA
 XX De Canck I, Rombout A, Rossau R;
 PI WPI; 2000-647426/52.
 DR
 XX
 XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using
 PT defined primer sets, useful for subtyping or typing of HLA Class I
 PT alleles -
 XX
 PS Claim 4; Page 40; 128pp; English.
 XX
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method.
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 other;
 XX
 Query Match 21.7%; Score 13; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 1.7e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 33 AGAGACTGACTCT 45
 |||||
 Db 15 AGAGACTGACTCT 3
 |||||
 RESULT 8
 AAV46219/c
 ID AAV46219 standard; DNA; 21 BP.
 XX
 AC AAV46219;
 XX
 DT 16-OCT-1998 (first entry)
 XX
 DE Human HLA-A primer 13-249.
 XX
 KW Histocompatibility locus antigen; HLA-A class I; human; class typing;
 KW donor; host; tissue transplantation; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9826091-A2.
 XX
 PD 18-JUN-1998.
 XX
 XX 12-DEC-1997; 97WO-CA00955.
 PF
 XX 12-DEC-1996; 96US-0766189.
 PR
 XX (VIST-) VISIBLE GENETICS INC.
 PA
 XX Blasczyk RH, Leushner J;
 PI WPI; 1998-348544/30.
 DR
 XX HLA Class I typing - by primer-based amplification of target DNA
 PT using group-specific untranslated region primer pair
 XX
 PS Claim 4; Page 127; 185pp; English.

CC (AA129513-AA13114) from the human genome which include polymorphic sites
 CC which can predispose individuals to disease. Various genes from a number
 CC of individuals were resequenced and single nucleotide polymorphisms
 CC (SNPs) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype or disorder (e.g.
 CC diabetes) associated with a particular genotype. The nucleic acids
 CC containing the polymorphic sites may be useful in forensics and paternity
 CC testing.

SQ Sequence 31 BP; 2 A; 11 C; 16 G; 2 T; 0 other;

Query Match 23.3%; Score 14; DB 22; Length 31;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCAGCCGCCCGAG 34

DB 19 CCAGCCGCCCGAG 6

RESULT 4

AAFP2154/C

AAFP2154 standard; DNA; 15 BP.

AC AAFP2154;

DT 15-MAY-2001 (first entry)

DE Human IGERB allele specific probe SEQ ID NO: 12.

KW Human; immunoglobulin E receptor beta chain; IGERB; chromosome 11q13;
 KW allergy; asthma; rhinitis; eczema; single nucleotide polymorphism; SNP;
 KW atopy; probe; PCR primer; ss.

OS Homo sapiens.

PN WO200114586-A1.

PD 01-MAR-2001.

PF 11-AUG-2000; 2000WO-US22175.

PR 24-AUG-1999; 99US-0150423.

PA (GENA-) GENAISANCE PHARM INC.

PI (NAND/) NANDABALAN K.

DR Denton RR, Klem SE, Stephens JC;

WPI; 2001-226623/23.

PT Novel polynucleotide useful for therapeutic purposes, comprises
 PT nucleotide polymorphisms in immunoglobulin E receptor beta chain gene

PS Claim 15; Page 61; 88pp; English.

CC The present invention provides the protein and coding sequences of
 CC several polymorphic variants of the human immunoglobulin E receptor beta
 CC chain (IGERB). These contain single nucleotide polymorphisms (SNPs) which
 CC may be indicative of a predisposition to atopy, allergy, asthma, rhinitis
 CC and eczema. Also provided are the sequences of probes and primers for use
 CC in identifying the genotype of an individual with regards to the IGERB
 CC gene. The IGERB gene is found at human chromosome 11q13. The sequences
 CC are all useful in therapeutics. The present sequence was used to isolate
 CC the IGERB gene.

SQ Sequence 15 BP; 4 A; 1 C; 8 G; 2 T; 0 other;

Query Match 21.7%; Score 13; DB 22; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTCCCGTTCCCC 17

DB 13 TTCCCGTTCCCC 1

RESULT 5

AAQ10624

AAQ10624 standard; DNA; 19 BP.

AC AAQ10624;

DT 29-APR-1991 (first entry)

DE HLA Class I locus-specific primer A2.2.

KW Human leukocyte antigen; major histocompatibility complex; MHC;
 KW restriction fragment length polymorphic analysis; RFLP;
 KW tissue typing; allele; PCR; ss.

OS Synthetic.

PN EP41469-A.

PD 27-FEB-1991.

PF 20-AUG-1990; 90EP-0309107.

PR 11-JUL-1990; 80US-0551239.

PR 25-AUG-1989; 89US-0398217.

PR 11-SEP-1989; 89US-0405499.

PR 16-JAN-1990; 90US-0465863.

PA (GENE-) GENETTYPE AG.

PI Simons MJ;

WPI; 1991-059664/09.

PT Detection of adjacent and non-adjacent locus, e.g. HLA alleles -
 PT by amplifying genomic DNA, for direct determination of haplotype

PS Claim 29; Page 49; 53pp; English.

CC The primer is specific for nt 1667-1685 of HLA Class I A2 locus.
 CC It is used in a method for the prodn. of RFLP fragments for an HLA
 CC locus, together with a second primer making up a locus-specific
 CC primer (LSP) pair. It is pref. used with a Class I-specific
 CC primer which hybridises with at least two different Class I loci,
 CC pref. at least one of each of A, B, and C, and most pref. all of
 CC these. The Class I primer esp. hybridises with intervening
 CC sequence (IVS) III or IVS I sequences. Direct determination of
 CC the haplotype is possible, providing useful information for
 CC identity of individuals for e.g. paternity case and forensic
 CC investigations.
 CC See also AAQ10621-Q10669.

SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 other;

Query Match 21.7%; Score 13; DB 12; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45

DB 3 AGAGAGTACTCT 15

RESULT 6

AAV9218/C

AAV9218 standard; DNA; 20 BP.

AC AAV9218;

XX Disclosure; Fig 15; 109pp; English.

XX
XX
XX The invention relates to promoter regions from mouse and human telomerase
CC RNA (TR) component genes. The TR gene promoter can be linked to a
CC heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC of cancer, especially neoplasias. The telomerase is necessary for the
CC unrestricted proliferative capacity of many human cancers. Mutation or
CC dysregulation of the telomerase repression pathway may cause reactivation
CC or upregulation of telomerase expression in cancer. Substances,
CC identified in the methods, can be used to block transcription from the TR
CC gene promoter through interaction of the 5' regulatory sequences. These
CC substances, e.g. antisense oligonucleotides, transcription factors,
CC peptide nucleic acids and factors that disrupt signal transduction, are
CC useful for cancer therapy. In particular, gene therapy vectors
CC (especially pG162-codupp) comprising the promoter and a viral thymidine
CC kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC neoplasia can be controlled or treated. Direct down-regulation of
CC telomerase RNA gene through manipulation of transcription factors may be
CC effective anticancer therapy and the cloning of the hTR gene promoter
CC allows the analysis of therapeutic molecules which modulate hTR promoter
CC activity. The present sequence represents an oligo comprising a Sp1 site.

XX
SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 other;

Query Match 33.3%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCAGCCCCGCCGAGAGAGT 39
Db 1 ACCAGCCCCGCCGAGAGAGT 20

RESULT 2
AA207318
ID AA207318 standard; DNA; 20 BP.

XX
AC AA207318;
DT 22-OCT-1999 (first entry)
XX
DE Human telomerase RNA gene (hTR) promoter specific primer h4.
XX
KM Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KM gene therapy; thymidine kinase gene; anticancer therapy; human;
KM mutagenesis; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9938964-A2.
XX
PD 05-AUG-1999.
XX
PF 29-JAN-1999; 99WO-GB00308.
XX
PR 29-JAN-1998; 98GB-0001902.
XX
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Keith MN;
XX
DR WPI; 1999-479183/40.
XX
PT Mouse and human telomerase RNA gene promoters, useful for tumor
PT specific gene therapy
XX
PS Disclosure; Fig 12; 109pp; English.
XX
CC The invention relates to promoter regions from mouse and human
CC telomerase RNA (TR) component genes. The TR gene promoter can be linked
CC to a heterologous gene, especially a gene encoding a cytotoxin, for

CC therapy of cancer, especially neoplasias. The telomerase is necessary for
CC the unrestricted proliferative capacity of many human cancers. Mutation
CC or dysregulation of the telomerase repression pathway may cause
CC reactivation or upregulation of telomerase expression in cancer.
CC Substances, identified in the methods, can be used to block transcription
CC from the TR gene promoter through interaction of the 5' regulatory
CC sequences. These substances, e.g. antisense oligonucleotides,
CC transcription factors, peptide nucleic acids and factors that disrupt
CC signal transduction, are useful for cancer therapy. In particular, gene
CC therapy vectors (especially pG162-codupp) comprising the promoter and a
CC viral thymidine kinase gene can be used to convert a prodrug, e.g.
CC gancyclovir, so that neoplasia can be controlled or treated. Direct
CC down-regulation of telomerase RNA gene through manipulation of
CC transcription factors may be effective anticancer therapy and the cloning
CC of the hTR gene promoter allows the analysis of therapeutic molecules
CC which modulate hTR promoter activity. Sequences AA207696-321 represent
CC PCR primers used in cloning and mutagenesis of human TR gene (hTR)
CC promoter region

XX
SQ Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 other;

Query Match 33.3%; Score 20; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCAGCCCCGCCGAGAGAGT 39
Db 1 ACCAGCCCCGCCGAGAGAGT 20

RESULT 3
AA13062/c
ID AA13062 standard; DNA; 31 BP.

XX
AC AA13062;
DT 18-OCT-2001 (first entry)
XX
DE Human single nucleotide polymorphism (SNP) 74.
XX
KM Human, resesquence; genotype; disease; forensic; paternity testing;
KM single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
FH Key
FH Variation Location/Qualifiers
FT rebase(16,T)
FT /*tag= a
XX /strand_name= "single nucleotide polymorphism"
XX
PN WO200166800-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-US07268.
XX
PR 07-MAR-2000; 2000US-0187510.
XX
PR 22-MAY-2000; 2000US-0206129.
XX
PA (WHEED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Cargill M, Ireland JS, Lander ES;
XX
DR WPI; 2001-522952/57.
XX
PT Nucleic acid molecules from the human genome which include polymorphic
PT sites, useful in methods for predicting the presence, absence or
PT severity of a particular phenotype or disorder (e.g. diabetes)
PT associated with a particular genotype -
XX
PS Claim 1; Page 65; 145pp; English.
XX
CC The invention relates to the identification of nucleic acid molecules

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:14:29 ; Search time 227.107 Seconds
(without alignments)
594.960 Million cell updates/sec

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Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

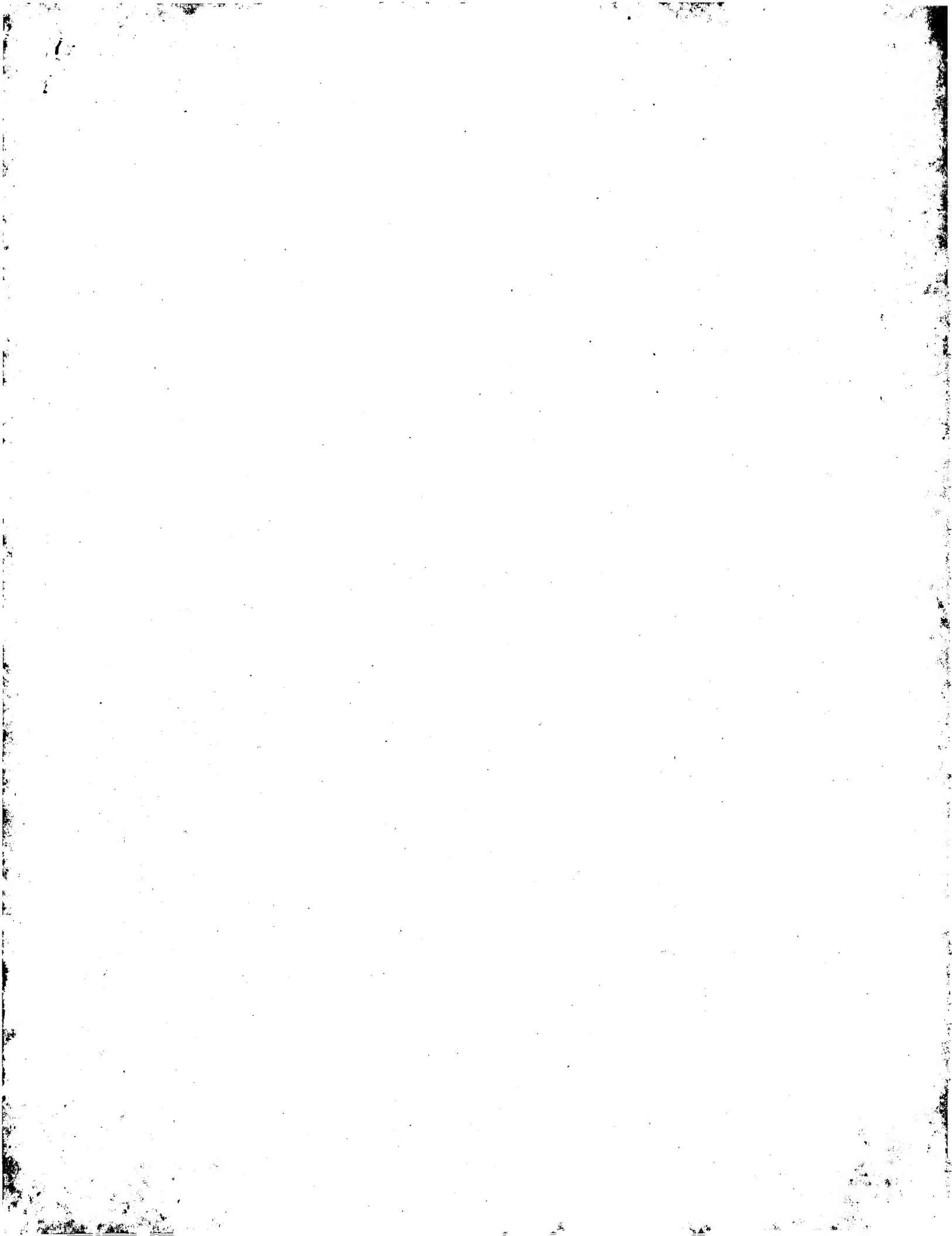
SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	33.3	20	AA207255	Wild-type oligo h4
2	20	33.3	20	AA207318	Human telomerase R
3	14	23.3	31	AA130062	Human single nucle
4	13	21.7	15	AA192154	Human IGERB allele
5	13	21.7	19	AAQ10624	HLA Class I locus-
6	13	21.7	20	AAV99218	Antisense primer f
7	13	21.7	20	AAV99218	Reverse primer #10
8	13	21.7	21	AAV46219	Human HLA-A primer
9	13	21.7	21	AAV46221	Human HLA-A primer

C	10	13	21.7	21	20	AAV38044	HLA-A untranslated
C	11	13	21.7	21	20	AAV38046	HLA-A untranslated
C	12	13	21.7	21	20	AAV38048	Reverse primer #10
C	13	13	21.7	22	21	AAV380281	Reverse primer #10
C	14	13	21.7	22	21	AAV380282	Reverse primer #11
C	15	13	21.7	22	21	AAV380283	Reverse primer #11
C	16	13	21.7	25	21	AAV380284	Reverse primer #11
C	17	13	21.7	25	21	AAV380285	Reverse primer #11
C	18	13	21.7	25	24	AAV380286	Reverse primer #11
C	19	13	21.7	39	14	AAV380287	Reverse primer #11
C	20	13	21.7	39	14	AAV380288	Reverse primer #11
C	21	13	21.7	39	14	AAV380289	Reverse primer #11
C	22	13	21.7	39	14	AAV380290	Reverse primer #11
C	23	13	21.7	39	14	AAV380291	Reverse primer #11
C	24	13	21.7	39	14	AAV380292	Reverse primer #11
C	25	13	21.7	39	14	AAV380293	Reverse primer #11
C	26	13	21.7	39	14	AAV380294	Reverse primer #11
C	27	13	21.7	39	14	AAV380295	Reverse primer #11
C	28	13	21.7	39	14	AAV380296	Reverse primer #11
C	29	13	21.7	39	14	AAV380297	Reverse primer #11
C	30	13	21.7	39	14	AAV380298	Reverse primer #11
C	31	13	21.7	39	14	AAV380299	Reverse primer #11
C	32	13	21.7	39	14	AAV380300	Reverse primer #11
C	33	13	21.7	39	14	AAV380301	Reverse primer #11
C	34	13	21.7	39	14	AAV380302	Reverse primer #11
C	35	13	21.7	39	14	AAV380303	Reverse primer #11
C	36	13	21.7	39	14	AAV380304	Reverse primer #11
C	37	13	21.7	39	14	AAV380305	Reverse primer #11
C	38	13	21.7	39	14	AAV380306	Reverse primer #11
C	39	13	21.7	39	14	AAV380307	Reverse primer #11
C	40	13	21.7	39	14	AAV380308	Reverse primer #11
C	41	13	21.7	39	14	AAV380309	Reverse primer #11
C	42	13	21.7	39	14	AAV380310	Reverse primer #11
C	43	13	21.7	39	14	AAV380311	Reverse primer #11
C	44	13	21.7	39	14	AAV380312	Reverse primer #11
C	45	13	21.7	39	14	AAV380313	Reverse primer #11

ALIGNMENTS

RESULT 1	AA207255	standard; DNA; 20 BP.
ID	AA207255;	
XX	AA207255;	
XX	22-OCT-1999	(first entry)
XX	Wild-type oligo h41 comprising Spt site.	
XX	Telomerase RNA; TR; promoter; cytotocin; cancer; neoplasia; hTR;	
XX	gene therapy; thymidine kinase gene; anticancer therapy; human; ss.	
XX	Synthetic.	
XX	Homo sapiens.	
XX	WO9338964-A2.	
XX	05-AUG-1999.	
XX	PD	
XX	29-JAN-1999;	99MO-GB00308.
XX	PF	
XX	29-JAN-1998;	98GB-0001902.
XX	PR	
XX	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.	
XX	Keitch WN;	
XX	WPI; 1999-479183/40.	
XX	DR	
XX	Mouse and human telomerase RNA gene promoters; useful for tumor	
XX	specific gene therapy	
XX	PT	



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SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,484
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2270
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: guanine attached to aminoethyl-lysine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: thymine attached to aminoethyl-lysine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: cytosine attached to aminoethyl-lysine
US-08-685-484-18
Query Match
Best Local Similarity 20.0%; Score 12; DB 1; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTTCCCCCAAC 21
DB 9 GTTCCCCCAAC 20
RESULT 15
US-08-847-108-18
Sequence 18, Application US/08847108
Patent No. 5736336
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5736336
TITLE OF INVENTION: and Solubility
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5736336r18 LLP
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/847,108
FILING DATE: 01-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/686,116
FILING DATE: JULY 24, 1996
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2271
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: guanine attached to aminoethyl-lysine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: thymine attached to aminoethyl-lysine
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 15
OTHER INFORMATION: cytosine attached to aminoethyl-lysine
US-08-847-108-18
Query Match
Best Local Similarity 20.0%; Score 12; DB 1; Length 20;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GTTCCCCCAAC 21
DB 9 GTTCCCCCAAC 20
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Search completed: June 24, 2003, 16:54:53
Job time : 61.5207 secs

GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER ANALOGS SPECIFIC FOR
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237,973
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,921
FILING DATE: 06-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCY J.
REGISTRATION NUMBER: 28,216
REFERENCE/DOCKET NUMBER: 24610-20032.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-237-973-36

Query Match 20.0%; Score 12; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CCCAACGAGCC 27
Db 17 CCCAACGAGCC 6

RESULT 13
US-08-686-116A-18
Sequence 18, Application US/08686116A
Patent No. 5714331
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Enhanced
TITLE OF INVENTION: Binding Affinity, Sequence Specificity
Patent No. 5714331
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5714331ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,116A
FILING DATE: July 24, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/108,591
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Michael P. Straher
REGISTRATION NUMBER: 38,325
REFERENCE/DOCKET NUMBER: ISIS-2271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: guanine attached to aminoethyl-lysine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: thymine attached to aminoethyl-lysine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: cytosine attached to aminoethyl-lysine
OTHER INFORMATION: backbone
FEATURE:
NAME/KEY: Modified-site
LOCATION: 16
OTHER INFORMATION: cytosine attached to aminoethyl-lysine
OTHER INFORMATION: backbone
US-08-686-116A-18

Query Match 20.0%; Score 12; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTCCCCCAGC 21
Db 9 GTTCCCCCAGC 20

RESULT 14
US-08-685-484-18
Sequence 18, Application US/08685484
Patent No. 5719262
GENERAL INFORMATION:
APPLICANT: Buchardt et al.
TITLE OF INVENTION: Peptide Nucleic Acids Having Amino Acid
TITLE OF INVENTION: Side Chains
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5719262ris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCES/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-290-793B-10

Query Match 20.0%; Score 12; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45
DB 16 GAGAGTACTCT 5

RESULT 10
US-08-234-613-23/c
Sequence 23, Application US/08234613
Patent No. 5582381
GENERAL INFORMATION:
APPLICANT: TOOLE, JOHN J.
APPLICANT: LATHAM, JOHN
APPLICANT: BOCK, LOUIS C.
APPLICANT: GRIFFIN, LINDA C.
TITLE OF INVENTION: APTAMER TARGET ELUTION METHOD
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/234,613
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/744,870
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCEY J.
REGISTRATION NUMBER: 28,216
REFERENCES/DOCKET NUMBER: 24610-20030.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-234-613-23

Query Match 20.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACCGCC 27
DB 17 CCCAACCGCC 6

RESULT 11
US-08-484-192-95/c
Sequence 95, Application US/08484192
Patent No. 575291
GENERAL INFORMATION:
APPLICANT: GRIFFIN, LINDA C.
APPLICANT: ALBRECHT, GLENN
APPLICANT: LATHAM, JOHN
APPLICANT: LEUNG, LAWRENCE
APPLICANT: VERNAS, ERIC
APPLICANT: TOOLE, JOHN J.
TITLE OF INVENTION: APTAMERS SPECIFIC FOR BIOMOLECULES AND
NUMBER OF SEQUENCES: 181
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,192
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,387
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: GRACEY, NANCEY J.
REGISTRATION NUMBER: 28,216
REFERENCES/DOCKET NUMBER: 246102002221
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-192-95

Query Match 20.0%; Score 12; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCCAACCGCC 27
DB 17 CCCAACCGCC 6

RESULT 12
US-08-237-973-36/c
Sequence 36, Application US/08237973
Patent No. 5640867

TELEPHONE: (908) 298-2987
TELEFAX: (908) 298-5388
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-744-10

Query Match 20.0%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45
|||||
DB 16 GAGAGTACTCT 5

RESULT 8
US-08-469-557-10/c
Sequence 10, Application US/08469557
Patent No. 5770403
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Le, Hung, Kenneth
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,557
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/113,623
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/881,553
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986

APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-557-10

Query Match 20.0%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTACTCT 45
|||||
DB 16 GAGAGTACTCT 5

RESULT 9
US-08-290-793B-10/c
Sequence 10, Application US/08290793B
Patent No. 5863537
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Le, Hung, Kenneth
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,793B
FILING DATE: August 16, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 24-OCT-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-MAY-1990
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/113,623
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/881,553
FILING DATE: 25-MAR-1986

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RESULT 5
PCT-US92-10359-1/c
Sequence 1, Application PC/US9210359
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Escobedo, Maria A.
APPLICANT: Preeto, Larry J.
TITLE OF INVENTION: Inhibitory Immunoglobulin Polypeptides
TITLE OF INVENTION: to Human PDGF Beta Receptor
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10359
FILING DATE: 19921201
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,795
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 12418-18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2422
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US92-10359-1

Query Match          21.7%; Score 13; DB 5; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 AATTCCCGTTCC 14
DB      19 AATTCCCGTTCC 7

RESULT 6
US-08-208-886C-10/c
Sequence 10, Application US/0820886C
Patent No. 5597710
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/208,886C
FILING DATE: March 10, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2987
TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-208-886C-10

Query Match          20.0%; Score 12; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      34 GAGAGTACTCT 45
DB      16 GAGAGTACTCT 5

RESULT 7
US-08-704-744-10/c
Sequence 10, Application US/08704744
Patent No. 5705154
GENERAL INFORMATION:
APPLICANT: Daille, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSER: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:

```

COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,394
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,574
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: S1237/7005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-08-927-394-8

Query Match 21.7%; Score 13; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 CGAGAGCCGCGAG 60
|||
Db 15 CGAGAGCCGCGAG 3

RESULT 3
US-08-927-394-7
Sequence 7, Application US/08927394
Patent No. 5990092
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: GATA-6 TRANSCRIPTION FACTOR: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,394
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,574
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: S1237/7005
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-927-394-7

Query Match 21.7%; Score 13; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 48 CGAGAGCCGCGAG 60
|||
Db 14 CGAGAGCCGCGAG 26

RESULT 4
US-08-258-283-1/c
Sequence 1, Application US/08258283
Patent No. 5817310
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Escobedo, Maria A.
TITLE OF INVENTION: INHIBITORY IMMUNOGLOBULIN POLYPEPTIDES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,283
FILING DATE: 10 JUN 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Karen B. Dow
REGISTRATION NUMBER: 29,684
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-08-258-283-1

Query Match 21.7%; Score 13; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AATTCCCGTTCC 14
|||
Db 19 AATTCCCGTTCC 7

QY 42 CTCTCAGGAG 53
DB 25 CTCTCAGGAG 14

RESULT 15
US-10-098-263B-24180/c
; Sequence 24180, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mitterman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 24180
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-24180

Query Match 20.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 42 CTCTCAGGAG 53
DB 25 CTCTCAGGAG 14

Search completed: June 24, 2003, 20:39:34
Job time : 733.909 secs

MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-003-810-1

Query Match 21.7%; Score 13; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTTCCCGTTCC 14
DB 19 AATTTCCCGTTCC 7

RESULT 11
US-09-419-076-1/C
Sequence 1, Application US/09419076
Patent No. US2002009443A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Vanitha
APPLICANT: Pectro, Larry U.
TITLE OF INVENTION: Inhibitory Immunoglobulin Polypeptides to Human PDGF
FILE REFERENCE: 44481-5017-04-US
CURRENT APPLICATION NUMBER: US/09/419,076
PRIOR FILING DATE: 1999-10-15/801,795
PRIOR APPLICATION NUMBER: US 07/801,795
PRIOR FILING DATE: 1991-12-02
PRIOR APPLICATION NUMBER: US 08/253,440
PRIOR FILING DATE: 1994-06-07
PRIOR APPLICATION NUMBER: US 08/258,263
PRIOR FILING DATE: 1994-06-10
PRIOR APPLICATION NUMBER: US 09/003,810
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide for creating PDGF beta receptor
US-09-419-076-1

Query Match 21.7%; Score 13; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AATTTCCCGTTCC 14
DB 19 AATTTCCCGTTCC 7

RESULT 12
US-09-932-300-66
Sequence 66, Application US/09932300
Publication No. US2003003788A1
GENERAL INFORMATION:
APPLICANT: GARNER, Eric
APPLICANT: TU, Guang-Chou
APPLICANT: ISRAEL, Yedy
TITLE OF INVENTION: METHODS OF INHIBITING ALCOHOL CONSUMPTION
FILE REFERENCE: 9855-3U2
CURRENT APPLICATION NUMBER: US/09/932,300
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: US 60/051,705
PRIOR FILING DATE: 1997-07-03
PRIOR APPLICATION NUMBER: US 09/109,663
PRIOR FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 111

SOFTWARE: Patent Ver. 2.1
SEQ ID NO 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Known
OTHER INFORMATION: effective ASO
US-09-932-300-66

Query Match 20.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCCCCCAAC 21
DB 9 GTTCCCCCAAC 20

RESULT 13
US-10-016-149-62/C
Sequence 62, Application US/10016149
Publication No. US20030100524A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP V (CA2+-DEPENDENT) EXPRESSION
FILE REFERENCE: RTS-0325
CURRENT APPLICATION NUMBER: US/10/016,149
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 62
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-016-149-62

Query Match 20.0%; Score 12; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGACTCT 45
DB 12 GAGAGTGACTCT 1

RESULT 14
US-10-098-263B-24179/C
Sequence 24179, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
PRIOR FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 24179
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-24179

Query Match 20.0%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 21.7%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AGAGAGTACTCT 45
 |||||
 DB 20 AGAGAGTACTCT 8

RESULT 7
 US-10-098-263B-8500
 ; Sequence 8500, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitterman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; PRIOR FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 8500
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-8500

Query Match 21.7%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 CTCACGAGAGCCG 56
 |||||
 DB 12 CTCACGAGAGCCG 24

RESULT 8
 US-10-098-263B-24815/C
 ; Sequence 24815, Application US/10098263B
 ; Publication No. US20030104410A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mitterman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/098,263B
 ; PRIOR FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/276,759
 ; PRIOR FILING DATE: 2001-03-16
 ; NUMBER OF SEQ ID NOS: 131066
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 24815
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-098-263B-24815

Query Match 21.7%; Score 13; DB 9; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ACTCTCAGAGAG 53
 |||||
 DB 25 ACTCTCAGAGAG 13

RESULT 9
 US-09-971-611-37/C
 ; Sequence 37, Application US/09971611
 ; Patent No. US20020123124A1
 ; GENERAL INFORMATION:

APPLICANT: ARAKI, HIROYUKI
 ; APPLICANT: ENDO, KEIJI
 ; APPLICANT: HASEGAWA, HIROSHI
 ; APPLICANT: IGARASHI, KAZUAKI
 ; APPLICANT: HAYASHI, YASUHIRO
 ; APPLICANT: OZAKI, KATSUYA
 ; TITLE OF INVENTION: HIGHLY PRODUCTIVE ALPHA-AMYLASES
 ; FILE REFERENCE: 214377USO
 ; CURRENT APPLICATION NUMBER: US/09/971,611
 ; PRIOR FILING DATE: 2001-10-09
 ; PRIOR APPLICATION NUMBER: JP 2000/310605
 ; PRIOR FILING DATE: 2001-10-11
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 37
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic DNA
 US-09-971-611-37

Query Match 21.7%; Score 13; DB 10; Length 25;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TTCCCCCAACCA 23
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 DB 15 TTCCCCCAACCA 3

RESULT 10
 US-09-003-810-1/C
 ; Sequence 1, Application US/09003810
 ; Publication No. US20030059425A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ramakrishnan, Vanitha
 ; Escobedo, Maria A.
 ; Pretto, Larry J.
 ; TITLE OF INVENTION: INHIBITORY IMMUNOGLOBULIN POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Knourle and Crew
 ; STREET: 379 Lytton Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/003,810
 ; FILING DATE: 07-Jan-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/258,283
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Karen B. Dow
 ; REGISTRATION NUMBER: 29,684
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 326-2400
 ; TELEFAX: (415) 326-2422
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 40 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear


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; FILE REFERENCE: ICG-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-199

Query Match          21.7%; Score 13; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      16 AGAGAGTGACTCT 4

RESULT 3
US-09-964-261-200/c
; Sequence 200, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ICG-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 200
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-200

Query Match          21.7%; Score 13; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      17 AGAGAGTGACTCT 5

RESULT 4
US-09-964-261-201/c
; Sequence 201, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ICG-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
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; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 201
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-201

Query Match          21.7%; Score 13; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      18 AGAGAGTGACTCT 6

RESULT 5
US-09-964-261-202/c
; Sequence 202, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ICG-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 202
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-202

Query Match          21.7%; Score 13; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTGACTCT 45
Db      19 AGAGAGTGACTCT 7

RESULT 6
US-09-964-261-203/c
; Sequence 203, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: ICG-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-203
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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11: /cgn2_6/ptodaca/2/pubpna/US10_NEW_PUB.seq:*
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14: /cgn2_6/ptodaca/2/pubpna/US60_PUBCOMB.seq:*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 3	13	21.7	22	9 US-09-964-261-200	Sequence 200, App
C 4	13	21.7	23	9 US-09-964-261-201	Sequence 201, App
C 5	13	21.7	24	9 US-09-964-261-202	Sequence 202, App
C 6	13	21.7	25	9 US-09-964-261-203	Sequence 203, App
C 7	13	21.7	25	9 US-10-098-263B-8500	Sequence 8500, App
C 8	13	21.7	25	9 US-10-098-263B-24815	Sequence 24815, A
C 9	13	21.7	25	10 US-09-971-611-37	Sequence 37, Appl
C 10	13	21.7	40	9 US-09-003-810-1	Sequence 1, Appl
C 11	13	21.7	40	10 US-09-419-076-1	Sequence 66, Appl
C 12	13	21.7	20	9 US-09-932-300-66	Sequence 62, Appl
C 13	13	21.7	20	9 US-10-016-149-62	Sequence 24160, A
C 14	13	21.7	25	9 US-10-098-263B-44179	Sequence 24160, A
C 15	13	21.7	25	9 US-10-098-263B-44160	Sequence 24160, A
C 16	13	21.7	25	9 US-10-098-263B-44816	Sequence 24816, A
C 17	13	21.7	25	9 US-10-098-263B-40334	Sequence 40334, A
C 18	13	21.7	25	9 US-10-098-263B-40334	Sequence 40334, A
C 19	13	21.7	25	9 US-10-098-263B-44135	Sequence 44135, A

C 20	12	20.0	25	9 US-10-098-263B-48690	Sequence 48690, A
C 21	12	20.0	25	9 US-10-098-263B-49760	Sequence 49760, A
C 22	12	20.0	25	9 US-10-098-263B-75176	Sequence 75176, A
C 23	12	20.0	25	9 US-10-098-263B-86702	Sequence 86702, A
C 24	12	20.0	25	9 US-10-098-263B-99417	Sequence 99417, A
C 25	12	20.0	25	9 US-10-098-263B-110168	Sequence 110168, A
C 26	12	20.0	25	9 US-10-098-263B-117410	Sequence 117410, A
C 27	12	20.0	25	10 US-09-971-611-30	Sequence 30, Appl
C 28	12	20.0	31	9 US-10-163-552-1392	Sequence 1392, App
C 29	11	18.3	17	9 US-09-904-968A-104	Sequence 104, App
C 30	11	18.3	17	9 US-09-780-533A-277	Sequence 277, App
C 31	11	18.3	17	9 US-09-780-533A-1150	Sequence 1150, App
C 32	11	18.3	17	9 US-09-780-533A-1151	Sequence 1151, App
C 33	11	18.3	17	9 US-09-780-533A-1935	Sequence 1935, App
C 34	11	18.3	17	9 US-09-930-423-287	Sequence 287, App
C 35	11	18.3	17	9 US-09-930-423-288	Sequence 288, App
C 36	11	18.3	17	9 US-09-930-423-289	Sequence 289, App
C 37	11	18.3	17	9 US-09-930-423-291	Sequence 291, App
C 38	11	18.3	17	9 US-09-930-423-1146	Sequence 1146, App
C 39	11	18.3	18	9 US-09-853-526-387	Sequence 387, App
C 40	11	18.3	18	10 US-09-901-484A-1387	Sequence 121, App
C 41	11	18.3	20	9 US-09-824-322B-121	Sequence 121, App
C 42	11	18.3	20	9 US-09-888-326-688	Sequence 688, App
C 43	11	18.3	20	9 US-10-112-653-112	Sequence 312, App
C 44	11	18.3	20	9 US-10-017-995-123	Sequence 323, App
C 45	11	18.3	20	9 US-09-776-479-323	Sequence 323, App

ALIGNMENTS

RESULT 1
US-09-964-261-198/c
; Sequence 198, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES
; FILE REFERENCE: 163-002
; CURRENT APPLICATION NUMBER: US/09/964,261
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: EP 99870068.6
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/138,614
; PRIOR FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 198
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-261-198

Query Match 21.7%; Score 13; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 33 AGAGAGTACTCT 45
Db 15 AGAGAGTACTCT 3

RESULT 2
US-09-964-261-199/c
; Sequence 199, Application US/09964261
; Publication No. US20020197613A1
; GENERAL INFORMATION:
; APPLICANT: De Canck, Ilse
; APPLICANT: Rombout, Annelies
; APPLICANT: Rossau, Rudi
; TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES

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; SOFTWARE: Proprietary
; SEQ ID NO 15330
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Deinococcus radiodurans R1 complete genome, plasmid
; FEATURE:
; LOCATION: (1850407)..(1850421)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 17904
PCT-US02-25940-15330

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Query Match          21.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

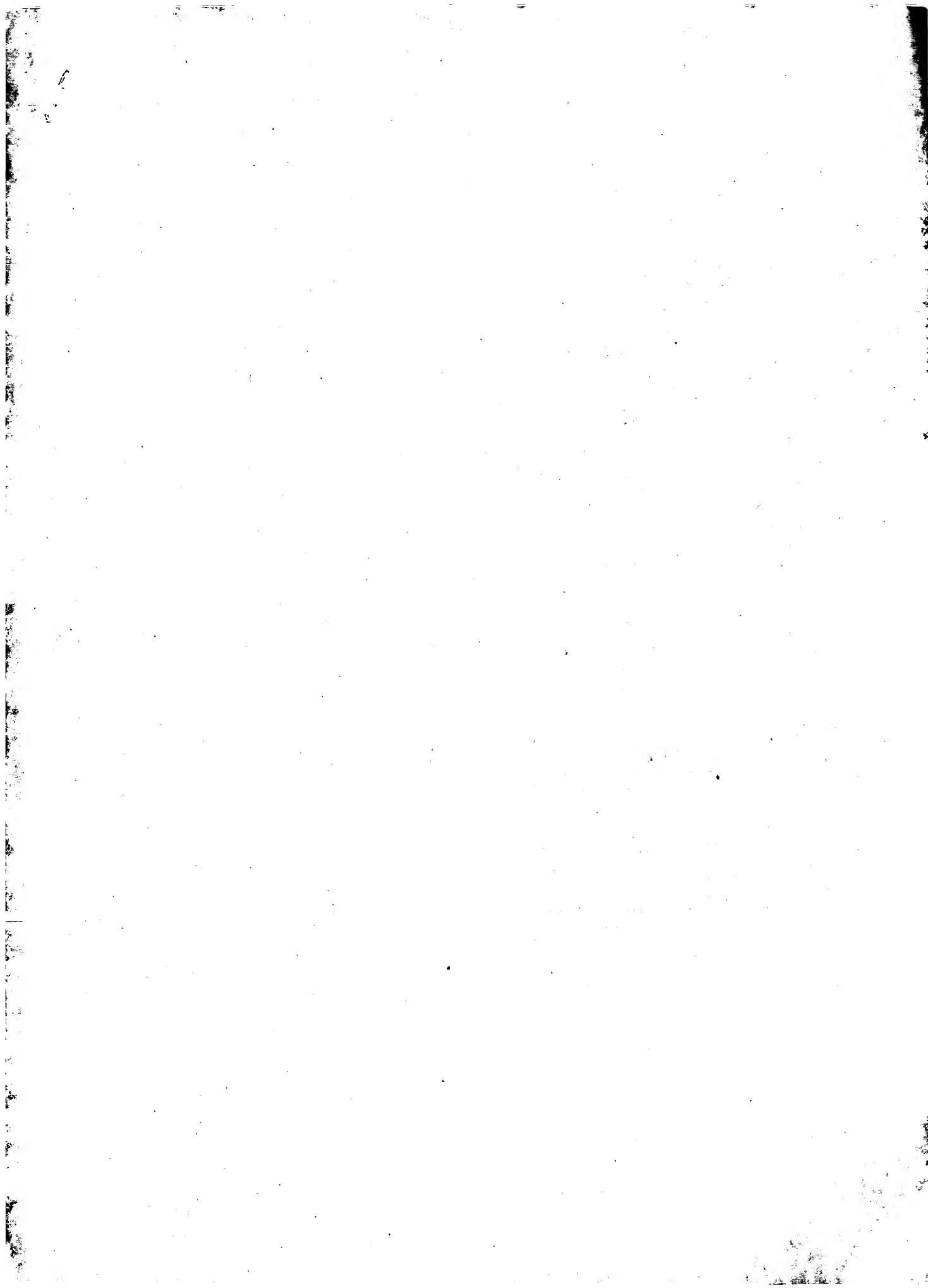
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Qy 24 GCGCGCGCGAGAG 36
Db 1 GCGCGCGCGAGAG 13

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Search completed: June 24, 2003, 18:22:27
 Job time : 2598.88 secs



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APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196F
CURRENT FILING DATE: 2001-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41222
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196F-41222

Query Match
Best Local Similarity 100.0%; Score 14; DB 17; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GCCCGAGAGAGTGA 41
DB 9 GCCCGAGAGAGTGA 22

RESULT 11
US-09-396-196G-41222
Sequence 41222, Application US/09396196G
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41222
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-41222

Query Match
Best Local Similarity 100.0%; Score 14; DB 17; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GCCCGAGAGAGTGA 41
DB 9 GCCCGAGAGAGTGA 22

RESULT 12
US-60-353-987-314865
Sequence 314865, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 314865
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
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```
US-60-353-987-314865

Query Match
Best Local Similarity 100.0%; Score 14; DB 79; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ACGAGAGCCCGCAG 60
DB 12 ACGAGAGCCCGCAG 25

RESULT 13
US-60-353-987-847501
Sequence 847501, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 847501
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-353-987-847501

Query Match
Best Local Similarity 100.0%; Score 14; DB 79; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 ACGAGAGCCCGCAG 60
DB 10 ACGAGAGCCCGCAG 23

RESULT 14
US-60-353-987-952021/C
Sequence 952021, Application US/60353987
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/60/353,987
CURRENT FILING DATE: 2002-02-01
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 952021
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-60-353-987-952021

Query Match
Best Local Similarity 100.0%; Score 14; DB 79; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 CGAGAGAGTGATTC 44
DB 21 CGAGAGAGTGATTC 8

RESULT 15
PCT-US02-25940-15330
Sequence 15330, Application PCT/TUS0225940
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Deinococcus radiodurans RI complete genome, Plasmid
FILE REFERENCE: Jim Zeigler Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: PCT/US02/25940
CURRENT FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 25502
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RESULT 5
US-60-234-017-339051
; Sequence 339051, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 339051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339051

Query Match      28.3%; Score 17; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCAGC 49
DB      4 AGAGAGTACTCTCAGC 20

RESULT 6
US-60-353-987-351034/c
; Sequence 351034, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 351034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-351034

Query Match      26.7%; Score 16; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 GAGTGACTCTCAGCAG 51
DB      18 GAGTGACTCTCAGCAG 3

RESULT 7
US-09-956-584-328898
; Sequence 328898, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328898
; LENGTH: 25

; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328898

Query Match      25.0%; Score 15; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCA 47
DB      11 AGAGAGTACTCTCA 25

RESULT 8
US-60-234-017-339061
; Sequence 339061, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltmann, M
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 339061
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339061

Query Match      25.0%; Score 15; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 AGAGAGTACTCTCA 47
DB      11 AGAGAGTACTCTCA 25

RESULT 9
US-60-353-987-448107
; Sequence 448107, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-448107

Query Match      25.0%; Score 15; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 GCCCGAGAGAGTGAC 42
DB      8 GCCCGAGAGAGTGAC 22

RESULT 10
US-09-396-196F-41222
; Sequence 41222, Application US/09396196F
; GENERAL INFORMATION:
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22 13 21.7 16 1 PCT-US02-25940-18174 Sequence 18174, A
23 13 21.7 16 1 PCT-US02-25940-22043 Sequence 22043, A
24 13 21.7 16 42 US-10-327-563-18174 Sequence 18174, A
25 13 21.7 16 42 US-10-327-563-22043 Sequence 22043, A
26 13 21.7 18 1 PCT-US02-25940-17148 Sequence 17148, A
27 13 21.7 18 1 PCT-US02-25940-17149 Sequence 17149, A
28 13 21.7 18 1 PCT-US02-25940-18156 Sequence 18156, A
29 13 21.7 18 42 US-10-327-563-17148 Sequence 17148, A
30 13 21.7 18 42 US-10-327-563-17149 Sequence 17149, A
31 13 21.7 19 38 US-10-327-563-18156 Sequence 18156, A
32 13 21.7 19 38 US-10-005-626A-33 Sequence 33, Appl
33 13 21.7 20 30 US-09-777-525-129 Sequence 129, App
34 13 21.7 20 36 US-09-964-261-198 Sequence 198, App
35 13 21.7 21 11 US-08-766-1898-200 Sequence 200, App
36 13 21.7 21 11 US-08-766-1898-202 Sequence 202, App
37 13 21.7 21 11 US-08-766-189C-200 Sequence 200, App
38 13 21.7 21 11 US-08-766-189C-202 Sequence 202, App
39 13 21.7 21 13 US-08-909-290-200 Sequence 200, App
40 13 21.7 21 13 US-08-909-290-202 Sequence 202, App
41 13 21.7 21 36 US-09-964-261-199 Sequence 199, App
42 13 21.7 22 8 US-08-472-801-625 Sequence 625, App
43 13 21.7 22 10 US-08-668-235-626 Sequence 626, App
44 13 21.7 22 36 US-09-964-261-200 Sequence 200, App
45 13 21.7 23 1 PCT-US00-35593A-61 Sequence 61, Appl

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ALIGNMENTS

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RESULT 1
US-09-601-267-62
; Sequence 62, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol KEITH
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601,267
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-601-267-62
Query Match 33.3%; Score 20; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ACCGAGCCGCCGCGAGAGT 39
Db 1 ACCGAGCCGCCGCGAGAGT 20

RESULT 2
US-09-956-584-328887
; Sequence 328887, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20

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; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328887

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```

Query Match 28.3%; Score 17; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 AGAGAGTGACTCTCAG 49
Db 4 AGAGAGTGACTCTCAG 20

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RESULT 3
US-09-956-584-328890
; Sequence 328890, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 328890
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-328890

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Query Match 28.3%; Score 17; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 AGAGAGTGACTCTCAG 49
Db 9 AGAGAGTGACTCTCAG 25

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```

RESULT 4
US-60-234-017-339049
; Sequence 339049, Application US/60234017
; GENERAL INFORMATION:
; APPLICANT: Miltman, M
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus
; FILE REFERENCE: 3115
; CURRENT APPLICATION NUMBER: US/60/234,017
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339049
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA982370
US-60-234-017-339049

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Query Match 28.3%; Score 17; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 AGAGAGTGACTCTCAG 49
Db 9 AGAGAGTGACTCTCAG 25

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:01:44 ; Search time 2594.88 Seconds
(Without alignments)
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Title: US-08-770-564a-1_COPY_137_196

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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Listing first 45 summaries

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3	17	28.3	25	US-09-956-584-328890	Sequence 328890,
4	17	28.3	25	US-60-234-017-339049	Sequence 339049,
5	17	28.3	25	US-60-234-017-339051	Sequence 339051,
6	16	26.7	25	US-60-353-987-314655	Sequence 314655,
7	15	25.0	25	US-09-956-584-328898	Sequence 328898,
8	15	25.0	25	US-60-234-017-339061	Sequence 339061,
9	15	25.0	25	US-60-353-987-448107	Sequence 448107,
10	14	23.3	25	US-09-396-196F-41222	Sequence 41222, A
11	14	23.3	25	US-09-396-196G-41222	Sequence 41222, A
12	14	23.3	25	US-60-353-987-314655	Sequence 314655,
13	14	23.3	25	US-60-353-987-847501	Sequence 847501,
14	14	23.3	25	US-60-353-987-847501	Sequence 847501,
15	13	21.7	15	PCT-US02-25940-15330	Sequence 15330, A
16	13	21.7	15	PCT-US02-25940-15330	Sequence 15330, A
17	13	21.7	15	PCT-US02-25940-15330	Sequence 15330, A
18	13	21.7	15	US-09-889-866A-12	Sequence 12, Appl
19	13	21.7	15	US-10-227-563-15330	Sequence 15330, A
20	13	21.7	15	US-10-227-563-19741	Sequence 19741, A
21	13	21.7	15	US-10-227-563-23260	Sequence 23260, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

QY 36 GAGTGACTCTCAG 49
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 Db 25 GAGTGACTCTCAG 12

RESULT 12
 US-60-417-190-41679/c
 ; Sequence 41679, Application US/60417190
 ; GENERAL INFORMATION:
 ; APPLICANT: Giulia Kennedy
 ; APPLICANT: Hajime Matsuzaki
 ; APPLICANT: Mei-Mei Shen
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
 ; FILE REFERENCE: 3522
 ; CURRENT APPLICATION NUMBER: US/60/417,190
 ; CURRENT FILING DATE: 2002-10-02
 ; NUMBER OF SEQ ID NOS: 122930
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 41679
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-60-417-190-41679

Query Match 23.3%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAG 48
 |||||
 Db 24 AGAGTGACTCTCAG 11

RESULT 13
 US-60-417-190-41680/c
 ; Sequence 41680, Application US/60417190
 ; GENERAL INFORMATION:
 ; APPLICANT: Giulia Kennedy
 ; APPLICANT: Hajime Matsuzaki
 ; APPLICANT: Mei-Mei Shen
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
 ; FILE REFERENCE: 3522
 ; CURRENT APPLICATION NUMBER: US/60/417,190
 ; CURRENT FILING DATE: 2002-10-02
 ; NUMBER OF SEQ ID NOS: 122930
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 41680
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-60-417-190-41680

Query Match 23.3%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAG 48
 |||||
 Db 23 AGAGTGACTCTCAG 10

RESULT 14
 US-60-427-808-34731/c
 ; Sequence 34731, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 34731

; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-34731

Query Match 23.3%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 GAGAGTGACTCTCA 47
 |||||
 Db 22 GAGAGTGACTCTCA 9

RESULT 15
 US-60-427-808-709610
 ; Sequence 709610, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 709610
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-60-427-808-709610

Query Match 23.3%; Score 14; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 CTCTCAGAGAGCC 55
 |||||
 Db 8 CTCTCAGAGAGCC 21

Search completed: June 24, 2003, 20:14:42
 Job time: 3335.23 secs

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/ SEQ ID NO 41675
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-41675
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Query Match
Best Local Similarity 100.0%; Score 15; DB 12; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 35 AGAGTACTCTCAGC 49
Db 23 AGAGTACTCTCAGC 9
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```
RESULT 7
US-60-470-475-42235/c
/ Sequence 42235, Application US/60470475
/ GENERAL INFORMATION:
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Shen, Mei-Mei
/ APPLICANT: Kennedy, Giulia
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522.1
/ CURRENT APPLICATION NUMBER: US/60/470,475
/ PRIOR FILING DATE: 2003-05-14
/ PRIOR APPLICATION NUMBER: 60/417,190
/ NUMBER OF SEQ ID NOS: 124031
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 42235
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-470-475-42235
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```
Query Match
Best Local Similarity 100.0%; Score 15; DB 13; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 35 AGAGTACTCTCAGC 49
Db 23 AGAGTACTCTCAGC 9
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```
RESULT 8
US-10-355-577-314865
/ Sequence 314865, Application US/10355577
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/10/355,577
/ PRIOR FILING DATE: 2003-01-31
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 314865
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-355-577-314865
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 47 ACGAGAGCCGCGAG 60
Db 12 ACGAGAGCCGCGAG 25
```

```
RESULT 9
US-10-355-577-847501
```

```
/ Sequence 847501, Application US/10355577
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/10/355,577
/ PRIOR FILING DATE: 2003-01-31
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 847501
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-355-577-847501
```

```
Query Match
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 47 ACGAGAGCCGCGAG 60
Db 10 ACGAGAGCCGCGAG 23
```

```
RESULT 10
US-10-355-577-952021/c
/ Sequence 952021, Application US/10355577
/ GENERAL INFORMATION:
/ APPLICANT: Miltmann, Michael
/ TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
/ FILE REFERENCE: 3121
/ CURRENT APPLICATION NUMBER: US/10/355,577
/ PRIOR FILING DATE: 2003-01-31
/ NUMBER OF SEQ ID NOS: 997516
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 952021
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-355-577-952021
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```
Query Match
Best Local Similarity 100.0%; Score 14; DB 9; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 31 CGAGAGTACTC 44
Db 21 CGAGAGTACTC 8
```

```
RESULT 11
US-60-417-190-41673/c
/ Sequence 41673, Application US/60417190
/ GENERAL INFORMATION:
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Shen, Mei-Mei
/ APPLICANT: Kennedy, Giulia
/ TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
/ FILE REFERENCE: 3522
/ CURRENT APPLICATION NUMBER: US/60/417,190
/ PRIOR FILING DATE: 2002-10-02
/ NUMBER OF SEQ ID NOS: 122930
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO 41673
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-60-417-190-41673
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Query Match
Best Local Similarity 100.0%; Score 14; DB 12; Length 25;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 35 AGAGTGACTCTCAGAGAG 53
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Db 1 AGAGTGACTCTCAGAGAG 19

RESULT 2

PCT-US03-04088-265/c
; Sequence 265, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 265
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; PCT-US03-04088-265

Query Match 31.7%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGAGAG 53
|||:|||||
Db 19 AGAGTGACTCTCAGAGAG 1

RESULT 3
US-10-355-577-351034/c
; Sequence 351034, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 351034
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-355-577-351034

Query Match 26.7%; Score 16; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAGTGACTCTCAGAG 51
|||:|||||
Db 18 GAGTGACTCTCAGAG 3

RESULT 4

US-10-355-577-448107
; Sequence 448107, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Miltmann, Michael
; APPLICANT: Hajime Matsuzaki
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 448107
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-355-577-448107

Query Match 25.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GCCCGAGAGAGTGAC 42
|||:|||||
Db 8 GCCCGAGAGAGTGAC 22

RESULT 5

US-60-417-190-41674/c
; Sequence 41674, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 41674
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
; US-60-417-190-41674

Query Match 25.0%; Score 15; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 AGAGTGACTCTCAGC 49
|||:|||||
Db 24 AGAGTGACTCTCAGC 10

RESULT 6
US-60-417-190-41675/c
; Sequence 41675, Application US/60417190
; GENERAL INFORMATION:
; APPLICANT: Giulia Kennedy
; APPLICANT: Hajime Matsuzaki
; APPLICANT: Mei-Mei Shen
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522
; CURRENT APPLICATION NUMBER: US/60/417,190
; CURRENT FILING DATE: 2002-10-02
; NUMBER OF SEQ ID NOS: 122930
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

Query Match 26.7%; Score 16; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6
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OW nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 3332.23 Seconds
(without alignments)
125.426 Million cell updates/sec

Title: US-08-770-564a-1_COPY_137_196

Perfect score: 60

Sequence: 1 TAAATCCCGTCCCGCCCA.....ACTCAGAGCGCGAG 60

Scoring table: OLIGO.MNC

Searched: 7821610 seqs, 348290355 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8654690

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending Patents_NA_New:*

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- 2: /cgn2_6/pdata/2/pna/US06-NEW_COMB.seq:*
- 3: /cgn2_6/pdata/2/pna/US08-NEW_COMB.seq:*
- 4: /cgn2_6/pdata/2/pna/US08-NEW_COMB.seq:*
- 5: /cgn2_6/pdata/2/pna/US09-NEW_COMB.seq:*
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- 10: /cgn2_6/pdata/2/pna/US10-NEW_COMB.seq:*
- 11: /cgn2_6/pdata/2/pna/US60-NEW_COMB.seq:*
- 12: /cgn2_6/pdata/2/pna/US60-NEW_COMB.seq:*
- 13: /cgn2_6/pdata/2/pna/US60-NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	31.7	19	1	PCT-US03-04088-1
3	16	26.7	25	9	US-10-355-577-351034
4	15	25.0	25	12	US-10-355-577-448107
5	15	25.0	25	12	US-10-355-577-448107
6	15	25.0	25	12	US-10-355-577-448107
7	15	25.0	25	12	US-10-355-577-448107
8	14	23.3	25	9	US-10-355-577-847501
9	14	23.3	25	9	US-10-355-577-847501
10	14	23.3	25	9	US-10-355-577-847501
11	14	23.3	25	12	US-60-417-190-41679
12	14	23.3	25	12	US-60-417-190-41679
13	14	23.3	25	12	US-60-417-190-41679
14	14	23.3	25	12	US-60-417-190-41679
15	14	23.3	25	12	US-60-417-190-41679
16	14	23.3	25	12	US-60-417-190-41679
17	14	23.3	25	12	US-60-417-190-41679
18	14	23.3	25	12	US-60-417-190-41679
19	14	23.3	25	12	US-60-417-190-41679
20	13	21.7	15	10	US-10-367-892-19741

21	13	21.7	16	10	US-10-367-892-18174	Sequence 18174, A
22	13	21.7	16	10	US-10-367-892-22043	Sequence 22043, A
23	13	21.7	18	10	US-10-367-892-17148	Sequence 17148, A
24	13	21.7	18	10	US-10-367-892-17148	Sequence 17148, A
25	13	21.7	18	10	US-10-367-892-18156	Sequence 18156, A
26	13	21.7	19	5	US-09-935-9984-33	Sequence 33, Appl
27	13	21.7	23	10	US-10-367-892-17147	Sequence 17147, A
28	13	21.7	25	9	US-10-098-263B-8500	Sequence 8500, Ap
29	13	21.7	25	9	US-10-098-263B-8500	Sequence 24815, A
30	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
31	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
32	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
33	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
34	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
35	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
36	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
37	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
38	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
39	13	21.7	25	9	US-10-355-577-151514	Sequence 151514, A
40	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A
41	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A
42	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A
43	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A
44	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A
45	13	21.7	25	12	US-60-417-190-41679	Sequence 41679, A

ALIGNMENTS

RESULT 1
PCT-US03-04088-1
Sequence 1, Application PC/US0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelsen, James
TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 19
TYPE: RNA
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
OTHER INFORMATION: region
PCT-US03-04088-1

Query Match 31.7%; Score 19; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 16; Conservative 3; Mismatches 0;

DIFFUSION ;, mRNA sequence.

ACCESSION

H27426

VERSION

H27426.1 GI:897416

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 34)

AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucada, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE

The WashU-Merck EST Project

JOURNAL

Unpublished (1995)

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 735

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LNL

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 735

Std Error: 0.00

Seq primer: M13Rev

High quality sequence stop: 1.

FEATURES

source

Location/Qualifiers

1..34

/organism="Homo sapiens"

/db_xref="GDB:575254"

/db_xref="taxon:9606"

/clone="IMAGE:161139"

/clone.lib="Soares breast 3NBHbst"

/sex="Female"

/dev_stage="adult"

/lab_host="DH10B (ampicillin resistant)"

/note="Organ: breast; Vector: pTZ19 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAGTGGAGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot = 20. Library constructed by Bento Soares and M.Fatima Bonaldo."

Bonaldo."

BASE COUNT

6 a 10 c 8 g 10 t

ORIGIN

Query Match

Best Local Similarity

18.3%; Score 11; DB 14; Length 34;

Matches

11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

15 CCCCAACCAGC 25

DB

30 CCCCAACCAGC 20

Search completed: June 24, 2003, 16:52:41
Job time : 1575.41 secs

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 DEFINITION EP(3)1001 Drosophila melanogaster EP line Drosophila melanogaster
 genomic sequence recovered from 5' end of P element, DNA sequence.
 ACCESSION A0025148
 VERSION A0025148.1 GI:3265500
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 30)
 Liao,G.-C., Rehm,E.J. and Rubin,G.M.
 Insertion site preferences of the P transposable element in
 Drosophila melanogaster
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
 JOURNAL 20202638
 MEDLINE
 COMMENT Contact: Gerald Rubin
 Berkeley Drosophila Genome Project
 University of California Berkeley
 LSA Building Berkeley, CA 94720-3200, USA
 Fax: 5106433947
 Email: ger@fruitfly.berkeley.edu
 Sequence recovery method was inverse PCR.
 Sequence orientation is forward strand relative to 5' end of P
 element
 The P element insertion position is base 23 in the 30 bases. This
 insertion position refers to the first base of the 8 base target
 recognition sequence.
 Class: transposon-tagged.
 Location/Qualifiers
 1. 30
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_1ib="Drosophila melanogaster EP line"
 /note="Inverse PCR was performed on Drosophila
 melanogaster strains each of which contains a single EP
 transposable element insertion. (The generation of these
 insertion strains is described in Roth P, Szabo K, Bailey
 A, Laverdy T, Rehm J, Rubin GM, Weigman K, Milan M, Benes
 V, Anorga W, Cohen SW, 1998. Systematic gain-of-function
 genetics in Drosophila. Development 6:1049-1057.) The
 resultant fragment for each strain was directly sequenced
 to determine the genomic sequence at the site of
 insertion. Details of the protocols used can be found at
 http://fruitfly.berkeley.edu/p_disrupt/inverse_pcr.html."
 BASE COUNT 0 a 11 c 10 g 9 t
 ORIGIN
 Query Match 18.3%; Score 11; DB 17; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 46 CACGAGACCG 56
 DB 16 CACGAGACCG 6
 RESULT 14
 LOCUS A1793967
 DEFINITION f56604.x1 zebrafish Mashu MPing EST Danio rerio cDNA clone
 IMAGE:3725430 3' similar to TR:Q61888 PROLINE RICH PROTEIN.
 ACCESSION A1793967
 VERSION A1793967.1 GI:5341683
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes

REFERENCE 1 (bases 1 to 31)
 AUTHORS Clark,M., Johnson,S.T., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
 S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
 K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
 Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritzer,E.,
 Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
 and Wilson,R.
 TITLE Mashu Zebrafish EST Project 1998
 JOURNAL Unpublished (1998)
 COMMENT Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@wustl.edu
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 ResSourceZentrumPirmardatenbank, Berlin, Germany (web address:
 www.rzp.de)
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 Seq primer: T7 ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 31
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone_1ib="IMAG:3725430"
 /clone_1ib="zebrafish Mashu MPing EST"
 /sex="mixed"
 /tissue="mixed"
 /tissue_type="26 somite embryos, adult livers, shield
 stage embryos"
 /lab_host="X11-blue MPF"
 /note="Vector: pSPORT1, Site_1: NotI, Site_2: SalI; 1st
 strand cDNA was primed with a NotI oligo(dT)15 primer
 (5'-pGCTGTTTCAATCGACGCGCGCTTTTCTTTT3');
 (5'-pGCTGTTTCAATCGACGCGCGCTTTTCTTTT3');
 digested with NotI and ligated into the NotI and SalI
 sites of the pSPORT1 vector (BRV). Library was constructed
 by Matthew Clark (Lehrach lab); ICRF, London and Max Planck
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST
 analysis were selected following oligonucleotide
 hybridization fingerprinting of arrayed clones from
 zebrafish late somitogenesis (26 ss), adult liver or
 embryonic shield stage (5.6 h) libraries. Fingerprint
 data were used to computationally cluster cDNAs, and a
 single cDNA from each cluster was chosen for sequencing.
 In some cases multiple members of the same cluster were
 sequenced to assess clustering parameters or single clones
 were sequenced additional times to assess quality
 control."
 BASE COUNT 9 a 20 c 2 g 0 t
 ORIGIN
 Query Match 18.3%; Score 11; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 CCCCCAACCA 23
 DB 15 CCCCCAACCA 25
 RESULT 15
 LOCUS H27426/c
 DEFINITION Y14402.c1 Soares breast 3MBHst Homo sapiens cDNA clone
 IMAGE:161139 5' similar to SP:PDUF_SALTY P37451 PROPANEDIOL

LOCUS AZ809974 27 bp DNA linear GSS 20-FEB-2001
 DEFINITION 2M0074C18F Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 clone UNGC2M0074C18 F, DNA sequence.
 ACCESSION AZ809974
 VERSION AZ809974.1 GI:12976775
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 27)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weis,R. R. 2003. Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0074 row: C column: 18
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers
 1..27
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG2M0074C18"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

8 a 6 c 11 g 2 t

ORIGIN

Query Match 18.3%; Score 11; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CCGTTCCCCC 18
 |||||
 Db 21 CCGTTCCCCC 11

RESULT 12
AZ307173

LOCUS AZ307173 28 bp DNA linear GSS 29-SEP-2000
 DEFINITION 1M0008N03R Mouse 10kb plasmid UNGC1M library Mus musculus genomic
 clone UNGC1M0008N03 R, DNA sequence.
 ACCESSION AZ307173
 VERSION AZ307173.1 GI:10345909
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
 and Wright,D., Weis,R. R. 2003. Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0008 row: N column: 03
 Seq primer: CACACAGAAACGATATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1..28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UNG1M0008N03"
 /clone_lib="Mouse 10kb plasmid UNGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (GI14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

2 a 13 c 5 g 8 t

ORIGIN

Query Match 18.3%; Score 11; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.2e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 CCAGCCCGCCC 31
 |||||
 Db 4 CCAGCCCGCCC 14

RESULT 13
AQ025148/c

LOCUS A2653028 22 bp DNA linear GSS 27-APR-2001
 DEFINITION 2M0218003F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
 clone UUGC2M0218003 F, DNA sequence.
 ACCESSION A2653028
 VERSION A2653028.1 GI:13824255
 KEYWORDS GSS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 22)
 REFERENCE Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0218 row: 0 column: 03
 Seq primer: CGTTGTAAACGACGCGCTACT
 Class: plasmid ends
 High quality sequence stop: 22.
 Location/Qualifiers
 1..22
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0218003"
 /clone_1fb="Mouse 10kb plasmid UUGC2M library"
 /sex="Female"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (female) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g11473214|9b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 1 a 0 c 14 g 7 t
 ORIGIN
 Query Match 18.3%; Score 11; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 CCCCCCAACCA 23
 DB 12 CCCCCCAACCA 2

LOCUS A2653869 23 bp DNA linear GSS 14-DEC-2000
 DEFINITION 1M0527D14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0527D14 R, DNA sequence.
 ACCESSION A2653869
 VERSION A2653869.1 GI:11791015
 KEYWORDS GSS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 23)
 REFERENCE Dun, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weis
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0527 row: D column: 14
 Seq primer: CACACGAGAAACGCTATACAC
 Class: plasmid ends
 High quality sequence stop: 23.
 Location/Qualifiers
 1..23
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0527D14"
 /clone_1fb="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g11473214|9b|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."
 BASE COUNT 4 a 1 c 13 g 5 t
 ORIGIN
 Query Match 18.3%; Score 11; DB 17; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CCGTCCCCCCC 18
 DB 11 CCGTCCCCCCC 1

RESULT 10
 A2653869/c

RESULT 11
 A2609974/c

Query Match 20.0%; Score 12; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 CCAGCCGCCCGC 32
 DB 25 CCAGCCGCCCGC 14

RESULT 7
 AZ921814/c 50 bp DNA linear GSS 17-DEC-2001
 LOCUS 1006032PF07.xl 1006 - Rescemu Grid G Zea mays genomic, DNA
 DEFINITION

ACCESSION AZ921814
 VERSION AZ921814.1 GI:13393834
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Walbot, V.
 TITLE Maize genomic sequences found using engineered Rescemu transposon
 JOURNAL Unpublished. (2001)
 COMMENT Contact: Walbot, V.
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1006032 row: 45
 Class: transposon-tagged.
 Location/Qualifiers

FEATURES
 source

1..50
 /organism="Zea mays"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /clone_lib="1006 - Rescemu Grid G"
 /issue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: leaf; Vector: Rescemu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescemu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescemu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescemu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
 13 c 18 g 8 t

BASE COUNT
 ORIGIN

Query Match 20.0%; Score 12; DB 17; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 CACGAGAGCCGC 57
 DB 15 CACGAGAGCCGC 4

RESULT 8
 AZ769086/c

LOCUS AZ769086 21 bp DNA linear GSS 16-FEB-2001
 DEFINITION 1M0569G22F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
 clone UUGCIM0569G22 F, DNA sequence.

ACCESSION AZ769086
 VERSION AZ769086.1 GI:12888857
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 21)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A., and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 JOURNAL Unpublished (2000)
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0569 row: G column: 22
 Seq primer: CGTTGTAAACGACGCGCAGT
 Class: plasmid ends
 High quality sequence stop: 21.
 Location/Qualifiers

FEATURES
 source

1..21
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone_lib="Mouse 10kb plasmid UUGCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-gold, TI-resistant, F-"
 /note="Vector: PWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g14732114/3d/AF12072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
 2 a 1 c 14 g 4 t

BASE COUNT
 ORIGIN

Query Match 18.3%; Score 11; DB 17; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 TCCCCCAACC 22
 DB 17 TCCCCCAACC 7

RESULT 9
 AZ953028/c

```

Query Match      21.7%; Score 13; DB 13; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 CAACGCGCCGCC 30
          |||||
Db       29 CAAACGCGCCGC 17

```

RESULT 4	
Bj048330/c	
LOCUS	Bj048330 49 bp mRNA linear EST 07-DEC-2001
DEFINITION	Bj048330 N18B Mochii normalized xenopus neurula library
ACCESSION	Bj048330
VERSION	Bj048330.1 GI:17408746
KEYWORDS	EST
SOURCE	African clawed frog.
ORGANISM	Xenopus laevis

REFERENCE	1 (bases 1 to 49)
AUTHORS	Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Koharata, Y.
TITLE	Expressed genes in X. laevis embryo
JOURNAL	Unpublished (2001)
COMMENT	Contact: Tadasu Shin-I

TITLE Expressed genes in *X. laevis* embryo
JOURNAL Unpublished (2001)
COMMENT Contract: Tadaeu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6885
Fax: 81-559-81-6885
Email: tshin@genes.nig.ac.jp
FEATURES Location/Qualifiers
SOURCE 1..49

```

/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XU019110"
/clone_id="NIBB Mochizuki normalized Xenopus neurula
library"
/issue_type="whole embryo"
/dev_stage="stage 15"
/note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; CDNA
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is substracted
and was constructed by N. Garrett and A.M. Zorn,
(Welcomme/CRC Institute)."
BASE COUNT      15 a      16 c      12 g      4 t      2 others
ORIGIN

```

Query Match	20.0%;	Score 12;	DB 13;	Length 49;
Best Local Similarity	100.0%;	Pred. No. 3.9e+04;		
Matches	12;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
QY	8	CCGTTCCCCCA	19	
DB	44	CCGTTCCCCCA	33	

RESULT 5				
AU102328/c				
LOCUS	AU102328	50 bp	mRNA	linear EST 30-AUG-2001
DEFINITION	Sugano Homo sapiens cdna library	Homo sapiens	cdna clone	
ACCESSION	KR060602		mRNA sequence.	
VERSION	AU102328			
KEYWORDS	AU102328.1	GI:13551948		
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 50)			

AUTHORS Suzuki, Y., Taira, H., Tannoda, T., Mizushima-Sugano, Y., See, J., Hatai, H., Oht, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites

JOURNAL EMBO Rep. 2 (5), 388-393 (2001)

MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
E-mail: yutaka@mol.f.u-tokyo.ac.jp

FEATURES
SOURCE
1-50 (49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1)
Location/Qualifiers

```

BASE COUNT
ORIGIN
2 a 18 c 15 g 15 t
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    /note="differential display comparison of untreated and
    dimethylfumarate treated U937 cells"

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Best Local Similarity	100.0%	Pred. No. 3.9e+04;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	45	CCCCCAACGAC	34	

RESULT 6	AU105457/c	50 bp	linear	EST 30-AUG-2001
LOCUS	AU105457			
DEFINITION	Sugano Homo sapiens cDNA library Homo sapiens cDNA clone			
ACCESSION	AB020120	mRNA sequence.		
VERSION	AU105457			
KEYWORDS	AU105457.1	GI:1354978		
SOURCE	EST.			
ORGANISM	human.			
	Homo sapiens			

REFERENCE
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Teunoda,T., Mizushima-Sugano,J., Seoe,J., Hata,
H., Oka,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,
Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE
mapping of mRNA start sites
JOURNAL
EMBO REP. 2 (5), 388-393 (2001)
MEDLINE
21270072
COMMENT
Contact: Yutaka Suzuki

FEATURES	SOURCE	COMMENT
		Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8633, Japan Email: yusuzuki@ims.u-tokyo.ac.jp Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
		Location/Qualifiers 1..50

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/organism="Homo sapiens"
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/clone="ADSU02120"
/clone_1fb="Sugano Homo sapiens cDNA library"
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BASE COUNT
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ORIGIN

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FEATURES

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 /db_xref="taxon:9606"
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 /tissue="NCI CGAP_Gas4"
 /tissue_type="poorly differentiated adenocarcinoma with
 signed ring cell features"
 /lab_host="DH10B"
 /note="Organ: stomach; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

BASE COUNT 18 a 4 c 25 g 2 t
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 49 TTCCCGTTCCCGCC 36

RESULT 2

A2444521

LOCUS A2444521 47 bp DNA linear GSS 04-OCT-2000
 DEFINITION 1M0239F13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0239F13 R, DNA sequence.

ACCESSION A2444521 GI:10593472
 VERSION A2444521.1
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 47)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weis, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
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 Class: plasmid ends
 High quality sequence stop: 47.
 Location/Qualifiers

FEATURES

SOURCE

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 /db_xref="taxon:10090"
 /clone="UGCG1M0239F13"
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 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: PMD42ntv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 12 a 10 c 11 g 14 t
 ORIGIN

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 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 12 GAGAGAGTACTC 24

RESULT 3

B1526845/c

LOCUS B1526845 50 bp mRNA linear EST 29-AUG-2001
 DEFINITION 602927364F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5059839 5',
 mRNA sequence.

ACCESSION B1526845
 VERSION B1526845.1 GI:15351637
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 50)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM1161 row: P column: 16
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 High quality sequence stop: 4.
 Location/Qualifiers

COMMENT

FEATURES

SOURCE

1. 50
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 /strain="FVB/N-3"
 /db_xref="taxon:10090"
 /clone="IMAGE:5059839"
 /clone_1ib="NCI CGAP Mam2"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

BASE COUNT 9 a 11 c 19 g 11 t
 ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 16:08:34 ; Search time 1570.41 Seconds
(without alignments)
618.773 Million cell updates/sec

Title: US-08-770-564A-1_COPY_137_196

Perfect score: 60
Sequence: 1 TAAATCCCGTCCCGCCCA.....ACTTCACGAGCGCGAG 60

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size: 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estbna:*
3: em_estca:*
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12: gb_est4:*
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14: gb_est6:*
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16: em_estcom:*
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18: em_gsa_hum:*
19: em_gsa_inv:*
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25: em_gsa_other:*
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27: em_gsa_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14	23.3	49	A1802512
2	13	21.7	17	A2444521
3	13	21.7	50	B1526845
4	12	20.0	49	B048330
5	12	20.0	50	AU102328
6	12	20.0	50	AU105457

C	7	12	20.0	50	17	A2921814	A2921814
C	8	11	18.3	21	17	A2769086	A2769086
C	9	11	18.3	22	17	A2953028	A2953028
C	10	11	18.3	23	17	A2653869	A2653869
C	11	11	18.3	27	17	A2809974	A2809974
C	12	11	18.3	28	17	A2307173	A2307173
C	13	11	18.3	30	17	AQ025148	AQ025148
C	14	11	18.3	31	9	A1793967	A1793967
C	15	11	18.3	34	14	H27426	H27426
C	16	11	18.3	36	17	BH862765	BH862765
C	17	11	18.3	37	9	AA912047	AA912047
C	18	11	18.3	37	13	B1549647	B1549647
C	19	11	18.3	37	13	B1550102	B1550102
C	20	11	18.3	37	13	B1552796	B1552796
C	21	11	18.3	40	17	AL766731	AL766731
C	22	11	18.3	42	10	AM250581	AM250581
C	23	11	18.3	42	13	B1546340	B1546340
C	24	11	18.3	43	17	HSWC17D09	HSWC17D09
C	25	11	18.3	44	13	B1825999	B1825999
C	26	11	18.3	46	9	AA969300	AA969300
C	27	11	18.3	46	9	A1544460	A1544460
C	28	11	18.3	46	9	A1591356	A1591356
C	29	11	18.3	47	17	AA072163	AA072163
C	30	11	18.3	49	9	A1723140	A1723140
C	31	11	18.3	50	9	AU102860	AU102860
C	32	11	18.3	50	9	AU104726	AU104726
C	33	11	18.3	50	9	AU105453	AU105453
C	34	11	18.3	50	9	AU105456	AU105456
C	35	11	18.3	50	9	AU105772	AU105772
C	36	11	18.3	50	9	AU105773	AU105773
C	37	11	18.3	50	9	AU105843	AU105843
C	38	11	18.3	50	17	A2351333	A2351333
C	39	11	18.3	50	17	A2918120	A2918120
C	40	11	16.7	21	17	A2645749	A2645749
C	41	10	16.7	22	10	AM247820	AM247820
C	42	10	16.7	22	17	A2454940	A2454940
C	43	10	16.7	24	17	A2836988	A2836988
C	44	10	16.7	25	9	AA931385	AA931385
C	45	10	16.7	25	9	A1474586	A1474586

ALIGNMENTS

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LOCUS A1802512/c 49 bp mRNA linear EST 14-DEC-1999
DEFINITION tp08h04.x1 NCI CGAP Gasa Homo sapiens cDNA clone IMAGE:2187223 3'
similar to TR:048805 O48809 F2401.18. ; mRNA sequence.

ACCESSION A1802512
VERSION A1802512.1 GI:5367984

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLES

COMMENT

Human
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases) (to 49)
NCI-CCGAP http://www.nci.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: CGAP@femail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LMW at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality

Fr1-Jun 27 07:41:55 2003

us-08-770-564a-1_copy_290_319.oligo.rge

Page 5

ACCESSION AX019586
VERSION AX019586.1 GI:10043500
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE artificial sequences.
1 (bases 1 to 38)
AUTHORS Keith, W.N.
TITLE Promoter regions of the mouse and human telomerase rna component
genes
JOURNAL Patent: WO 938964-A 40 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGGTGTGCC 12
Db 27 GGGGTGTGCC 38

Search completed: June 23, 2003, 20:29:41
Job time : 301.008 secs

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGGTGGCCAT 14
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Db 23 GGTGGTGGCCAT 12

RESULT 11
LOCUS AR079889 30 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 2 from patent US 5968506.
ACCESSION AR079889
VERSION AR079889.1 GI:10006642
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
AUTHORS Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vassero,A.P.,
Prizan,R.A. and Kealey,J.T.
TITLE Purified telomerase
JOURNAL Patent: US 5968506-A 2 19-OCT-1999;
FEATURES Location/Qualifiers
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Db 30 TGTCTAACCTA 19

RESULT 12
LOCUS A84592 31 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 2 from Patent WO9845450.
ACCESSION A84592
VERSION A84592.1 GI:6733508
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Atkinson,E.M. and Kealey,J.T.
TITLE PURIFIED TELOMERASE
JOURNAL Patent: WO 9845450-A 2 15-OCT-1998;
FEATURES Location/Qualifiers
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/db_xref="taxon:32644"

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mod_base=OTHER
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Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 TGTCTAACCTA 30

Db 30 TGTCTAACCTA 19
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RESULT 13
LOCUS AX268979 31 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 60 from Patent WO0175165.
ACCESSION AX268979
VERSION AX268979.1 GI:16541998
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Mcconlogue,L.C., Games,K.D., Yednock,T.A., Hua,T., Messersmith,E.
and Baird,F.
TITLE Screening markers and methods for neurodegenerative disorders
JOURNAL Patent: WO 0175165-A 60 11-OCT-2001;
FEATURES Location/Qualifiers
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/note="probe 140T"

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGGCCATTTT 12

RESULT 14
LOCUS A76106 33 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 45 from Patent WO9320210.
ACCESSION A76106
VERSION A76106.1 GI:6088247
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Taylor,G. and Stott,E.J.
TITLE ANTIBODIES FOR TREATMENT AND PREVENTION OF RESPIRATORY SYNCYTIAL
JOURNAL VIRUS INFECTION
Patent: WO 9320210-A 45 14-OCT-1993;
FEATURES Location/Qualifiers
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/db_xref="taxon:32644"

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGGTGGCCAT 14
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Db 28 GGTGGTGGCCAT 17

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LOCUS AX019586 38 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 40 from Patent WO9338964.

DEFINITION Sequence 45 from Patent. WO9318964.
ACCESSION AX019591.1 GI:10043505
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Keith, W.N.
TITLE Promoter regions of the mouse and human telomerase rna component
JOURNAL Patent: WO 9308964-A 45 05-AUG-1993;
FEATURES KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
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/note="Oligonucleotide"
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 9 GGGGTGGTGGCC 20
RESULT 7
LOCUS AR067095 22 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 443 from patent US 5851760.
ACCESSION AR067095
VERSION AR067095.1 GI:598317
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evans, G.A. and Smith, M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 443 22-DEC-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
LOCUS AX037834 26 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 185 from Patent WO0059917.
ACCESSION AX037834
VERSION AX037834.1 GI:11227216
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Howard, J.C., Feldkamp, U., Rauhe, H. and Banzhaf, W.
TITLE Information-carrying and information-processing polymers
JOURNAL Patent: WO 0059917-A 185 12-OCT-2000;

HOWARD JONATHAN C (DE) ; FELDKAMP UDO (DE) ; RAUHE HILMAR (DE) ;
BANZHAF WOLFGANG (DE)
FEATURES Location/Qualifiers
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/db_xref="taxon:32630"
/note="X80U: Unique non-biological sequence for representation of data."
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11 TTGTCTAACCT 22
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LOCUS AX037835 26 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 186 from Patent WO0059917.
ACCESSION AX037835
VERSION AX037835.1 GI:11227217
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 26)
AUTHORS Howard, J.C., Feldkamp, U., Rauhe, H. and Banzhaf, W.
TITLE Information-carrying and information-processing polymers
JOURNAL Patent: WO 0059917-A 186 12-OCT-2000;
HOWARD JONATHAN C (DE) ; FELDKAMP UDO (DE) ; RAUHE HILMAR (DE) ;
BANZHAF WOLFGANG (DE)
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 18 TTGTCTAACCT 29
Db 20 TTGTCTAACCT 9
RESULT 10
LOCUS ARI45878 29 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 22 from patent US 6218131.
ACCESSION ARI45878
VERSION ARI45878.1 GI:15109067
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Keesee, S.K., Obar, R. and Wu, Y.-J.
TITLE Materials and methods for detection of breast cancer
JOURNAL Patent: US 6218131-A 22 17-APR-2001;
FEATURES Location/Qualifiers
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ORIGIN

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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TTGTCTAACCTA 30
 DB 20 TTGTCTAACCTA 7

RESULT 2
 AR075544/c
 LOCUS AR075544 20 bp DNA linear PAT 30-AUG-2000
 DEFINITION Sequence 41 from patent US 5958680.
 ACCESSION AR075544
 VERSION AR075544.1 GI:10002290
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Valleponteau,B., Feng,J., Funk,W. and Andrews,W.H.
 TITLE Mammalian telomerase
 JOURNAL Patent: US 5958680-A 41 28-SEP-1999;
 FEATURES Location/Qualifiers
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Query Match 46.7%; Score 14; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TTGTCTAACCTA 30
 DB 20 TTGTCTAACCTA 7

RESULT 3
 I31751/c
 LOCUS I31751 20 bp DNA linear PAT 06-FEB-1997
 DEFINITION Sequence 4 from patent US 5583016.
 ACCESSION I31751
 VERSION I31751.1 GI:1822542
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Valleponteau,B., Feng,J., Funk,W. and Andrews,W.H.
 TITLE Mammalian telomerase
 JOURNAL Patent: US 5583016-A 4 10-DEC-1996;
 FEATURES Location/Qualifiers
 source 1. .20
 /organism="unknown"

BASE COUNT 7 a 3 c 5 g 5 t
 ORIGIN

Query Match 46.7%; Score 14; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TTGTCTAACCTA 30
 DB 20 TTGTCTAACCTA 7

RESULT 4

AX471972/c

LOCUS AX471972 29 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 3 from Patent WO02054073.
 ACCESSION AX471972
 VERSION AX471972.1 GI:22207029
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Deslauriers,M., Quinn,F.D., Beall,D.S., King,P. and Bitkess,K.A.
 TITLE Latent human tuberculosis model, diagnostic antigens, and methods of use
 JOURNAL Patent: WO 02054073-A 3 11-JUL-2002;
 FEATURES Location/Qualifiers
 source 1. .29
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Synthetic oligonucleotide"

BASE COUNT 5 a 14 c 6 g 4 t
 ORIGIN

Query Match 46.7%; Score 14; DB 6; Length 29;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GGGTGTGGCCATT 15
 DB 23 GGGTGTGGCCATT 10

RESULT 5
 AX405383
 LOCUS AX405383 44 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 77 from Patent WO0222830.
 ACCESSION AX405383
 VERSION AX405383.1 GI:21438478
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Reschlimann,D.P. and Grenard,P.M.
 TITLE Transglutaminase gene products
 JOURNAL Patent: WO 0222830-A 77 21-MAR-2002;
 FEATURES Location/Qualifiers
 source 1. .44
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 CDS
 <30. .>44
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAD34664.1"
 /db_xref="GI:21438479"
 /translation="GLEVA"

BASE COUNT 7 a 13 c 12 g 12 t
 ORIGIN

Query Match 46.7%; Score 14; DB 6; Length 44;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 TTGTCTAACCTT 29
 DB 1 TTGTCTAACCTT 14

RESULT 6
 AX019591
 LOCUS AX019591 20 bp DNA linear PAT 07-SEP-2000

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:17:23 ; Search time 299.008 Seconds

(without alignment) 2919.933 Million cell updates/sec

Title: US-08-770-564A-1_COPY_290_319

Perfect score: 30 1 GGGGTGGTGGCCATTCTTTGTCTAACCTTA 30

Sequence: 1 GGGGTGGTGGCCATTCTTTGTCTAACCTTA 30

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
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14: gb_vi:*
15: gb_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hlg_hum:*
31: em_hlg_iny:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_red:*
36: em_hlg_vic:*
37: em_hlg_vic:*
38: em_hlg_vic:*
39: em_hlg_vic:*
40: em_hlg_vic:*
41: em_hlg_vic:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14	46.7	20	6	AR059219
C 2	14	46.7	20	6	AR075544
C 3	14	46.7	20	6	AR075544
C 4	14	46.7	20	6	AR075544
C 5	14	46.7	20	6	AR075544
C 6	14	46.7	20	6	AR075544
C 7	14	46.7	20	6	AR075544
C 8	14	46.7	20	6	AR075544
C 9	14	46.7	20	6	AR075544
C 10	14	46.7	20	6	AR075544
C 11	14	46.7	20	6	AR075544
C 12	14	46.7	20	6	AR075544
C 13	14	46.7	20	6	AR075544
C 14	14	46.7	20	6	AR075544
C 15	14	46.7	20	6	AR075544
C 16	14	46.7	20	6	AR075544
C 17	14	46.7	20	6	AR075544
C 18	14	46.7	20	6	AR075544
C 19	14	46.7	20	6	AR075544
C 20	14	46.7	20	6	AR075544
C 21	14	46.7	20	6	AR075544
C 22	14	46.7	20	6	AR075544
C 23	14	46.7	20	6	AR075544
C 24	14	46.7	20	6	AR075544
C 25	14	46.7	20	6	AR075544
C 26	14	46.7	20	6	AR075544
C 27	14	46.7	20	6	AR075544
C 28	14	46.7	20	6	AR075544
C 29	14	46.7	20	6	AR075544
C 30	14	46.7	20	6	AR075544
C 31	14	46.7	20	6	AR075544
C 32	14	46.7	20	6	AR075544
C 33	14	46.7	20	6	AR075544
C 34	14	46.7	20	6	AR075544
C 35	14	46.7	20	6	AR075544
C 36	14	46.7	20	6	AR075544
C 37	14	46.7	20	6	AR075544
C 38	14	46.7	20	6	AR075544
C 39	14	46.7	20	6	AR075544
C 40	14	46.7	20	6	AR075544
C 41	14	46.7	20	6	AR075544
C 42	14	46.7	20	6	AR075544
C 43	14	46.7	20	6	AR075544
C 44	14	46.7	20	6	AR075544
C 45	14	46.7	20	6	AR075544

ALIGNMENTS

RESULT 1	AR059219/c	20 bp	DNA	linear	PAT 29-SEP-1993
LOCUS	AR059219	Sequence 26 from patent US 5837857.			
DEFINITION	Sequence 26 from patent US 5837857.				
ACCESSION	AR059219				
VERSION	AR059219.1	GI:5984796			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.				
TITLE	Mammalian telomerase				
JOURNAL	Patent: US 5837857-A 26 17-NOV-1998;				
FEATURES	Location/Qualifiers				

XX Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
 PI Marhenda MA, Villeponteau B;
 XX WPI; 1996-097428/10.
 XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX
 PS Disclosure; Page 23; 85pp; English.
 XX The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation. The
 CC antisense oligonucleotide is synthesised as a 2-O-methyl RNA
 CC oligonucleotide and is more resistant to hydrolysis than unmodified
 CC RNA oligonucleotides (See AAT1032-35).
 CC
 SQ Sequence 20 BP; 7 A; 3 C; 5 G; 5 U; 0 other;

Query Match 46.7%; Score 14; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 17 TTTGCTACCTTA 30
 Db 20 TTTGCTACCTTA 7

RESULT 15
 AAT89245
 ID AAT89245 standard; DNA; 24 BP.
 XX
 AC AAT89245;
 XX
 DT 12-MAY-1998 (first entry)
 XX
 DE DNA oligonucleotide 1, used in the measurement of Tm values.
 XX
 KW Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
 KW inhibitor; human telomerase RNA; htr; PCR; oligonucleotide; ss.
 XX
 OS Synthetic.
 XX
 PN WO9738013-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 09-APR-1997; 97WO-US05931.
 XX
 PR 09-APR-1996; 96US-0630019.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Corey D, Norton JC, Piatyszek MA, Shay JW, Wright WE;
 XX WPI; 1997-512647/47.
 DR
 XX New peptide nucleic acids hybridising to mammalian telomerase RNA -
 PT used to inhibit telomerase, for treating tumours and other
 PT proliferative diseases, also for diagnosis
 XX
 PS Example 2; Page 49; 76pp; English.
 CC This is an oligonucleotide used in the measurement of Tm values and
 CC their complementary peptide nucleic acids (PNAs), (e.g. AAT89228-T89233,
 CC

CC AAT89243-T89244). PNAs hybridise specifically to an RNA component of
 CC mammalian telomerase, and include the sequence GGG for specific
 CC hybridisation to the template region of this component. PNAs can be
 CC used as probes to detect the RNA component of mammalian telomerase and
 CC as inhibitors of telomerase activity, especially in the treatment of
 CC cancer.
 CC
 SQ Sequence 24 BP; 7 A; 5 C; 5 G; 7 T; 0 other;

Query Match 46.7%; Score 14; DB 18; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTACCTTA 30
 Db 1 TTTGCTACCTTA 14

Search completed: June 23, 2003, 20:09:18
 Job time : 113.554 secs

htr gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
 KM autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
 KM HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytostatic;
 KM acquired immunodeficiency syndrome; anti-inflammatory; ss.

OS Homo sapiens.

FX Key Location/Qualifiers
 FT tag= a
 FT /note= "Telomerase RNA active site"

PN US6294650-B1.

PD 25-SEP-2001.

PF 08-JUL-1999; 99US-0349532.

PR 09-APR-1997; 97US-0838545.

PR 09-APR-1996; 96US-0630019.

XX (TEXA) UNIV TEXAS SYSTEM.

PI Shay JW, Wright WB, Piatyzek MA, Corey DR, Norton JC;

DR WPI; 2001-638024/73.

XX New peptide nucleic acids that hybridises to the RNA component of
 PT mammalian telomerase, useful for treating or preventing cancer,
 PT inflammation, lymphoproliferative diseases, autoimmune disease, or
 PT neurodegenerative diseases -
 XX Example 2; Column 37-38; 46p; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
 CC mammalian cells by hybridising to the RNA component of mammalian
 CC telomerase. The PNAs are useful as probes to detect the RNA component
 CC of mammalian telomerase and as inhibitors of telomerase activity, or to
 CC detect and/or quantitate polynucleotide having the human telomerase
 CC RNA component (hTR) sequence, as well as in forensic identification of
 CC individuals, such as paternity testing or identification of criminal
 CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
 CC PNA can be further used for treating or preventing cancer, inflammation,
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
 CC diseases. The PNAs in combination with other pharmaceuticals (such as
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
 CC diseases characterised by abnormal telomere metabolism or telomerase
 CC activity. The present sequence representing hTR RNA strand #2 is used
 CC to test the inhibition of telomerase activity by the PNAs of the
 CC present invention.

SQ Sequence 31 BP; 8 A; 6 C; 8 G; 9 U; 0 other;

Query Match 50.0%; Score 15; DB 23; Length 31;

Best Local Similarity 53.3%; Pred. No. 55;

Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTGTGCTAACCTTA 30

DB 1 UUUUGUCUAAACCUA 15

RESULT 13
 AAT10286/c

ID AAT10286 standard; DNA; 20 BP.

AC AAT10286;

DT 09-SEP-1996 (first entry)

XX

DE RNA component of mammalian telomerase antisense oligonucleotide T3.

XX RNA component; mammalian; telomerase; antisense oligonucleotide;
 KM triple helix; inhibition; neoplastic; cells; activity; ss.

OS Synthetic.

PN WO9601835-A1.

PD 25-JAN-1996.

PF 06-JUL-1995; 95WO-US08530.

PR 07-JUN-1995; 95US-0482115.

PR 07-JUL-1994; 94US-0272102.

PR 27-OCT-1994; 94US-0330123.

PR 07-JUN-1995; 95US-0472802.

PA (GERO-) GERON CORP.

PI Andrews WH, Feng J, Funk W, Villeponteau B;

DR WPI; 1996-097581/10.

XX RNA component of mammalian telomerase, esp. human - useful in
 PT identifying e.g. candidate telomerase-modulating agents

XX Disclosure; Page 38; 114p; English.

XX The present sequence is a RNA component of mammalian telomerase,
 CC antisense oligonucleotide, which can be used, along with triple
 CC helix forming sequences, to inhibit telomerase activity in cells,
 CC esp. neoplastic cells.

SQ Sequence 20 BP; 7 A; 3 C; 5 G; 5 T; 0 other;

Query Match 46.7%; Score 14; DB 17; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTGCTAACCTTA 30

DB 20 TTGTGCTAACCTTA 7

RESULT 14
 AAT1032/c

ID AAT1032 standard; DNA; 20 BP.

AC AAT1032;

DT 09-JUN-1996 (first entry)

DE Antisense oligonucleotide (T3) inhibiting telomerase activity.

XX Telomerase; mammal; antisense; triple forming oligonucleotide;

KM plasmid; probe; primer; ribozyme; ss.

OS Synthetic.

PN WO9601614-A2.

PD 25-JAN-1996.

PF 07-JUL-1995; 95WO-US08620.

PR 07-JUN-1995; 95US-0485778.

PR 07-JUL-1994; 94US-0272102.

PR 27-OCT-1994; 94US-0330123.

PR 13-FEB-1995; 95US-0387524.

PA (COLD-) COLD SPRING HARBOR LAB.

PA (GERO-) GERON CORP.

XX

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OS Synthetic.
XX
XX PN W09938964-A2.
XX
XX PD 05-AUG-1999.
XX
XX PF 29-JAN-1999; 99MO-GB00308.
XX
XX PR 29-JAN-1998; 98GB-0001902.
XX
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
XX PI Keith MN;
XX
XX DR WPI; 1999-479183/40.
XX
XX PT Mouse and human telomerase RNA gene promoters, useful for tumor
XX specific gene therapy
XX
XX PS Disclosure; Fig 19; 109pp; English.
XX
XX CC The invention relates to promoter regions from mouse and human
XX telomerase RNA (TR) component genes. The TR gene promoter can be linked
XX to a heterologous gene, especially a gene encoding a cytotoxin, for
XX therapy of cancer, especially neoplasias. The telomerase is necessary for
XX the unrestricted proliferative capacity of many human cancers. Mutation
XX or dysregulation of the telomerase repression pathway may cause
XX reactivation or upregulation of telomerase expression in cancer.
XX Substances, identified in the methods, can be used to block transcription
XX from the TR gene promoter through interaction of the 5' regulatory
XX sequences. These substances, e.g. antisense oligonucleotides,
XX transcription factors, peptide nucleic acids and factors that disrupt
XX signal transduction, are useful for cancer therapy. In particular, gene
XX therapy vectors (especially pGT62-codapp) comprising the promoter and a
XX viral thymidine kinase gene can be used to convert a prodrug, e.g.
XX gancyclovir, so that neoplasia can be controlled or treated. Direct
XX down-regulation of telomerase RNA gene through manipulation of
XX transcription factors may be effective anticancer therapy and the cloning
XX of the hTR gene promoter allows the analysis of therapeutic molecules
XX which modulate hTR promoter activity. Sequences AA207324-332 and
XX CA000332-340 represent constructs with hTR promoter sequence element
XX mutations.
XX
XX SQ Sequence 47 BP; 11 A; 7 C; 15 G; 14 T; 0 other;
XX
XX Query Match 66.7%; Score 20; DB 20; Length 47;
XX Best Local Similarity 100.0%; Pred. No. 0.1;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 8 TGGCCATTTTGTCTAACC 27
XX Db 28 TGGCCATTTTGTCTAACC 47
XX
XX RESULT 11
XX ID AAA37591 standard; RNA; 31 BP.
XX
XX AC AAA37591;
XX
XX DT 15-AUG-2000 (first entry)
XX
XX DE Telomerase target sequence.
XX
XX KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
XX inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
XX AIDS; HIV; fungal infection; forensic identification; detect; tumour;
XX paternity testing; ss.
XX
XX OS Synthetic.
XX
XX PN US6046307-A.
XX

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PD 04-APR-2000.
XX
XX PP 09-APR-1997; 97US-0836545.
XX
XX PR 09-APR-1996; 96US-0630019.
XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX
XX PI Wright WE, Platyszek MA, Shay JW, Norton JC, Corey DR;
XX
XX DR WPI; 2000-292432/25.
XX
XX PT New peptide nucleic acid (PNA) compounds that inhibit telomerase
XX activity in mammalian cells is useful as probes to detect the RNA
XX component of a mammalian telomerase
XX
XX PS Example 2; Column 37; 45pp; English.
XX
XX CC The present sequence represents a telomerase target sequence. The
XX invention relates to an antisense oligonucleotide used as a control
XX sequence alongside a peptide nucleic acid molecule which hybridizes to
XX the mRNA component of mammalian telomerase, and inhibits telomerase
XX activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
XX strand of the telomeric DNA, using as a template an 11 nucleotide
XX sequence contained within the RNA component of the enzyme. The invention
XX relates to PNA molecules having a sequence of no more than 25 bases,
XX which include the sequence GTTAGG. The unchanged nature of the PNA
XX backbone increases the melting temperature of associating strands,
XX increases the rate of association with targeted nucleic acids, and
XX affords greater resistance of degradation by proteases or nucleases. The
XX therapeutic PNAs may be used for treating disease conditions such as
XX cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
XX immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
XX syndrome) and associated pathologies, fungal infections, and other
XX diseases characterized by abnormal telomere metabolism or telomerase
XX activity, in combination with antineoplastic and other cytotoxic or
XX cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
XX used for molecular diagnostics. Labelled PNAs are used as hybridization
XX probes to detect or quantitate polynucleotides having a human telomerase
XX RNA (hTR) sequence. PNA probes are also used for forensic identification
XX of individuals, e.g. paternity testing, based on hTR gene restriction
XX fragment length polymorphism (RFLP) pattern. PNAs are also useful as
XX probes to detect the RNA component of a mammalian telomerase and as
XX inhibitors of telomerase activity. The method of the present invention
XX allows cancerous conditions to be detected with increased confidence and
XX possibly at an earlier stage, before cells are detected as cancerous
XX based on pathological characteristics. The diagnostic and prognostic
XX methods of the present invention can be used to detect an immortal or
XX neoplastic cell or tumour tissue or cancer of any origin, provided the
XX cell expresses telomerase activity and its RNA component.
XX
XX SQ Sequence 31 BP; 8 A; 6 C; 8 G; 9 U; 0 other;
XX
XX Query Match 50.0%; Score 15; DB 21; Length 31;
XX Best Local Similarity 53.3%; Pred. No. 55;
XX Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 16 TTTTGCTAACCCTA 30
XX Db 1 UUUUGUCUAAACCCTA 15
XX
XX RESULT 12
XX ID AAS15462 standard; RNA; 31 BP.
XX
XX AC AAS15462;
XX
XX DT 14-FEB-2002 (first entry)
XX
XX DE Human telomerase RNA (hTR) strand #2.
XX
XX KW Mammalian; forensic; paternity testing; human telomerase RNA component;
XX

```

CC screening a genomic library of mouse D3 embryonic stem cells.
 XX Sequence 27 BP; 2 A; 4 C; 12 G; 9 T; 0 other;

Query Match 66.7%; Score 20; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGTTGGCCATTCTTTTG 20
 |||||
 DB 8 GGGGTGTTGGCCATTCTTTTG 27

RESULT 8
 AAX90787
 ID AAX90787 standard; DNA; 28 BP.

AC AAX90787;
 DT 13-JAN-2000 (first entry)

DE Human telomerase RNA specific PCR primer-1.
 XX PCR primer; human telomerase RNA; hTR; amplify; human strafen cDNA;
 XX hSTau; synthesized; random hexamer primer;
 KM Superscript II reverse transcriptase; ss.

OS Synthetic.
 OS Homo sapiens.

XX WO951255-A1.

XX 14-OCT-1999.

XX 06-APR-1999; 99MO-US07533.

XX 06-APR-1998; 98US-0080783.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Greider CM, Le S;

XX WPI; 1999-620168/53.

XX Human strafen polypeptide useful in methods for identifying telomerase

XX inhibitors

XX Disclosure; Page 15; 50pp; English.

XX The present sequence is a PCR primer specific to human telomerase
 CC RNA (hTR). It is used to amplify human strafen (hSTau) cDNA synthesized
 CC using random hexamer primers and Superscript II reverse transcriptase.

XX Sequence 28 BP; 2 A; 4 C; 13 G; 9 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGTGTTGGCCATTCTTTTG 20
 |||||
 DB 9 GGGGTGTTGGCCATTCTTTTG 28

RESULT 9
 AAZ00339
 ID AAZ00339 standard; DNA; 47 BP.

AC AAZ00339;

XX 22-OCT-1999 (first entry)

DE Mutated hTR promoter fragment containing construct 115.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
 KM gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

OS Homo sapiens.

OS Synthetic.

XX WO938964-A2.

XX 05-AUG-1999.

XX 23-JAN-1999; 99MO-GB00308.

XX 23-JAN-1998; 98GB-0001902.

XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.

XX Keith MN;

XX WPI; 1999-479183/40.

XX Mouse and human telomerase RNA gene promoters, useful for tumor

XX specific gene therapy

XX Disclosure; Fig 19; 109pp; English.

XX The invention relates to promoter regions from mouse and human

XX telomerase RNA (TR) component genes. The TR gene promoter can be linked

XX to a heterologous gene, especially a gene encoding a cytotoxin, for

XX therapy of cancer, especially neoplasia. The telomerase is necessary for

XX the unrestricted proliferative capacity of many human cancers. Mutation

XX or dysregulation of the telomerase repression pathway may cause

XX substances, identified in the methods, can be used to block transcription

XX from the TR gene promoter through interaction of the 5' regulatory

XX sequences. These substances, e.g. antisense oligonucleotides,

XX transcription factors, peptide nucleic acids and factors that disrupt

XX signal transduction, are useful for cancer therapy. In particular, gene

XX therapy vectors (especially pGTR2-codupp) comprising the promoter and a

XX viral thymidine kinase gene can be used to convert a produg, e.g.

XX gancyclovir, so that neoplasia can be controlled or treated. Direct

XX down-regulation of telomerase RNA gene through manipulation of

XX transcription factors may be effective anticancer therapy and the cloning

XX of the hTR gene promoter allows the analysis of therapeutic molecules

XX CC AAZ00332-340 represent constructs with hTR promoter sequence element

XX mutations.

XX Sequence 47 BP; 8 A; 7 C; 18 G; 14 T; 0 other;

Query Match 66.7%; Score 20; DB 20; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGCATTCTTTGCTAAC 27
 |||||
 DB 28 TGGCATTCTTTGCTAAC 47

RESULT 10
 AAZ00340
 ID AAZ00340 standard; DNA; 47 BP.

AC AAZ00340;

XX 22-OCT-1999 (first entry)

DE Mutated hTR promoter fragment containing construct 114.

XX Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;

XX KM gene therapy; thymidine kinase gene; anticancer therapy; human; ss.

OS Homo sapiens.

CC of individuals, e.g. paternity testing, based on htr gene restriction
 CC fragment length polymorphism (RFLP) pattern. PNA's are also useful as
 CC probes to detect the RNA component of a mammalian telomerase and as
 CC inhibitors of telomerase activity. The method of the present invention
 CC allows cancerous conditions to be detected with increased confidence and
 CC possibly at an earlier stage, before cells are detected as cancerous
 CC based on pathological characteristics. The diagnostic and prognostic
 CC methods of the present invention can be used to detect an immortal or
 CC neoplastic cell or tumour tissue or cancer of any origin, provided the
 CC cell expresses telomerase activity and its RNA component.

SQ Sequence 23 BP; 5 A; 7 C; 1 G; 10 T; 0 other;

Query Match 66.7%; Score 20; DB 23; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCATTTTGTCTAACCTTA 30
 Db 1 CCATTTTGTCTAACCTTA 20

RESULT 6
 AAS15446
 ID AAS15446 standard; DNA; 23 BP.

XX AAS15446;

XX 14-FEB-2002 (first entry)

XX Oligonucleotide #2 used in melting temperature studies of PNA's.

XX Mammalian; paternity testing; human telomerase RNA component;
 KM htr gene RFLP pattern; cancer; inflammation; forensic;
 KM lymphoproliferative disease; autoimmune disease; hyperplasia;
 KM neurodegenerative disease; neoplasia; HIV; AIDS; cytostatic;
 KM human immunodeficiency virus; acquired immunodeficiency syndrome;
 KM telomere metabolism; anti-inflammatory; immunosuppressive; ss.

XX Homo sapiens.
 OS Synthetic.

XX US6294650-B1.

XX 25-SEP-2001.

XX 08-JUL-1999; 99US-0349532.

XX 09-APR-1997; 97US-0838545.

XX 09-APR-1996; 96US-0630019.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;

XX WPI; 2001-638024/73.

XX New peptide nucleic acids that hybridises to the RNA component of
 PT mammalian telomerase, useful for treating or preventing cancer,
 PT inflammation, lymphoproliferative diseases, autoimmune disease, or
 PT neurodegenerative diseases

XX Example 2; Column 34; 46pp; English.

XX The present invention relates to peptide nucleic acids (PNAs), comprising
 CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
 CC mammalian cells by hybridising to the RNA component of mammalian
 CC telomerase. The PNAs are useful as probes to detect the RNA component
 CC of mammalian telomerase and as inhibitors of telomerase activity, or to
 CC detect and/or quantitate polynucleotide having the human telomerase
 CC RNA component (htr) sequence, as well as in forensic identification of
 CC individuals, such as paternity testing or identification of criminal
 CC suspects or unknown descendants based on the htr gene RFLP pattern. The

CC PNA can be further used for treating or preventing cancer, inflammation,
 CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
 CC diseases. The PNAs in combination with other pharmaceuticals (such as
 CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
 CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
 CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
 CC diseases characterised by abnormal telomere metabolism or telomerase
 CC activity. The present sequence representing a DNA oligonucleotide is
 CC complementary to some of the PNAs of the present invention, and is
 CC used in melting temperature studies.

SQ Sequence 23 BP; 5 A; 7 C; 1 G; 10 T; 0 other;

Query Match 66.7%; Score 20; DB 23; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CCATTTTGTCTAACCTTA 30
 Db 1 CCATTTTGTCTAACCTTA 20

RESULT 7
 AAT11045
 ID AAT11045 standard; DNA; 27 BP.

XX AAT11045;

XX 02-JUL-1996 (first entry)

XX Primer used for producing telomerase probe.

XX Telomerase; mammal; antisense; triplex forming oligonucleotide;
 KM plasmid; probe; primer; ribozyme; ss.

XX Synthetic.

XX MO9601614-A2.

XX 25-JUN-1996.

XX 07-JUL-1995; 95WO-US08620.

XX 07-JUN-1995; 95US-0485778.

XX 27-JUL-1994; 94US-0272102.

XX 27-OCT-1994; 94US-0330123.

XX 13-FEB-1995; 95US-0387524.

XX (COLD-) COLD SPRING HARBOR LAB.

XX (GERO-) GERON CORP.

XX Andrews WH, Avillion AA, Feng J, Funk W, Greider C;

XX Marhunda MA, Villeponteau B;

XX WPI; 1996-097428/10.

XX RNA components of (non)human mammalian telomerase(s) - useful in
 PT studying cell senescence and immortalisation
 XX Example 10; Page 55; 85pp; English.

XX The RNA components of (non) human mammalian telomerase(s) especially
 CC from mouse, rat and chinese hamster are all claimed. Antisense
 CC oligonucleotides can be used to block the activity of the
 CC telomerase; probes and primers can be used in detection; vectors and
 CC host cells transformed with the isolated telomerase genes can be
 CC used for production of telomerases; RNA and DNA ribozymes and triplex
 CC forming oligonucleotides directed against the telomerase genes can
 CC be used therapeutically as can plasmids. A mouse which lacks the
 CC telomerase gene (also claimed) can be used for study of telomere
 CC regulation in vivo, and the role it plays in immortalisation.
 CC Two primers (AAT11045, AAT11046) were used to amplify a fragment of the
 CC human telomerase encoding enzyme for its use as a probe in

PS	Disclosure: Fig 19; 109pp; English.
XX	
CC	The invention relates to promoter regions from mouse and human
CC	telomerase RNA (TR) component genes. The TR gene promoter can be linked
CC	to a heterologous gene, especially a gene encoding a cytotoxin, for
CC	therapy of cancer, especially neoplasias. The telomerase is necessary for
CC	the unrestricted proliferative capacity of many human cancers. Mutation
CC	or dysregulation of the telomerase repression pathway may cause
CC	substances, identified in the methods, can be used to block transcription
CC	from the TR gene promoter through interaction of the 5' regulatory
CC	sequences. These substances, e.g. antisense oligonucleotides,
CC	transcription factors, peptide nucleic acids and factors that disrupt
CC	signal transduction, are useful for cancer therapy. In particular, gene
CC	therapy vectors (especially pGR62-codAupp) comprising the promoter and a
CC	viral thymidine kinase gene can be used to convert a prodruq, e.g.
CC	gancyclovir, so that neoplasia can be controlled or treated. Direct
CC	down-regulation of telomerase RNA gene through manipulation of
CC	transcription factors may be effective anticancer therapy and the cloning
CC	of the hTR gene promoter allows the analysis of therapeutic molecules
CC	which modulate hTR promoter activity. Sequences AA207324-332 and
CC	AA200332-340 represent constructs with hTR promoter sequence element
CC	mutations.
CC	
XX	
SO	Sequence 47 BP; 8 A; 7 C; 19 G; 13 T; 0 other;
	Query Match 90.0%; Score 27; DB 20; Length 47;
	Best Local Similarity 100.0%; Pred. No. 1.6e-05;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGGGTGGTGGCCATTTTGTCTAAC 27
Db	21 GGGGTGGTGGCCATTTTGTCTAAC 47
RESULT 2	
AAZ00337	
ID	AAZ00337 standard; DNA; 47 BP.
XX	
AC	AAZ00337;
XX	
DT	22-OCT-1999 (first entry)
XX	
DE	Mutated hTR promoter fragment containing construct 112(RCE).
XX	
KW	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW	gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO9938964-A2.
XX	
PD	05-AUG-1999.
XX	
PF	29-JAN-1999; 99WO-GB00308.
XX	
PR	29-JAN-1998; 98GB-0001902.
XX	
PA	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX	
PI	Keith WN;
XX	
DR	WPI; 1999-479183/40.
XX	
PT	Mouse and human telomerase RNA gene promoters, useful for tumor
PT	specific gene therapy
XX	
PS	Disclosure; Fig 19; 109pp; English.
XX	
CC	The invention relates to promoter regions from mouse and human
CC	telomerase RNA (TR) component genes. The TR gene promoter can be linked

CC	to a heterologous gene, especially a gene encoding a cytotoxin, for
CC	therapy of cancer, especially neoplasias. The telomerase is necessary for
CC	the unrestricted proliferative capacity of many human cancers. Mutation
CC	or dysregulation of the telomerase repression pathway may cause
CC	reactivation or upregulation of telomerase expression in cancer.
CC	Substances, identified in the methods, can be used to block transcription
CC	from the TR gene promoter through interaction of the 5' regulatory
CC	sequences. These substances, e.g., antisense oligonucleotides,
CC	transcription factors, peptide nucleic acids and factors that disrupt
CC	signal transduction, are useful for cancer therapy. In particular, gene
CC	therapy vectors (especially pGRG2-codAupp) comprising the promoter and a
CC	viral thymidine kinase gene can be used to convert a prodrug, e.g.,
CC	gancyclovir, so that neoplasia can be controlled or treated. Direct
CC	down-regulation of telomerase RNA gene through manipulation of
CC	transcription factors may be effective anticancer therapy and the cloning
CC	of the hTR gene promoter allows the analysis of therapeutic molecules
CC	which modulate hTR promoter activity. Sequences AA207324-332 and
CC	AA200332-340 represent constructs with hTR promoter sequence element
CC	mutations.
SO	
XX	Sequence 47 BP; 6 A; 7 C; 20 G; 14 T; 0 other;
QY	
Query Match	83.3%; Score 25; DB 20; Length 47;
Best Local Similarity	100.0%; Pred. No. 0.00019;
Matches 25; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	
3	GGTGGTGCCATTTTGTCTTACC 27
23	GGTGGTGCCATTTTGTCTTACC 47
RESULT 3	
AA200338	
ID	AA200338 standard; DNA; 47 BP.
AC	
XX	AA200338;
DT	
XX	22-OCT-1999 (first entry)
DE	
XX	Mutated hTR promoter fragment containing construct 113(msp1+mrCE).
KM	
XX	Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
XX	gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
OS	
XX	Homo sapiens.
OS	
XX	Synthetic.
FN	
XX	W09938964-A2.
PD	
XX	05-AUG-1999.
PF	
XX	29-JAN-1999; 99WO-GB00308.
XX	
XX	29-JAN-1998; 98GB-0001902.
XX	
XX	(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PI	
XX	Keith MN;
XX	
XX	WPI; 1999-479183/40.
PT	
XX	Mouse and human telomerase RNA gene promoters, useful for tumor
PT	specific gene therapy
XX	
XX	Disclosure; Fig 19, 109pp; English.
XX	
CC	The invention relates to promoter regions from mouse and human
CC	telomerase RNA (TR) component genes. The TR gene promoter can be linked
CC	to a heterologous gene, especially a gene encoding a cytotoxin, for
CC	therapy of cancer, especially neoplasias. The telomerase is necessary for
CC	the unrestricted proliferative capacity of many human cancers. Mutation
CC	or dysregulation of the telomerase repression pathway may cause
CC	reactivation or upregulation of telomerase expression in cancer.

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 10:14:29 ; Search time 113.554 Seconds
(without alignments)
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Perfect score: 30
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Scoring table: Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
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 - 19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
 - 20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
 - 21: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
 - 22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
 - 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
 - 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	90.0	47	20	AAZ00336
2	25	83.3	47	20	AAZ00337
3	25	83.3	47	20	AAZ00338
4	20	66.7	23	18	AA189246
5	20	66.7	23	21	AA189246
6	20	66.7	23	23	AA189246
7	20	66.7	23	23	AA189246
8	20	66.7	27	17	AA11045
9	20	66.7	28	20	AA190787
			47	20	AAZ00339

10	20	66.7	47	20	AAZ00340	Mutated htr promot
11	15	50.0	31	21	AA137591	Telomerase target
12	15	50.0	31	23	AA154562	Human telomerase R
13	14	46.7	20	17	AA110286	RNA component of m
14	14	46.7	20	17	AA110286	Antisense oligonuc
15	14	46.7	24	18	AA189245	DNA oligonucleotid
16	14	46.7	24	19	AA189245	Human telomerase R
17	14	46.7	24	19	AA137567	PNA sequence #25 u
18	14	46.7	24	23	AA154545	Oligonucleotide #1
19	14	46.7	25	21	AA137582	Telomerase RNA tar
20	14	46.7	25	21	AA154545	Human telomerase R
21	14	46.7	44	24	AA167765	Human telomerase R
22	13	43.3	13	18	AA189228	Peptide nucleic ac
23	13	43.3	13	20	AA137547	Human RRP-IC-A1 h
24	13	43.3	13	21	AA137547	PNA sequence #4 us
25	13	43.3	13	21	AA137588	Antisense sequence
26	13	43.3	13	21	AA137593	PNA sequence #51 u
27	13	43.3	13	21	AA137594	PNA sequence #52 u
28	13	43.3	13	22	AA181193	Phosphoramidate-11
29	13	43.3	13	22	AA126730	Phosphoramidate-11
30	13	43.3	13	22	AA126734	Phosphoramidate-11
31	13	43.3	13	23	AA154526	PNA 5/XII inhibiti
32	13	43.3	13	23	AA154526	PNA 3 inhibiting h
33	13	43.3	13	23	AA154565	PNA 2 inhibiting h
34	13	43.3	15	18	AA189229	PNA sequence #5 us
35	13	43.3	15	23	AA137548	PNA XII inhibiti
36	13	43.3	15	23	AA154527	Mycobacterium anti
37	13	43.3	24	18	AA159091	Antisense oligonuc
38	13	43.3	31	22	AA163645	Antisense oligonuc
39	13	43.3	31	22	AA163645	Antisense oligonuc
40	13	43.3	31	22	AA163645	Antisense oligonuc
41	13	43.3	33	18	AA159090	Human beta catenin
42	12	40.0	20	20	AA1207301	Human beta catenin
43	12	40.0	20	21	AA159359	Human POU1564 forw
44	12	40.0	23	21	AA137291	Probe #48 used in
45	12	40.0	23	22	AA154446	

ALIGNMENTS

RESULT 1	
AAZ00336	standard; DNA; 47 BP.
AAZ00336;	
22-OCT-1999	(first entry)
Mutated htr promoter fragment containing construct 111 (mspl.4).	
Telomerase RNA; TR; promoter; cytotocin; cancer; neoplasia; htr;	
gene therapy; thymidine kinase gene; anticancer therapy; human; ss.	
Homologous.	
Synthetic.	
WO9338964-A2.	
05-AUG-1999.	
29-JAN-1999;	99NO-GB00308.
29-JAN-1998;	98GB-0001902.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.	
Kelch W;	
WPI; 1999-479183/40.	
Mouse and human telomerase RNA gene promoters, useful for tumor	
specific gene therapy	


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FILING DATE: 25-May-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330,123
FILING DATE: Unknown
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William W
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-580-517-4

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Query Match      46.7%; Score 14; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 TTTGCTTACCCTA 30
DB 20 TTTGCTTACCCTA 7

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RESULT 15
US-08-838-545-25
Sequence 25, Application US/08838545
Patent No. 6046307
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Placzek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307on, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA)",
DESCRIPTION: where (deoxy/ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino N through a methylene carbonyl linker"
US-08-838-545-25

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Query Match      46.7%; Score 14; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 TTTGCTTACCCTA 30
DB 1 TTTGCTTACCCTA 14

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; Sequence 6, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-520-550A-6

Query Match      46.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TTTGCTAACCTA 30
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Db      20 TTGTCTAACCTA 7

RESULT 13
US-08-998-443-26/c
; Sequence 26, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Scirella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-998-443-26

Query Match      46.7%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TTTGCTAACCTA 30
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Db      20 TTGTCTAACCTA 7

RESULT 14
US-09-580-517-4/c
; Sequence 4, Application US/09580517
; Patent No. 6320039
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; FENG, Junli
; FUNK, Walter
; ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/580,517
```

NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-26

Query Match 46.7%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTA 30
Db 20 TTGTCTAACCTA 7

RESULT 10
US-08-485-778-6/c
Sequence 6, Application US/08485778
Patent No. 5878979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Greider, Carol
APPLICANT: Marhenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millita Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778
FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION/DOCKET NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-6

Query Match 46.7%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTA 30
Db 20 TTGTCTAACCTA 7

RESULT 11
US-08-472-802C-41/c
Sequence 41, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 514
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION/DOCKET NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-472-802C-41

Query Match 46.7%; Score 14; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTA 30
Db 20 TTGTCTAACCTA 7

RESULT 12
US-08-520-550A-6/c

Sequence 49, Application US/09349532
Patent No. 6294650
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatyzek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6294650ton, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
TITLE OF INVENTION: Peptide Nucleic Acids
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,532
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,545
FILING DATE: 09-APR-1997
APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-09-349-532-49

Query Match 50.0%; Score 15; DB 4; Length 31;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTGTCTAACCTTA 30
DB 1 UUUUGCUAACCTTA 15

RESULT 8
US-08-330-123A-4/c
Sequence 4, Application US/0830123A
Patent No. 5583016
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California

COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-330-123A-4

Query Match 46.7%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTTGTCTAACCTTA 30
DB 20 TTTGTCTAACCTTA 7

RESULT 9
US-08-660-678A-26/c
Sequence 26, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:

Fri Jun 27 07:41:57 2003

us-08-770-564a-1_copy_290_319_01igo.rml

Page 3

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/ APPLICANT: Greider, Carol
/ APPLICANT: Marhuende, Maria A. B.
/ APPLICANT: Valleponneau, Bryant
/ TITLE OF INVENTION: RNA Component of Telomerase
/ NUMBER OF SEQUENCES: 47
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
/ STREET: Two Militia Drive
/ CITY: Lexington
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02173
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/520,550A
/ FILING DATE: 29-AUG-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/387,524
/ FILING DATE: 13-FEB-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/330,123
/ FILING DATE: 27-OCT-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/272,102
/ FILING DATE: 07-JUL-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Granahan, Patricia
/ REGISTRATION NUMBER: 32,7227
/ REFERENCE/DOCKET NUMBER: CSHL94-05A3B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
/ US-08-520-550A-20
/
Query Match 66.7%; Score 20; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Cy 1 GGGGTGGTGGCCATTTTGG 20
Db 8 GGGGTGGTGGCCATTTTGG 27
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RESULT 5
/ US-09-286-959B-3
/ Sequence 3, Application US/09286959B
/ Patent No. 6300131
/ GENERAL INFORMATION:
/ APPLICANT: Johns Hopkins University
/ APPLICANT: Greider, Carol W.
/ APPLICANT: Le, Siyan
/ TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
/ FILE REFERENCE: 07265/157001
/ CURRENT APPLICATION NUMBER: US/09/286,959B
/ CURRENT FILING DATE: 1999-04-06
/ PRIOR APPLICATION NUMBER: 60/080,783
/ PRIOR FILING DATE: 1998-04-06
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 28
/ TYPE: DNA
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/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
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/ US-09-286-959B-3
/
Query Match 66.7%; Score 20; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Cy 1 GGGGTGGTGGCCATTTTGG 20
Db 9 GGGGTGGTGGCCATTTTGG 28
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RESULT 6
/ US-08-838-545-49
/ Sequence 49, Application US/08838545
/ Patent No. 6046307
/ GENERAL INFORMATION:
/ APPLICANT: Shay, Jerry M.
/ APPLICANT: Wright, Woodring E.
/ APPLICANT: Piatyvezek, Mieczyslaw A.
/ APPLICANT: Corey, David R.
/ APPLICANT: No. 6046307on, James C.
/ TITLE OF INVENTION: Modulation of Mammalian Telomerase by
/ TITLE OF INVENTION: Peptide Nucleic Acids
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838,545
/ FILING DATE: 09-APR-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/630,019
/ FILING DATE: 09-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Storella, John R.
/ REGISTRATION NUMBER: 32,944
/ REFERENCE/DOCKET NUMBER: 015389-001610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: RNA (genomic)
/
/ US-08-838-545-49
/
Query Match 50.0%; Score 15; DB 3; Length 31;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
/
Cy 16 TTGTGCTAACCCCTA 30
Db 1 UUUUGCUAACCCUA 15
/
RESULT 7
/ US-09-349-532-49
/
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US-08-838-545-26

Query Match 66.7%; Score 20; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30
Db 1 CCATTTTGTCTAACCTTA 20

RESULT 2

US-09-349-532-26
Sequence 26, Application US/09349532
Patent No. 6294650

GENERAL INFORMATION:

APPLICANT: Shay, Jerry W.

APPLICANT: Wright, Woodring E.

APPLICANT: Piatyszek, Mieczyslaw A.

APPLICANT: Corey, David R.

APPLICANT: No. 6294650ton, James C.

TITLE OF INVENTION: Modulation of Mammalian Telomerase by

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/349,532

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/838,545

FILING DATE: 09-APR-1997

APPLICATION NUMBER: US 08/630,019

FILING DATE: 09-APR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-001610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0300

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "peptide nucleic acid (PNA),

DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by

DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via

DESCRIPTION: "glycine amino N through a methylene carbonyl linker"

US-09-349-532-26

Query Match 66.7%; Score 20; DB 4; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CCATTTTGTCTAACCTTA 30

Db 1 CCATTTTGTCTAACCTTA 20

RESULT 3

US-08-485-778-20
Sequence 20, Application US/08485778
Patent No. 5876979

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avilion, Ariel Athena

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria Antonia Blasco

APPLICANT: Villeponteau, Bryant

TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,778

FILING DATE: 07-JE-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/367,524

FILING DATE: 13-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-485-778-20

Query Match 66.7%; Score 20; DB 2; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGTGGCCATTTTGG 20

Db 8 GGGGTGTGGCCATTTTGG 27

RESULT 4

US-08-520-550A-20
Sequence 20, Application US/08520550A
Patent No. 6013468

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avilion, Ariel A.

APPLICANT: Feng, Junli

APPLICANT: Funk, Walter

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 19:12:24 ; Search time 28.7603 Seconds
(without alignments)
319,896 Million cell updates/sec

Title: US-08-770-564a-1_COPY_290_319
Perfect score: 30
Sequence: 1 GGCGTGGTGGCCATTCTTGTACCCCTA 30

Scoring table: OLIGO_NUC
Gapop 60.0, Gapexc 60.0

Searched: 441362 seqs, 15338381 residues

Word size: 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Issued Patents NA: *
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2: /cgn2_6/ptodata/2/1na/5b_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	66.7	23	3	US-08-838-545-26 Sequence 26, Appl
2	20	66.7	23	4	US-09-349-532-26 Sequence 26, Appl
3	20	66.7	27	2	US-08-485-778-20 Sequence 20, Appl
4	20	66.7	27	3	US-08-520-550A-20 Sequence 20, Appl
5	20	66.7	28	4	US-09-286-959B-3 Sequence 3, Appl
6	15	50.0	31	3	US-08-838-545-49 Sequence 49, Appl
7	15	50.0	31	4	US-09-349-532-49 Sequence 49, Appl
8	14	46.7	20	1	US-08-330-123A-4 Sequence 4, Appl
9	14	46.7	20	2	US-08-660-678A-26 Sequence 26, Appl
10	14	46.7	20	2	US-08-485-778-6 Sequence 6, Appl
11	14	46.7	20	2	US-08-472-802C-4 Sequence 4, Appl
12	14	46.7	20	3	US-08-530-550A-6 Sequence 6, Appl
13	14	46.7	20	3	US-08-988-443-26 Sequence 26, Appl
14	14	46.7	20	4	US-08-380-517-4 Sequence 4, Appl
15	14	46.7	24	4	US-08-838-545-25 Sequence 25, Appl
16	14	46.7	24	4	US-09-349-532-25 Sequence 25, Appl
17	14	46.7	24	4	US-09-018-125-4 Sequence 4, Appl
18	14	46.7	25	3	US-08-630-019A-26 Sequence 26, Appl
19	14	46.7	25	3	US-08-630-019A-36 Sequence 36, Appl
20	14	46.7	25	3	US-08-838-545-40 Sequence 40, Appl
21	14	46.7	25	4	US-09-349-532-40 Sequence 40, Appl
22	13	43.3	13	3	US-08-630-019A-17 Sequence 17, Appl
23	13	43.3	13	3	US-08-630-019A-41 Sequence 41, Appl
24	13	43.3	13	3	US-08-838-545-46 Sequence 46, Appl
25	13	43.3	13	3	US-08-838-545-51 Sequence 51, Appl
26	13	43.3	13	3	US-08-838-545-52 Sequence 52, Appl
27	13	43.3	13	3	US-08-838-545-52 Sequence 52, Appl

c 28	13	43.3	13	4	US-09-349-532-4	Sequence 4, Appl
c 29	13	43.3	13	4	US-09-349-532-46	Sequence 46, Appl
c 30	13	43.3	13	4	US-09-349-532-51	Sequence 51, Appl
c 31	13	43.3	13	4	US-09-349-532-52	Sequence 52, Appl
c 32	13	43.3	15	3	US-08-630-019A-18	Sequence 18, Appl
c 33	13	43.3	15	3	US-08-838-545-5	Sequence 5, Appl
c 34	13	43.3	15	3	US-09-349-532-5	Sequence 5, Appl
c 35	13	43.3	24	5	PCT-US96-09473-15	Sequence 15, Appl
c 36	13	43.3	33	5	PCT-US96-09473-13	Sequence 13, Appl
c 37	12	40.0	22	2	US-08-117-952-443	Sequence 443, Appl
c 38	12	40.0	29	2	US-08-944-604-22	Sequence 22, Appl
c 39	12	40.0	29	2	US-08-833-377-2	Sequence 2, Appl
c 40	12	40.0	40	3	US-08-399-696-11	Sequence 11, Appl
c 41	12	40.0	43	1	US-08-836-922-12	Sequence 12, Appl
c 42	11	36.7	11	3	US-08-630-019A-14	Sequence 14, Appl
c 43	11	36.7	11	3	US-08-630-019A-16	Sequence 16, Appl
c 44	11	36.7	11	3	US-08-838-545-3	Sequence 3, Appl
c 45	11	36.7	11	3	US-08-838-545-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-838-545-26
Sequence 26, Application US/08838545
Patent No. 6046307
GENERAL INFORMATION:
APPLICANT: Shay, Jerry W.
APPLICANT: Wright, Woodring E.
APPLICANT: Piatydzek, Mieczyslaw A.
APPLICANT: Corey, David R.
APPLICANT: No. 6046307con, James C.
TITLE OF INVENTION: Modulation of Mammalian Telomerase by
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,545
FILING DATE: 09-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/630,019
FILING DATE: 09-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "peptide nucleic acid (PNA),
DESCRIPTION: where (deoxy/ribose-phosphate linkages are replaced by
DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
DESCRIPTION: glycine amino N through a methylencarbonyl linker"

OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-117A-348

Query Match 40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTTGGTGGCCAT 14
|||||
Db 6 GGTTGGTGGCCAT 17

RESULT 15

US-10-013-913A-348
Sequence 348, Application US/10013913A
Publication No. US20030083462A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2830F1C40
CURRENT APPLICATION NUMBER: US/10/013,913A
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 348
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-913A-348

Query Match 40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTTGGTGGCCAT 14
|||||
Db 6 GGTTGGTGGCCAT 17

Search completed: June 24, 2003, 20:39:35
Job time : 366.455 secs

PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101071
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/101471
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101472
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101474
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101479
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101738
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PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
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PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102330
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102331
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PRIOR APPLICATION NUMBER: 60/102570
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102571
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 60/102684
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102687
PRIOR FILING DATE: 1998-10-01
PRIOR APPLICATION NUMBER: 60/102965
PRIOR FILING DATE: 1998-10-02
PRIOR APPLICATION NUMBER: 60/103258
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103314
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103315
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103328
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103395
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103396
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103401
PRIOR FILING DATE: 1998-10-07
PRIOR APPLICATION NUMBER: 60/103449
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: 60/103633
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103678

PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103679
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/103711
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 60/104257
PRIOR FILING DATE: 1998-10-14
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PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105000
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 60/105002
PRIOR FILING DATE: 1998-10-20
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PRIOR FILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/105169
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: 60/105266
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PRIOR FILING DATE: 1998-10-26
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PRIOR APPLICATION NUMBER: 60/105881
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/105882
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: 60/106023
PRIOR FILING DATE: 1998-10-28

Query Match 40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 GGTGGTGGCCAT 14
Db 6 GGTGGTGGCCAT 17

RESULT 14
US-10-006-117A-348
Sequence 348, Application US/10006117A
Publication No. US20030082627A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan I.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830PC13
CURRENT APPLICATION NUMBER: US/10/006,117A
Prior Application removed - See File Wrapper or Palm
PRIOR FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 348
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

QY 3 GGTGGTGCCAT 14
|||||
Db 6 GGTGGTGCCAT 17

RESULT 12

US-10-015-869A-348
Sequence 348, Application US/10015869A
Publication No. US2003073130A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C45
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 348
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-869A-348

Query Match 40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGTGGTGCCAT 14
|||||
Db 6 GGTGGTGCCAT 17

RESULT 13

US-10-006-116A-348
Sequence 348, Application US/10006116A
Publication No. US20030082626A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P1C15
CURRENT FILING DATE: 2001-12-16
Prior Application Number: 60/098716

PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
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? PRIOR FILING DATE: 1998-09-18
? PRIOR APPLICATION NUMBER: 60/101068
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? PRIOR FILING DATE: 1998-10-02
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? PRIOR FILING DATE: 1998-10-06
? PRIOR APPLICATION NUMBER: 60/103314
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? PRIOR FILING DATE: 1998-10-08

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? PRIOR APPLICATION NUMBER: 60/103678
? PRIOR FILING DATE: 1998-10-08
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? PRIOR APPLICATION NUMBER: 60/104257
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? PRIOR APPLICATION NUMBER: 60/105002
? PRIOR FILING DATE: 1998-10-20
? PRIOR APPLICATION NUMBER: 60/105104
? PRIOR FILING DATE: 1998-10-21
? PRIOR APPLICATION NUMBER: 60/105169
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105266
? PRIOR FILING DATE: 1998-10-22
? PRIOR APPLICATION NUMBER: 60/105693
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? PRIOR APPLICATION NUMBER: 60/105694
? PRIOR FILING DATE: 1998-10-26
? PRIOR APPLICATION NUMBER: 60/105807

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Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 GGTGGTGGCCAT 14
DB      6 GGTGGTGGCCAT 17

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RESULT 11
US-10-012-121A-348
? Sequence 348, Application US/10012121A
? Publication No. US2003073810A1
? GENERAL INFORMATION:
? APPLICANT: Baker, Kevin P.
? APPLICANT: Botstein, David
? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan L.
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Fong, Sherman
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, Christopher J.
? APPLICANT: Gueney, Austin L.
? APPLICANT: Hillan, Kenneth J.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2830PIC20
? CURRENT APPLICATION NUMBER: US/10/012,121A
? PRIOR FILING DATE: 2001-12-07
? Prior Application removed - See File Wrapper or Palm
? NUMBER OF SEQ ID NOS: 477
? SEQ ID NO 348
? LENGTH: 23
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-348

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Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-015-393A-348
; Sequence 348, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC6
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 348
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-348

Query Match      40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GGGTGGGCGCAT 14
Db      6  GGGTGGGCGCAT 17

RESULT 10
US-09-946-374-348
; Sequence 348, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC1
; CURRENT FILING DATE: 2001-09-04
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; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
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; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
```

```

; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1
; OTHER INFORMATION: to 20 are phosphorothioates,
; OTHER INFORMATION: linkages between positions 22 to 34 are modified
; OTHER INFORMATION: by 14-(1-aminocetyl)glycine)methylene carbonyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: position 21 n(L) = linker is
; OTHER INFORMATION: -O(PO2)-OCH2-CH-(CH2COOH)-(CH2)4-NH
US-09-817-387-21

```

```

Query Match          43.3%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 18 TTGCTAACCTTA 30
DB 34 TTGCTAACCTTA 22

```

RESULT 6

```

US-09-817-387-7/c
; Sequence 7, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Delbruck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to
; OTHER INFORMATION: 19 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 19 to 35 are phosphodiester
; OTHER INFORMATION: positions 21 to 35 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
US-09-817-387-7

```

```

Query Match          43.3%; Score 13; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 18 TTGCTAACCTTA 30
DB 35 TTGCTAACCTTA 23

```

RESULT 7

```

US-10-006-856A-348
; Sequence 348, Application US/10006856A
; Publication No. US20030044841A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.

```

```

; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; CURRENT FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See file wrapper or Palm
; SEQ ID NO 348
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-856A-348

```

```

Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 3 GGTGGGGCCAT 14
DB 6 GGTGGGGCCAT 17

```

RESULT 8

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US-10-006-818A-348
; Sequence 348, Application US/10006818A
; Publication No. US20030054406A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P14
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 348
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-348

```

```

Query Match          40.0%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 GGTGGGGCCAT 14
DB 6 GGTGGGGCCAT 17

```

RESULT 9

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-09-057-351-40

Query Match 46.7%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
| | | | | | | | | | | | | | | | | | | | | |
DB 20 TTGTCTAACCTTA 7

RESULT 2
US-09-018-125-4
; Sequence 4, Application US/09018125A
; Patent No. US20010007902A1
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Kondo, Seiji
; APPLICANT: Cowell, John K.
; APPLICANT: Li, Guyling
; APPLICANT: Torrence, Paul F.
; TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
; TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES
; FILE REFERENCE: 8656-022
; CURRENT APPLICATION NUMBER: US/09/018, 125A
; EARLIER FILING DATE: 1999-02-03
; EARLIER APPLICATION NUMBER: 60/044,507
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-018-125-4

Query Match 46.7%; Score 14; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
| | | | | | | | | | | | | | | | | | | | | |
DB 1 TTGTCTAACCTTA 14

RESULT 3
US-09-817-387-8/C
; Sequence 8, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to
; OTHER INFORMATION: 15 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 15 to 17, 19 to 23 and 25 to 30 are
; OTHER INFORMATION: phosphodiester,
; OTHER INFORMATION: linkages between positions 17 to 19 and 23 to 25
; OTHER INFORMATION: are N3' to N5' phosphoramidates
US-09-817-387-8

Query Match 43.3%; Score 13; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTGTCTAACCTTA 30
| | | | | | | | | | | | | | | | | | | | | |
DB 30 TTGTCTAACCTTA 18

RESULT 4
US-09-817-387-9/C
; Sequence 9, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide, linkages between positions 1 to
; OTHER INFORMATION: 15 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 15 to 20 are phosphodiester,
; OTHER INFORMATION: position 21 n(l) = linker is
; OTHER INFORMATION: 3'-O(P02)CH2CH(CH2COOH)-(CH2)4-NH-,
; OTHER INFORMATION: linkages between positions 22 to 34 are
; OTHER INFORMATION: [N-(2-aminoethyl)glycine] methylene carbonyl
; OTHER INFORMATION: residues
US-09-817-387-9

Query Match 43.3%; Score 13; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TTGTCTAACCTTA 30
| | | | | | | | | | | | | | | | | | | | | |
DB 34 TTGTCTAACCTTA 22

RESULT 5
US-09-817-387-21/C
; Sequence 21, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Debruck-Centrum fur Molekulare Medizin
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: June 23, 2003, 20:29:49 ; Search time 365.455 Seconds

(without alignments)
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Title: US-08-770-564a-1_COPY_290_319

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Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 73373590 residues

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-Processing: Listing first 45 summaries

Database : Published Applications NA:*

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12: /cgn2_6/ptodata/2/pubna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	46.7	20	10	US-09-057-351-40
2	14	46.7	24	10	US-09-018-125-4
3	13	43.3	30	10	US-09-817-387-8
4	13	43.3	34	10	US-09-817-387-9
5	13	43.3	34	10	US-09-817-387-21
6	13	43.3	35	10	US-09-817-387-7
7	12	40.0	23	9	US-10-006-856A-348
8	12	40.0	23	9	US-10-006-818A-348
9	12	40.0	23	9	US-10-015-933A-348
10	12	40.0	23	9	US-08-946-374-348
11	12	40.0	23	9	US-10-012-121A-348
12	12	40.0	23	9	US-10-015-869A-348
13	12	40.0	23	9	US-10-006-116A-348
14	12	40.0	23	9	US-10-006-117A-348
15	12	40.0	23	9	US-10-013-913A-348
16	12	40.0	23	9	US-10-017-527A-348
17	12	40.0	23	9	US-10-007-194A-348
18	12	40.0	23	9	US-10-013-430A-348
19	12	40.0	23	9	US-10-011-671A-348

20	12	40.0	23	9	US-10-012-755A-348	Sequence 348, App
21	12	40.0	23	9	US-10-015-386A-348	Sequence 348, App
22	12	40.0	23	9	US-10-011-692A-348	Sequence 348, App
23	12	40.0	25	9	US-10-098-263B-14446	Sequence 14446, A
24	12	40.0	25	9	US-10-098-263B-116941	Sequence 116941, A
25	12	40.0	27	10	US-09-976-674-50	Sequence 38, App
26	11	36.7	16	9	US-10-206-833-38	Sequence 38, App
27	11	36.7	20	9	US-09-966-451-83	Sequence 83, App
28	11	36.7	20	9	US-09-902-176A-39	Sequence 39, App
29	11	36.7	20	10	US-09-988-915-3	Sequence 57, App
30	11	36.7	24	9	US-10-091-135-57	Sequence 58, App
31	11	36.7	24	9	US-10-091-135-58	Sequence 71, App
32	11	36.7	24	9	US-09-940-185-711	Sequence 4677, App
33	11	36.7	25	9	US-09-940-185-4677	Sequence 12672, A
34	11	36.7	25	9	US-10-098-263B-12672	Sequence 14445, A
35	11	36.7	25	9	US-10-098-263B-14445	Sequence 68494, A
36	11	36.7	25	9	US-10-098-263B-68494	Sequence 75989, A
37	11	36.7	25	9	US-10-098-263B-75989	Sequence 79564, A
38	11	36.7	25	9	US-10-098-263B-79736	Sequence 79736, A
39	11	36.7	25	9	US-10-098-263B-82962	Sequence 82962, A
40	11	36.7	25	9	US-10-098-263B-86266	Sequence 86266, A
41	11	36.7	25	9	US-10-098-263B-86266	Sequence 90337, A
42	11	36.7	29	9	US-09-863-040-54	Sequence 54, App
43	11	36.7	29	10	US-09-946-678-22	Sequence 22, App
44	11	36.7	30	10	US-09-750-373-37	Sequence 37, App
45	11	36.7	30	10	US-09-750-373-37	Sequence 37, App

ALIGNMENTS

RESULT 1
US-09-057-351-40/c
; Sequence 40, Application US/09057351
; Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Vallopreteu, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 06/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

APPLICANT: Feng, Junli
 APPLICANT: Funk, Walter
 APPLICANT: Greider, Carol
 APPLICANT: Marhuenda, Maria A.B.
 APPLICANT: Villeponteau, Bryant
 TITLE OF INVENTION: RNA Component of Telomerase
 FILE REFERENCE: CSHL94-05A7
 CURRENT APPLICATION NUMBER: US/09/259,943
 CURRENT FILING DATE: 1999-03-01
 EARLIER APPLICATION NUMBER: 08/623,166
 EARLIER FILING DATE: 1996-03-28
 EARLIER APPLICATION NUMBER: 08/520,550
 EARLIER FILING DATE: 1995-08-29
 EARLIER APPLICATION NUMBER: 08/485,778
 EARLIER FILING DATE: 1995-06-07
 EARLIER APPLICATION NUMBER: 08/387,524
 EARLIER FILING DATE: 1995-02-13
 EARLIER APPLICATION NUMBER: 08/330,123
 EARLIER FILING DATE: 1994-10-27
 EARLIER APPLICATION NUMBER: 08/272,102
 EARLIER FILING DATE: 1994-07-07
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO: 26
 LENGTH: 20
 TYPE: RNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic oligonucleotides
 US-09-259-943-26

Query Match 46.7%; Score 14; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
 20 TTGTCTAACCTTA 7

RESULT 15
 US-09-370-455-26
 Sequence 26; Application US/09370455
 GENERAL INFORMATION:
 APPLICANT: Shay, Jerry W.
 APPLICANT: Wright, Woodring E.
 APPLICANT: Piatysek, Mieczyslaw A.
 APPLICANT: Corey, David
 APPLICANT: Norton, James C.
 TITLE OF INVENTION: Modulation of Mammalian Telomerase by
 TITLE OF INVENTION: Peptide Nucleic Acids
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/370,455
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/630,019
 FILING DATE: 09-JUN-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.

REGISTRATION NUMBER: 32,944
 REFERENCE/DOCKET NUMBER: 015389-001600US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "peptide nucleic acid (PNA),
 DESCRIPTION: where (deoxy)ribose-phosphate linkages are replaced by
 DESCRIPTION: N-(2-aminoethyl)glycine units linked to nucleotide bases via
 DESCRIPTION: glycine amino nitrogen through a methylene-carbonyl linker"
 US-09-370-455-26

Query Match 46.7%; Score 14; DB 17; Length 25;
 Best Local Similarity 57.1%; Pred. No. 2.4e+03;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
 DB 1 UUUGUCUACCTTA 14

Search completed: June 24, 2003, 18:22:28
 Job time : 1298.44 secs

REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
ANTI-SENSE: YES
US-08-521-634-25

Query Match 46.7%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTA 30
Db 20 TTTGCTAACCTA 7

RESULT 12
US-08-660-678-4/c
Sequence 4, Application US/08660678
GENERAL INFORMATION:
APPLICANT: VILLEPONTAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000811
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-660-678-4

Query Match 46.7%; Score 14; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTA 30
Db 20 TTTGCTAACCTA 7

RESULT 13
US-09-057-351-40/c
Sequence 40, Application US/09057351
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-09-057-351-40

Query Match 46.7%; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTA 30
Db 20 TTTGCTAACCTA 7

RESULT 14
US-09-259-943-26/c
Sequence 26, Application US/09259943
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.

STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-482-115A-4

Query Match 46.7%; Score 14; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30
Db 20 TTTGCTAACCTTA 7

RESULT 10
US-08-520-550-6/C
Sequence 6, Application US/08520550
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550-6

Query Match 46.7%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TTTGCTAACCTTA 30
Db 20 TTTGCTAACCTTA 7

RESULT 11
US-08-521-634-25/C
Sequence 25, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-772-102-7

Query Match 46.7%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
DB 20 TTGTCTAACCTTA 7

RESULT 7
US-08-387-524-6/c
Sequence 6, Application US/08387524
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,524
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-387-524-6

Query Match 46.7%; Score 14; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
DB 20 TTGTCTAACCTTA 7

DB 20 TTGTCTAACCTTA 7

RESULT 8
US-08-472-802B-41/c
Sequence 41, Application US/08472802B
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-472-802B-41

Query Match 46.7%; Score 14; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TTGTCTAACCTTA 30
DB 20 TTGTCTAACCTTA 7

RESULT 9
US-08-482-115A-4/c
Sequence 4, Application US/08482115A
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco

Qy 1 GGGGTGGTGCCATTTTTG 20
|||
Db 8 GGGGTGGTGCCATTTTTG 27

RESULT 3

US-09-259-943-46
; Sequence 46, Application US/09259943
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Maruenda, Maria A.B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; FILE REFERENCE: CSHL94-05A7
; CURRENT APPLICATION NUMBER: US/09/259,943
; EARLIER FILING DATE: 1999-03-01
; EARLIER FILING DATE: 1996-03-28
; EARLIER APPLICATION NUMBER: 08/520,550
; EARLIER FILING DATE: 1995-08-29
; EARLIER APPLICATION NUMBER: 08/485,778
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/387,524
; EARLIER FILING DATE: 1995-02-13
; EARLIER APPLICATION NUMBER: 08/330,123
; EARLIER FILING DATE: 1994-10-27
; EARLIER APPLICATION NUMBER: 08/272,102
; EARLIER FILING DATE: 1994-07-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotides
US-09-259-943-46

Query Match 66.7%; Score 20; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGCCATTTTTG 20
|||
Db 8 GGGGTGGTGCCATTTTTG 27

RESULT 4

PCT-US99-07533-3
; Sequence 3, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157MO
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-3

Query Match 66.7%; Score 20; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGTGGTGCCATTTTTG 20
|||
Db 9 GGGGTGGTGCCATTTTTG 28

RESULT 5

PCT-US99-07533-3
; Sequence 3, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157MO
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-3

Query Match 66.7%; Score 20; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGTGGTGCCATTTTTG 20
|||
Db 9 GGGGTGGTGCCATTTTTG 28

RESULT 6

US-08-272-102-7/c
; Sequence 7, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTEAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: Funk, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:


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C 23 13 43.3 13 17 US-09-370-455-41 Sequence 41, Appl
C 24 13 43.3 13 25 US-09-657-445A-2 Sequence 2, Appl
C 25 13 43.3 13 42 US-10-255-535-3 Sequence 3, Appl
C 26 13 43.3 15 17 US-09-370-455-18 Sequence 18, Appl
C 27 13 43.3 17 28 US-09-708-690-7501 Sequence 7501, Ap
C 28 13 43.3 17 33 US-09-870-161-7501 Sequence 7501, Ap
C 29 13 43.3 17 40 US-10-138-674-7501 Sequence 7501, Ap
C 30 13 43.3 19 65 US-60-216-745-7916 Sequence 7916, Ap
C 31 13 43.3 20 41 US-10-187-659A-61 Sequence 61, Appl
C 32 13 43.3 20 41 US-10-187-659A-120 Sequence 120, Appl
C 33 13 43.3 24 8 US-08-484-169-15 Sequence 15, Appl
C 34 13 43.3 25 67 US-60-232-638-55299 Sequence 55299, A
C 35 13 43.3 25 67 US-60-233-620-68407 Sequence 68407, A
C 36 13 43.3 25 67 US-60-233-620-123435 Sequence 123435,
C 37 13 43.3 25 79 US-60-353-987-788561 Sequence 788561,
C 38 13 43.3 25 79 US-60-353-987-905467 Sequence 905467,
C 39 13 43.3 30 31 US-09-817-387-8 Sequence 8, Appl
C 40 13 43.3 31 9 US-08-510-736-1 Sequence 1, Appl
C 41 13 43.3 31 28 US-09-717-828A-1 Sequence 1, Appl
C 42 13 43.3 31 28 US-09-717-828B-1 Sequence 1, Appl
C 43 13 43.3 31 28 US-09-717-829A-1 Sequence 13, Appl
C 44 13 43.3 33 8 US-08-484-169-13 Sequence 9, Appl
C 45 13 43.3 34 31 US-09-817-387-9

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ALIGNMENTS

RESULT 1

Sequence 20, Application US/08387524

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avillion, Ariel A.

APPLICANT: Peng, Junli

APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria A. B.

APPLICANT: Villeponteau, Bryant

TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESSES:

ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,524

FILING DATE: 13-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULAR TYPE: DNA (genomic)
US-08-387-524-20

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Query Match 66.7%; Score 20; DB 7; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGGTGTCGCATTTTGG 20
Db 8 GGGGTGTCGCATTTTGG 27

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RESULT 2

Sequence 20, Application US/08520550

GENERAL INFORMATION:

APPLICANT: Andrews, William H.

APPLICANT: Avillion, Ariel A.

APPLICANT: Peng, Junli

APPLICANT: Greider, Carol

APPLICANT: Marhuenda, Maria A. B.

APPLICANT: Villeponteau, Bryant

TITLE OF INVENTION: RNA Component of Telomerase

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESSES:

ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/520,550

FILING DATE: 29-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/387,524

FILING DATE: 13-FEB-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A3B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-520-550-20

Query Match

Best Local Similarity 66.7%; Score 20; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:01:44 ; Search time 1297.44 Seconds
(without alignments)
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Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

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2	20	66.7	27	US-08-520-550-20	Sequence 46, Appl
3	20	66.7	27	US-09-259-943-46	Sequence 40, Appl
4	20	66.7	28	PCT-US99-07553-3	Sequence 26, Appl
5	20	66.7	28	PCT-US99-07553-3	Sequence 3, Appl
6	14	46.7	20	US-08-372-102-7	Sequence 7, Appl
7	14	46.7	20	US-08-387-524-20	Sequence 6, Appl
8	14	46.7	20	US-08-472-802B-41	Sequence 41, Appl
9	14	46.7	20	US-08-482-115A-4	Sequence 4, Appl
10	14	46.7	20	US-08-520-550-6	Sequence 23, Appl
11	14	46.7	20	US-08-521-631-25	Sequence 2, Appl
12	14	46.7	20	US-08-660-678-4	Sequence 4, Appl
13	14	46.7	20	US-09-057-351-40	Sequence 40, Appl
14	14	46.7	20	US-09-259-943-46	Sequence 26, Appl
15	14	46.7	25	US-09-370-455-36	Sequence 36, Appl
16	14	46.7	25	US-09-370-455-36	Sequence 46061, A
17	14	46.7	25	US-60-223-628-46061	Sequence 808955,
18	14	46.7	25	US-60-353-987-808955	Sequence 865819,
19	14	46.7	25	US-60-353-987-865819	Sequence 6, Appl
20	14	46.7	27	US-08-521-631-6	Sequence 3, Appl
21	13	43.3	13	PCT-US02-0918A-3	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Fri Jun 27 07:42:00 2003

us-08-770-564a-1_copy_290_319.oligo.rnpn

Page 5

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 13
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
PCT-US02-33146-13

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Matches 8; Conservative 5; Mismatches 0; Indels 0;
Gaps 0;
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Db 1 UUGGCUAACCCCUA 13

Search completed: June 24, 2003, 20:14:43
Job time : 1667.12 secs

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GTGGTGCCATT 17
Db 14 GTGGTGCCATT 1

RESULT 11

US-60-427-808-895384
; Sequence 895384, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 895384
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-895384

Query Match 46.7%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGGTGGCCATT 18
Db 1 TGGTGGCCATT 14

RESULT 12

US-60-427-836-475949
; Sequence 475949, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 639466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 475949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-475949

Query Match 46.7%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTGTCTAACCT 29
Db 8 TTTTGTCTAACCT 21

RESULT 13

PCT-US02-17674-490/C
; Sequence 490, Application PC/TUS0217674
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; FILE REFERENCE: 400/047 (02-325)
; CURRENT APPLICATION NUMBER: PCT/US02/17674

; CURRENT FILING DATE: 2003-03-25
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 09/708,690
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 09/870,161
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/334,461
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 5989
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 490
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
PCT-US02-17674-490

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Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGCCATT 20
Db 15 TGCCATT 3

RESULT 14

US-10-287-949A-7501/C
; Sequence 7501, Application US/10287949A
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7501
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7501

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Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGCCATT 20
Db 15 TGCCATT 3

RESULT 15

PCT-US02-33146-13
; Sequence 13, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: FP-71506-2/RFT/SRN
; CURRENT APPLICATION NUMBER: PCT/US02/33146

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COUNTRY: USA
ZIP: 94111-3814
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/359,935
FILING DATE: 07-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-10-359-935-40

Query Match          46.7%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TTTGCTACCCCTA 30
DB      20 TTTGCTACCCCTA 7

RESULT 7
US-09-953-570-46061
Sequence 46061, Application US/09953570
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
FILE REFERENCE: 3110.1
CURRENT APPLICATION NUMBER: US/09/953,570
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: 60/222,638
PRIOR FILING DATE: 2000-09-14
NUMBER OF SEQ ID NOS: 138410
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 46061
LENGTH: 25
TYPE: DNA
ORGANISM: Saccharomyces Cerevisiae
US-09-953-570-46061

Query Match          46.7%; Score 14; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GTGGCAATTTTGG 20
DB      12 GTGGCAATTTTGG 25

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RESULT 8
US-10-355-577-808955
Sequence 808955, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 808955
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-808955

Query Match          46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 CCATTTTGTGCTA 24
DB      2 CCATTTTGTGCTA 15

RESULT 9
US-10-355-577-865819
Sequence 865819, Application US/10355577
GENERAL INFORMATION:
APPLICANT: Miltmann, Michael
TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
FILE REFERENCE: 3121
CURRENT APPLICATION NUMBER: US/10/355,577
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 997516
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 865819
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-355-577-865819

Query Match          46.7%; Score 14; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TTTTGTCTACCC 27
DB      3 TTTTGTCTACCC 16

RESULT 10
US-60-427-808-4727/c
Sequence 4727, Application US/60427808
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528
CURRENT APPLICATION NUMBER: US/60/427,808
CURRENT FILING DATE: 2002-11-20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 4727
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-60-427-808-4727/c

Query Match          46.7%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 TTTTGTCTACCC 27
DB      3 TTTTGTCTACCC 16

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QY 8 TGGCCATTTTGTCTAAC 26
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 Db 1 UGGCCAUUUUUUGUCUAC 19

RESULT 2

PCT-US03-04088-272/c
 ; Sequence 272, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyne Pharmaceuticals, Inc.
 ; APPLICANT: MCSwigen, James
 ; APPLICANT: Betgelman, Leonid
 ; TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 272
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
 ; PCT-US03-04088-272

Query Match 63.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGCCATTTTGTCTAAC 26
 :|||||:|||||
 Db 19 TGGCCATTTTGTCTAAC 1

RESULT 3

PCT-US02-33146-9
 ; Sequence 9, Application PC/TUS0233146
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Rochester Medical Center
 ; APPLICANT: Rowley, Peter
 ; TITLE OF INVENTION: Telomerase Interference
 ; FILE REFERENCE: FP-71506-2/RFT/SRN
 ; CURRENT APPLICATION NUMBER: PCT/US02/33146
 ; CURRENT FILING DATE: 2002-12-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 22
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; PCT-US02-33146-9

Query Match 53.3%; Score 16; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 69;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGGTGGGCCATTT 16
 :|||||:|||||
 Db 7 GGGGTGGGCCATTT 22

RESULT 4

US-60-427-836-73/c
 ; Sequence 73, Application US/60427836
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
 ; FILE REFERENCE: 3527
 ; CURRENT APPLICATION NUMBER: US/60/427,836
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 699466
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 73
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; US-60-427-836-73

Query Match 53.3%; Score 16; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTGGTGGCCATTTT 19
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 Db 16 GTGGTGGCCATTTT 1

RESULT 5

US-60-427-808-749867
 ; Sequence 749867, Application US/60427808
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528
 ; CURRENT APPLICATION NUMBER: US/60/427,808
 ; CURRENT FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 749867
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-60-427-808-749867

Query Match 50.0%; Score 15; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 TTTTGTCTAACCT 29
 :|||||:|||||
 Db 7 TTTTGTCTAACCT 21

RESULT 6

US-10-359-935-40/c
 ; Sequence 40, Application US/10359935
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Funk, Walter
 ; APPLICANT: Andrews, William H.
 ; TITLE OF INVENTION: Mammalian Telomerase
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 20:09:29 ; Search time 1666.12 Seconds
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Title: US-08-770-564A-1_COPY_290_319

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Scoring table:

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Total number of hits satisfying chosen parameters: 8654690

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

Pending Patents NA New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	15	50.0	25	12	US-60-427-808-749867
6	14	46.7	20	9	US-10-359-935-40
7	14	46.7	25	9	US-09-953-570-46061
8	14	46.7	25	9	US-10-355-577-865819
9	14	46.7	25	12	US-60-427-808-749867
10	14	46.7	25	12	US-60-427-808-749867
11	14	46.7	25	12	US-60-427-808-749867
12	14	46.7	25	12	US-60-427-808-749867
13	13	43.3	17	10	PCT-US02-17674-490
14	13	43.3	17	10	US-10-287-949A-7501
15	13	43.3	19	9	PCT-US02-33146-13
16	13	43.3	19	9	US-10-310-188-45971
17	13	43.3	20	9	US-10-310-188-72791
18	13	43.3	21	1	PCT-US02-33146-1
19	13	43.3	25	7	US-09-953-570-55299
20	13	43.3	25	7	US-09-954-445A-68407

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C 23	13	43.3	25	9	US-10-355-577-905467	Sequence 905467
C 24	13	43.3	25	12	US-60-427-808-32047	Sequence 32047, A
C 25	13	43.3	25	12	US-60-427-808-31286	Sequence 31286, A
C 26	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
C 27	13	43.3	25	12	US-60-427-808-122370	Sequence 122370
C 28	13	43.3	25	12	US-60-427-808-387042	Sequence 387042
C 29	13	43.3	25	12	US-60-427-808-430998	Sequence 430998
C 30	13	43.3	25	12	US-60-427-808-654167	Sequence 654167
C 31	13	43.3	25	12	US-60-427-808-654167	Sequence 654167
C 32	13	43.3	25	12	US-60-427-836-3553	Sequence 3553, Ap
C 33	13	43.3	25	12	US-60-427-836-17687	Sequence 17687, A
C 34	13	43.3	25	12	US-60-427-836-220705	Sequence 220705
C 35	13	43.3	25	12	US-60-427-836-100545	Sequence 100545
C 36	13	43.3	31	10	US-10-330-872A-1	Sequence 1, Appl
C 37	13	43.3	31	10	US-10-330-872A-1	Sequence 1, Appl
C 38	12	40.0	15	10	US-10-287-787-14217	Sequence 14217, A
C 39	12	40.0	15	10	US-10-287-787-19188	Sequence 19188, A
C 40	12	40.0	17	1	PCT-US02-17674-491	Sequence 491, App
C 41	12	40.0	17	9	US-10-310-188-84645	Sequence 84645, A
C 42	12	40.0	17	9	US-10-310-188-84645	Sequence 84645, A
C 43	12	40.0	18	9	US-10-310-188-54892	Sequence 54892, Ap
C 44	12	40.0	19	9	US-10-310-188-70460	Sequence 70460, A
C 45	12	40.0	20	9	US-10-315-474-84	Sequence 84, Appl

ALIGNMENTS

RESULT 1

PCT-US03-04088-8

Sequence 8, Application PC/TUS0304088

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: McSwiggen, James

APPLICANT: Beigelman, Leonard

TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene

TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)

FILE REFERENCE: 02-708-A (400/080)

CURRENT APPLICATION NUMBER: PCT/US03/04088

CURRENT FILING DATE: 2003-04-28

PRIOR APPLICATION NUMBER: US 60/396,600

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11

PRIOR APPLICATION NUMBER: US 60/386,782

PRIOR FILING DATE: 2002-06-06

PRIOR APPLICATION NUMBER: US 60/406,784

PRIOR FILING DATE: 2002-08-29

PRIOR APPLICATION NUMBER: US 60/408,378

PRIOR FILING DATE: 2002-09-05

PRIOR APPLICATION NUMBER: US 60/409,293

PRIOR FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US 60/440,129

PRIOR FILING DATE: 2003-01-15

NUMBER OF SEQ ID NOS: 626

SOURCE: Patent version 3.2

SEQ ID NO: 8

LENGTH: 19

TYPE: RNA

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense

PCT-US03-04088-8

Query Match 63.3%; Score 19; DB 1; Length 19;

Best Local Similarity 52.6%; Pred. No. 1.6;

Matches 10; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Db |||||||
 29 TTTTGTCTAAC 19

Search completed: June 24, 2003, 16:52:45
Job time : 789.207 secs

Trace considered overall poor quality
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Seq primer: -40UP from Gibco
High quality sequence stop: 1.

FEATURES

Location/Qualifiers

source

1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGB:2264524"
/clone_1b="NCI-CCAP_Ut3"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: PCMV-SPORE6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.45 kb. Life Technologies catalog #: 11541-018"

BASE COUNT 14 a 12 c 18 g 2 t
ORIGIN

Query Match 36.7%; Score 11; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGGCATTTT 19
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30 GGGCATTTT 20

Db 30 GGGCATTTT 20

RESULT 14

AZ404140 46 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
100172J15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0172J15 F, DNA sequence.

ACCESSION

AZ404140

VERSION

AZ404140.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 46)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah
Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0172 Row: J Column: 15
Seq primer: CGTGTAAACACGCGCCAGT
Class: Plasmid ends
High quality sequence stop: 46.

FEATURES

Location/Qualifiers

source

1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0172J15"
/clone_1b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: PWD42uv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 19 a 10 c 10 g 7 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
24 GGGTGTGTGCG 34

Db 24 GGGTGTGTGCG 34

RESULT 15

AU105989/c 50 bp mRNA linear EST 30-AUG-2001
LOCUS
DEFINITION
AU105989 Sugano Homo sapiens CDNA library Homo sapiens CDNA clone
HS101865, mRNA sequence.

ACCESSION

AU105989

VERSION

AU105989.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 50)

AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isegaki, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki,
Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE

Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites

JOURNAL

EMBO Rep. 2 (5), 388-393 (2001)

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science,
University of Tokyo
4-6-1, Shirokane, Minato-ku, Tokyo 108-8639, Japan
Email: yusuk@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

Location/Qualifiers

source

1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HS101865"
/clone_1b="Sugano Homo sapiens CDNA library"
/note="Differential display comparison of untreated and
dimethylformate treated U937 cells"

BASE COUNT

15 a 14 c 8 g 13 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 TTTTGTCTAAC 26

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; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAACG 15
Db      1 GCTCTAGATGAACG 15

RESULT 13
US-10-330-872A-5
; Sequence 5, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-5

Query Match      100.0%; Score 15; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAACG 15
Db      1 GCTCTAGATGAACG 15

RESULT 14
US-10-310-188-36216/c
; Sequence 36216, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
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; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 36216
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-36216

Query Match      93.3%; Score 14; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAAC 14
Db      14 GCTCTAGATGAAC 1

RESULT 15
US-60-427-808-952738
; Sequence 952738, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 952738
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-952738

Query Match      93.3%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATGAAC 14
Db      3 GCTCTAGATGAAC 16

Search completed: June 26, 2003, 04:15:19
Job time : 359.634 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1272.79 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTTAGAATGAACG 15

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq.*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	1	PCT-US97-23619-10
2	15	100.0	15	11	US-08-770-564A-10
3	15	100.0	19	1	PCT-US97-23619-9
4	15	100.0	19	11	US-08-770-564A-9
5	15	100.0	25	16	US-09-250-336A-4
6	15	100.0	25	25	US-09-642-177-4
7	15	100.0	26	1	PCT-US96-14679A-27
8	15	100.0	26	1	PCT-US96-14679A-27
9	15	100.0	26	1	PCT-US99-03302-4
10	15	100.0	26	1	PCT-US99-07533-4
11	15	100.0	26	1	PCT-US99-07533-4
12	15	100.0	26	7	US-08-272-102-23
13	15	100.0	26	7	US-08-387-524-19
14	15	100.0	26	8	US-08-472-802A-34
15	15	100.0	26	8	US-08-472-802B-24
16	15	100.0	26	8	US-08-482-115A-23
17	15	100.0	26	9	US-08-520-550-19
18	15	100.0	26	9	US-08-521-634-41
19	15	100.0	26	10	US-08-660-678-23
20	15	100.0	26	13	US-08-911-312-23
21	15	100.0	26	13	US-08-911-312A-23

22 15 100.0 26 13 US-08-912-951-312
23 15 100.0 26 13 US-08-973-589-17
24 15 100.0 26 13 US-08-974-549-598
25 15 100.0 26 14 US-09-057-351-23
26 15 100.0 26 16 US-09-216-847-2
27 15 100.0 26 16 US-09-250-336-4
28 15 100.0 26 16 US-09-259-943-45
29 15 100.0 26 18 US-09-402-181A-598
30 15 100.0 26 18 US-09-402-181B-598
31 15 100.0 26 18 US-09-432-503-598
32 15 100.0 26 25 US-09-653-573-5
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36 15 100.0 26 33 US-09-895-606-26
37 15 100.0 26 38 US-10-044-539-312
38 15 100.0 27 1 PCT-US97-23619-26
39 15 100.0 27 1 PCT-US97-23619-26
40 15 100.0 30 9 US-08-510-736-5
41 15 100.0 30 9 US-08-521-634-10
42 15 100.0 30 11 US-08-770-564A-8
43 15 100.0 30 21 US-09-540-119B-10
44 15 100.0 30 28 US-09-717-828A-5
45 15 100.0 30 28 US-09-717-828A-5

ALIGNMENTS

RESULT 1
PCT-US97-23619-10
; Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-10
Query Match 100.0%; Score 15; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGACG 15
Db 1 GCTCTAGATGACG 15
RESULT 3
PCT-US97-23619-9
; Sequence 10, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-564A-10
Query Match 100.0%; Score 15; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGACG 15
Db 1 GCTCTAGATGACG 15

Sequence 9, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note= "oligo 21ab"
PCT-US97-23619-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15
DB 1 GCTCTAGATGAACG 15
RESULT 4
US-08-770-564A-9
Sequence 9, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-9
Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15
DB 1 GCTCTAGATGAACG 15
RESULT 5
US-09-250-336A-4
Sequence 4, Application US/09250336A
GENERAL INFORMATION:
APPLICANT: STROVEL, Jeffrey W.
APPLICANT: STAMBERG, Judith
APPLICANT: ABRUZZO, Lynne V.
APPLICANT: HIGHSMITH, Edward
TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS FOR CANCER SCREENING
TITLE OF INVENTION: AND ASSESSMENT OF DISEASE STAGE AND PROGNOSIS
FILE REFERENCE: 10460-4 (210460.0004)
CURRENT APPLICATION NUMBER: US/09/250,336A
CURRENT FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: US 60/074,793
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: PCT/US99/03302
PRIOR FILING DATE: 1999-02-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:R3c, Primer
US-09-250-336A-4
Query Match 100.0%; Score 15; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15
DB 1 GCTCTAGATGAACG 15

Db 4 GCTCTAGATGAACG 18

RESULT 6

US-09-642-177-4

Sequence 4, Application US/09642177

GENERAL INFORMATION:

APPLICANT: STROVEL, Jeffrey W.

APPLICANT: STAMBERG, Judith

APPLICANT: ABRUZZO, Lynne V.

APPLICANT: HIGSMITH, Edward

TITLE OF INVENTION: TELOMERASE ASSAY OF BODY FLUIDS

FILE REFERENCE: 10460-4U1 (210460.0019)

CURRENT APPLICATION NUMBER: US/09/642,177

CURRENT FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: US 60/074,793

PRIOR FILING DATE: 1998-02-16

PRIOR APPLICATION NUMBER: US 09/250,336

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: PCT/US99/03302

PRIOR FILING DATE: 1999-02-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 25

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism:R3c, Primer

US-09-642-177-4

Query Match 100.0%; Score 15; DB 25; Length 25;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 4 GCTCTAGATGAACG 18

RESULT 7

PCT-US96-14679-27

Sequence 27, Application PC/TUS9614679

GENERAL INFORMATION:

APPLICANT: VILLEPONTEAU, BRYANT

APPLICANT: FENG, JUNLI

APPLICANT: ANDREWS, WILLIAM H.

APPLICANT: ADAMS, ROBERT R.

TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: GERON CORPORATION

STREET: 200 CONSTITUTION DRIVE

CITY: MENLO PARK

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/14679

FILING DATE: 13-SEP-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: KASTER ESQ., KEVIN R.

REGISTRATION NUMBER: 32,704

REFERENCE/DOCKET NUMBER: 012/045PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 473-7779

TELEFAX: (415) 473-7750

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-14679A-27

Query Match 100.0%; Score 15; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 8

PCT-US96-14679A-27

Sequence 27, Application PC/TUS9614679A

GENERAL INFORMATION:

APPLICANT: VILLEPONTEAU, BRYANT

APPLICANT: FENG, JUNLI

APPLICANT: ANDREWS, WILLIAM H.

APPLICANT: ADAMS, ROBERT R.

TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: GERON CORPORATION

STREET: 200 CONSTITUTION DRIVE

CITY: MENLO PARK

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/14679A

FILING DATE: 13-SEP-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: KASTER ESQ., KEVIN R.

REGISTRATION NUMBER: 32,704

REFERENCE/DOCKET NUMBER: 012/045PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 473-7779

TELEFAX: (415) 473-7750

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-14679A-27

Query Match 100.0%; Score 15; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 9

PCT-US99-03302-4

TELEFAX: (415)473-7750

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-14679-27

Query Match 100.0%; Score 15; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 8

PCT-US96-14679A-27

Sequence 27, Application PC/TUS9614679A

GENERAL INFORMATION:

APPLICANT: VILLEPONTEAU, BRYANT

APPLICANT: FENG, JUNLI

APPLICANT: ANDREWS, WILLIAM H.

APPLICANT: ADAMS, ROBERT R.

TITLE OF INVENTION: METHODS AND REAGENTS FOR REGULATING

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: GERON CORPORATION

STREET: 200 CONSTITUTION DRIVE

CITY: MENLO PARK

STATE: CALIFORNIA

COUNTRY: U.S.A.

ZIP: 94025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/14679A

FILING DATE: 13-SEP-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: KASTER ESQ., KEVIN R.

REGISTRATION NUMBER: 32,704

REFERENCE/DOCKET NUMBER: 012/045PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 473-7779

TELEFAX: (415)473-7750

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US96-14679A-27

Query Match 100.0%; Score 15; DB 1; Length 26;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

Db 5 GCTCTAGATGAACG 19

RESULT 9

PCT-US99-03302-4

; Sequence 4, Application PC/TUS9903302
; GENERAL INFORMATION:
; APPLICANT: Strovel, Jeffrey W
; APPLICANT: Stamborg, Judith
; APPLICANT: Abruzzo, Lynne V
; APPLICANT: Highsmith, Edward

; TITLE OF INVENTION: Telomerase Assay of Body Fluids for Cancer Screening
; TITLE OF INVENTION: and Assessment of Disease Stage and Prognosis
; FILE REFERENCE: 1489JS 60/074,793
; CURRENT APPLICATION NUMBER: PCT/US99/03302
; CURRENT FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/074,793
; EARLIER FILING DATE: 1998-02-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn.Ver. 2.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: R3c,
; OTHER INFORMATION: synthesized, Gibco-BRL
PCT-US99-03302-4

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTGAACG 15
|||||
DB 5 GCTCTAGAGTGAACG 19

RESULT 10

PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783
; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTGAACG 15
|||||
DB 5 GCTCTAGAGTGAACG 19

RESULT 11

PCT-US99-07533-4
; Sequence 4, Application PC/TUS9907533A
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157W01
; CURRENT APPLICATION NUMBER: PCT/US99/07533A
; CURRENT FILING DATE: 1999-04-06
; EARLIER APPLICATION NUMBER: 60/080,783

; EARLIER FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
PCT-US99-07533-4

Query Match 100.0%; Score 15; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTGAACG 15
|||||
DB 5 GCTCTAGAGTGAACG 19

RESULT 12

US-08-272-102-23
; Sequence 23, Application US/08272102
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTIEU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/272,102
; FILING DATE: 07-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000800
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-272-102-23

Query Match 100.0%; Score 15; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAGTGAACG 15
|||||
DB 5 GCTCTAGAGTGAACG 19

RESULT 13

US-08-387-524-19

Sequence 19, Application US/08387524
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,524
FILING DATE: 13-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-387-524-19
Query Match 100.0%; Score 15; DB 7; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19
RESULT 14
US-08-472-802A-24
Sequence 24, Application US/08472802A
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802A-24
Query Match 100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATGAACG 15
DB 5 GCTCTAGATGAACG 19
RESULT 15
US-08-472-802B-24
Sequence 24, Application US/08472802B
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

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; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-472-802B-24

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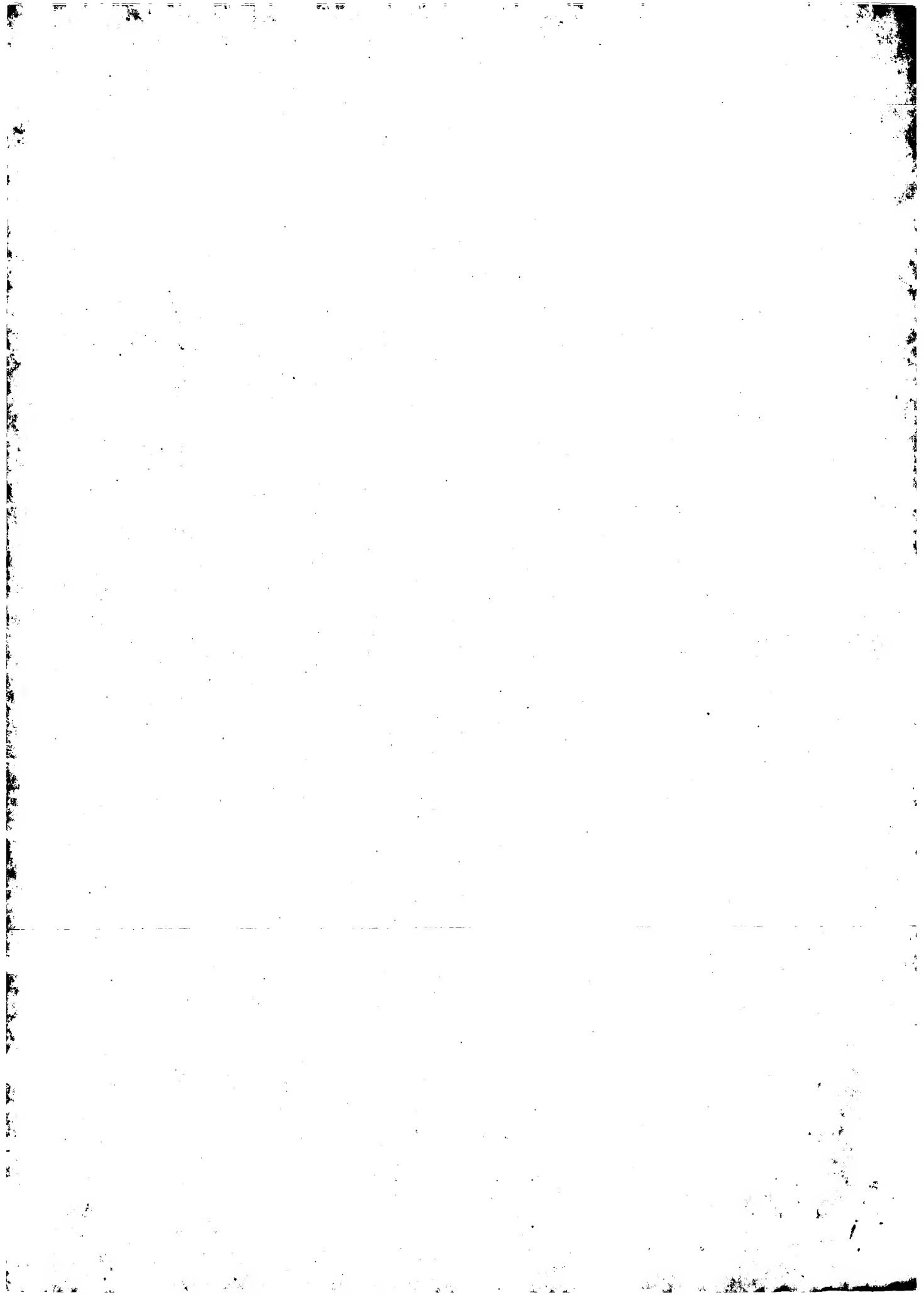
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Query Match      100.0%; Score 15; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATGAACG 15
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Db       5 GCTCTAGATGAACG 19

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Search completed: June 25, 2003, 06:20:26
Job time : 1273.4 secs



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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 45.5976 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-10

Perfect score: 15
Sequence: 1 GCTCTAGATGAACG 15

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	26	9	US-10-044-692-312 Sequence 312, App
2	15	100.0	26	9	US-10-044-539-312 Sequence 312, App
3	15	100.0	26	10	US-09-057-351-23 Sequence 23, Appl
4	13	86.7	25	9	US-10-098-263B-118949 Sequence 118949
5	13	86.7	26	9	US-09-952-522B-19 Sequence 19, Appl
6	13	86.7	26	10	US-09-844-086A-3 Sequence 3, Appl
7	12.4	82.7	23	9	US-09-952-522B-31 Sequence 31, Appl
8	12.4	82.7	26	9	US-10-011-366-16 Sequence 16, Appl
9	12	80.0	23	9	US-09-952-522B-17 Sequence 17, Appl
10	12	80.0	25	9	US-10-215-112-6862 Sequence 6862, Ap
11	12	80.0	25	9	US-10-098-263B-64498 Sequence 64498, A
12	11.8	78.7	25	9	US-10-215-112-12114 Sequence 12114, A
13	11.8	78.7	25	9	US-10-098-263B-74741 Sequence 74741, A
14	11.8	78.7	26	9	US-10-118-495-13 Sequence 13, Appl
15	11.8	78.7	40	9	US-10-090-182A-255 Sequence 255, App
16	11.8	78.7	41	9	US-10-090-182A-234 Sequence 234, App
17	11.8	78.7	42	10	US-09-947-305-5 Sequence 5, Appl
18	11.8	78.7	45	9	US-10-090-182A-435 Sequence 235, App
19	11.8	78.7	45	9	US-10-090-182A-409 Sequence 409, App

20	11.4	76.0	23	9	US-10-079-429-51 Sequence 51, Appl
21	11.4	76.0	24	9	US-10-245-813-2 Sequence 2, Appl
22	11.4	76.0	25	9	US-10-098-263B-4340 Sequence 4340, Ap
23	11.4	76.0	25	9	US-10-098-263B-30035 Sequence 30035, A
24	11.4	76.0	25	9	US-10-098-263B-33532 Sequence 33532, A
25	11.4	76.0	25	9	US-10-098-263B-34691 Sequence 34691, A
26	11.4	76.0	25	9	US-10-098-263B-118950 Sequence 118950, Sequence 5, Appl
27	11.4	76.0	29	10	US-09-905-992-5 Sequence 18, Appl
28	11.4	76.0	36	9	US-10-127-816-18 Sequence 58, Appl
29	11.4	76.0	46	9	US-09-876-082-58 Sequence 13, Appl
30	11.4	76.0	46	9	US-09-875-082-58 Sequence 5, Appl
31	11	73.3	21	9	US-09-997-868-13 Sequence 13, Appl
32	11	73.3	22	10	US-09-765-873A-5 Sequence 9, Appl
33	11	73.3	23	9	US-09-952-522B-9 Sequence 10750, A
34	11	73.3	25	9	US-10-098-263B-10750 Sequence 44593, A
35	11	73.3	25	9	US-10-098-263B-44593 Sequence 44594, A
36	11	73.3	25	9	US-10-098-263B-104702 Sequence 104702, Sequence 11, Appl
37	11	73.3	25	9	US-10-118-495-11 Sequence 8, Appl
38	11	73.3	26	9	US-09-784-508-8 Sequence 2, Appl
39	11	73.3	27	10	US-10-162-223-2 Sequence 40, Appl
40	11	73.3	29	9	US-09-905-983-40 Sequence 12, Appl
41	11	73.3	31	10	US-09-848-616-12 Sequence 7, Appl
42	11	73.3	33	9	US-09-964-895-7 Sequence 15, Appl
43	11	73.3	33	9	US-09-964-895-15 Sequence 10, Appl
44	11	73.3	33	9	US-09-964-895-15 Sequence 10, Appl
45	11	73.3	34	10	US-09-784-508-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692
FILING DATE: 11-Jan-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
DB 5 GCTCTAGAAATGAACG 19

RESULT 2

US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Query Match 100.0%; Score 15; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
DB 5 GCTCTAGAAATGAACG 19

RESULT 3

US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:

APPLICANT: Vilpenteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 15; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAACG 15
|||||
Db 5 GCTCTAGAAATGAACG 19

RESULT 4

US-10-098-263B-118949/c
; Sequence 118949, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 118949
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-118949

Query Match 86.7%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGAAATGAACG 15
|||||
Db 20 TCTAGAAATGAACG 8

RESULT 5

US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: sialoprotein forward primer

US-09-952-522B-19

Query Match 86.7%; Score 13; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 6

US-09-844-006A-3
; Sequence 3, Application US/09844006A
; Patent No. US20020083496A1
; GENERAL INFORMATION:
; APPLICANT: Wyatt, Sarah
; APPLICANT: Tsou, Pei-Lan
; APPLICANT: Robertson, Dominique
; APPLICANT: Boss, Wendy
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH INCREASES IN CALCIUM STORES
; FILE REFERENCE: 5051.503
; CURRENT APPLICATION NUMBER: US/09/844,006A
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 60/200,233
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(28)
; OTHER INFORMATION: Synthetic Oligonucleotide.
US-09-844-006A-3

Query Match 86.7%; Score 13; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAAATGAA 13
|||||
Db 1 GCTCTAGAAATGAA 13

RESULT 7

US-09-952-522B-31
; Sequence 31, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Liull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23

QY 1 GCTCTAGATGA 12
| | | | | | | | | |
DB 15 GCTCTAGATGA 4

RESULT 11

US-10-098-263B-64498/c
; Sequence 64498, Application US/10098263B
; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 64498

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-64498

Query Match

Best Local Similarity 80.0%; Score 12; DB 9; Length 25;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TCTAGATGAAC 14

| | | | | | | | | |

DB 23 TCTAGATGAAC 12

RESULT 12

US-10-215-112-12114/c

; Sequence 12114, Application US/10215112

; Publication No. US20030082596A1

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; TITLE OF INVENTION: Method of Genetic Analysis of Probes:

; FILE REFERENCE: Test3

; CURRENT APPLICATION NUMBER: US/10/215,112

; CURRENT FILING DATE: 2002-08-08

; NUMBER OF SEQ ID NOS: 14936

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12114

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-12114

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 9; Length 25;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

| | | | | | | | | |

DB 21 GCTCTAGACGGACG 7

RESULT 13

US-10-098-263B-74741/c

; Sequence 74741, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 74741

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-74741

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 9; Length 25;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

| | | | | | | | | |

DB 22 GCTCTAGATGAACG 8

RESULT 14

US-10-118-495-13

; Sequence 13, Application US/10118495

; Publication No. US20030074688A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; FILE REFERENCE: MSU-06897

; CURRENT APPLICATION NUMBER: US/10/118,495

; CURRENT FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: 60/283,812

; PRIOR FILING DATE: 2001-04-13

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 26

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic

US-10-118-495-13

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 9; Length 26;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACG 15

| | | | | | | | | |

DB 1 GCTCTAGATGGCCG 15

RESULT 15

US-10-090-182A-255

; Sequence 255, Application US/10090182A

; Publication No. US20030103936A1

; GENERAL INFORMATION:

; APPLICANT: Abrams, Mark A.

; Bauer, S. C.

; Bradford-Goldberg, Sarah R.

; Caparon, Mairé H.

; Easton, Alan M.

; Klein, Barbara K.

; McKearn, John P.

; Oline, Peter O.

; Paik, Kumanan

; Thomas, John W.

; TITLE OF INVENTION: Methods of Ex-vivo Expansion of

; Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple

; Mutation Polypeptides

; NUMBER OF SEQUENCES: 415

CORRESPONDENCE ADDRESS:
 ADDRESSEE: S. Christopher Bauer, Pharmacia Corp
 STREET: 800 N. Lindbergh Blvd.
 CITY: St. Louis
 STATE: Missouri
 COUNTRY: USA
 ZIP: 63167
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US/10/090,182A
 FILING DATE: 03-Apr-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/764,114
 FILING DATE: 09-DEC-1996
 APPLICATION NUMBER: US 07/981,044
 FILING DATE: 24-NOV-1992
 APPLICATION NUMBER: PCT/US93/11197
 FILING DATE: 22-NOV-1993
 APPLICATION NUMBER: 08/411,795
 FILING DATE: 04-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: S. Christopher Bauer
 REGISTRATION NUMBER: 42,305
 REFERENCE/DOCKET NUMBER: C2713/12
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (636)737-6257
 TELEFAX: (736)737-6257
 INFORMATION FOR SEQ ID NO: 255:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 255:
 US-10-090-182A-255

Query Match 78.7%; Score 11.8; DB 9; Length 40;
 Best Local Similarity 86.7%; Pred. No. 2.1e+03;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GCTCTAGATGACG 15
 Db 12 GCTCTATATGATCG 26

Search completed: June 25, 2003, 22:25:07
 Job time : 45.5976 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 46.9721 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30
Sequence: 1 GCTCTAGTAATGAACGGTGGAGGCGGCAGG 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	US-08-770-565-8	Sequence 8, Appli
2	29	96.7	30	US-08-833-377-6	Sequence 6, Appli
3	23	76.7	27	US-08-770-565-26	Sequence 26, Appli
4	22	73.3	26	US-08-330-123A-23	Sequence 23, Appli
5	22	73.3	26	US-08-482-115B-23	Sequence 23, Appli
6	22	73.3	26	US-08-660-678A-23	Sequence 23, Appli
7	22	73.3	26	US-08-710-249-26	Sequence 26, Appli
8	22	73.3	26	US-08-485-778-19	Sequence 19, Appli
9	22	73.3	26	US-08-472-802C-24	Sequence 24, Appli
10	22	73.3	26	US-08-520-550A-19	Sequence 19, Appli
11	22	73.3	26	US-08-998-443-23	Sequence 23, Appli
12	22	73.3	26	US-08-974-549A-598	Sequence 598, Appli
13	22	73.3	26	US-09-060-523-23	Sequence 23, Appli
14	22	73.3	26	US-09-220-157A-26	Sequence 26, Appli
15	22	73.3	26	US-09-286-959B-4	Sequence 4, Appli
16	22	73.3	26	US-09-580-517-23	Sequence 23, Appli
17	19	63.3	19	US-08-770-565-9	Sequence 9, Appli
18	15	50.0	15	US-08-770-565-10	Sequence 10, Appli
19	14	46.7	27	US-08-630-172-24	Sequence 24, Appli
20	14	46.7	27	US-09-375-419-24	Sequence 24, Appli
21	13	43.3	18	US-08-974-549A-543	Sequence 543, Appli
22	12	40.0	26	US-08-480-604A-16	Sequence 16, Appli
23	12	40.0	26	US-08-405-496A-16	Sequence 16, Appli
24	12	40.0	26	US-08-915-136-16	Sequence 16, Appli
25	12	40.0	26	US-08-957-310-16	Sequence 16, Appli
26	12	40.0	30	US-08-349-006-3	Sequence 3, Appli
27	12	40.0	30	US-08-495-743-50	Sequence 50, Appli

28	12	40.0	30	1	US-08-495-739-50	Sequence 50, Appli
29	12	40.0	30	1	US-08-495-741-50	Sequence 50, Appli
30	12	40.0	30	4	US-08-062-023-50	Sequence 50, Appli
31	12	40.0	30	5	PCT-US94-02107-3	Sequence 3, Appli
32	12	40.0	33	3	US-08-630-172-22	Sequence 22, Appli
33	12	40.0	33	4	US-03-375-419-22	Sequence 22, Appli
34	11	36.7	11	2	US-08-770-565-11	Sequence 11, Appli
35	11	36.7	15	1	US-08-363-240A-659	Sequence 659, App
36	11	36.7	15	1	US-08-363-240A-660	Sequence 660, App
37	11	36.7	18	1	US-08-363-240A-1203	Sequence 1203, Ap
38	11	36.7	20	3	US-08-974-180-4	Sequence 4, Appli
39	11	36.7	21	4	US-08-026-143B-13	Sequence 13, Appli
40	11	36.7	21	5	PCT-US92-10621-13	Sequence 13, Appli
41	11	36.7	21	5	PCT-US94-02233-13	Sequence 13, Appli
42	11	36.7	22	4	US-09-627-216A-5	Sequence 5, Appli
43	11	36.7	23	3	US-08-973-068-46	Sequence 46, Appli
44	11	36.7	24	4	US-08-697-610-11	Sequence 11, Appli
45	11	36.7	24	4	US-08-349-357-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-770-565-8
; Sequence 8, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-8

Query Match 100.0%; Score 30; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGTAATGAACGGTGGAGGCGGCAGG 30

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Db      1  GCTCTAGATGAACGGTGGGAAGCGCGCAGG 30
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RESULT 2
US-08-833-377-6
; Sequence 6, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/833,377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5' biotinylated guanosine"
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 14"
US-08-833-377-6
Query Match      96.7%; Score 29; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2  CTCCTAGATGAACGGTGGGAAGCGCGCAGG 30
Db      2  CTCCTAGATGAACGGTGGGAAGCGCGCAGG 30
|||||
RESULT 3
US-08-770-565-26
; Sequence 26, Application US/08770565
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; Patent No. 5946723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-26
Query Match      76.7%; Score 23; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCTCTAGATGAACGGTGGGAAGG 23
Db      5  GCTCTAGATGAACGGTGGGAAGG 27
|||||
RESULT 4
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FENG, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGAACGGTGAAG 22
|||||
DB 5 GCTCTAGAATGAACGGTGAAG 26

RESULT 5
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 73.3%; Score 22; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGAACGGTGAAG 22
|||||
DB 5 GCTCTAGAATGAACGGTGAAG 26

RESULT 6
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGAACGGTGAAG 22

Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 7
US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Vilponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US/08/583,808
; APPLICATION DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO. 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAG 22
Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 8
US-08-485-778-19
; Sequence 19, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol

; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Vilponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 08/387,524
; APPLICATION NUMBER: 13-FEB-1995
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA: US 08/330,123
; APPLICATION NUMBER: 27-OCT-1994
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA: US 08/272,102
; APPLICATION NUMBER: 07-JUL-1994
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO. 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-778-19

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGGAAG 22
Db 5 GCTCTAGATGAACGGTGGGAAG 26

RESULT 9
US-08-472-802C-24
; Sequence 24, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Vilponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/472,802C
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/330,123
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 73.3%; Score 22; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAG 22
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Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 10
US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avillion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuela, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A3B
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-520-550A-19

Query Match 73.3%; Score 22; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATGAACGGTGGAG 22
|||||
Db 5 GCTCTAGATGAACGGTGGAG 26

RESULT 11
US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid

INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-060-523-23

Query Match 73.3%; Score 22; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
 DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 14
 US-09-220-157A-26
 ; Sequence 26, Application US/09220157A
 ; Patent No. 6300110
 ; GENERAL INFORMATION:
 ; APPLICANT: Villeponteau, Bryant
 ; APPLICANT: Feng, Junli
 ; APPLICANT: Andrews, William H.
 ; APPLICANT: Adams, Robert R.
 ; TITLE OF INVENTION: Methods and Reagents for Regulating
 ; TITLE OF INVENTION: Telomere Length and Telomerase Activity
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/220,157A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/710,249
 ; FILING DATE: 13-SEP-1996
 ; APPLICATION NUMBER: US 08/583,808
 ; FILING DATE: 05-JAN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/003,492
 ; FILING DATE: 08-SEP-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-001220US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-09-220-157A-26

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 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

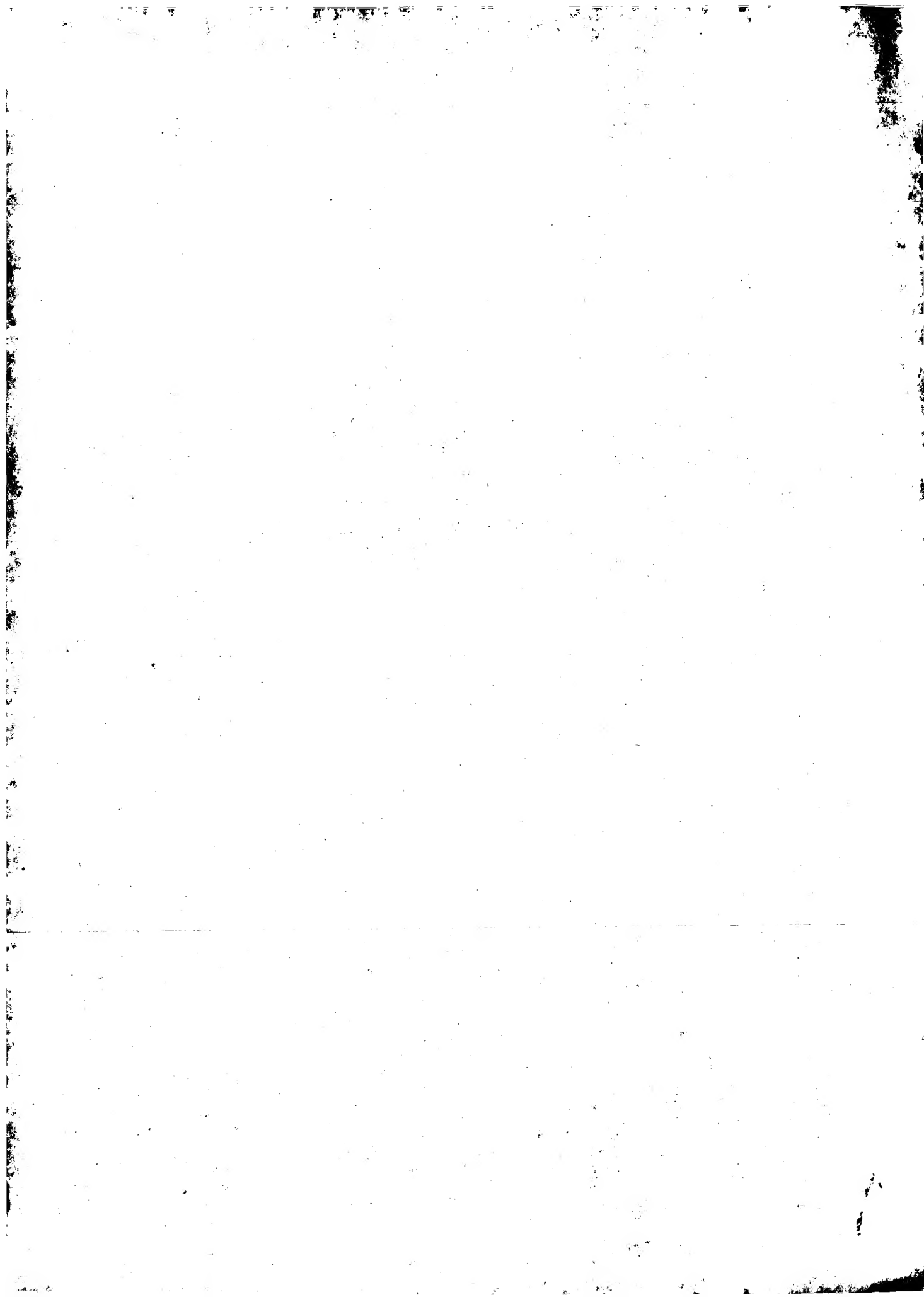
QY 1 GCTCTAGATGAACGGTGAAG 22
 DB 5 GCTCTAGATGAACGGTGAAG 26

RESULT 15
 US-09-286-959B-4
 ; Sequence 4, Application US/09286959B
 ; Patent No. 6300131
 ; GENERAL INFORMATION:
 ; APPLICANT: Johns Hopkins University
 ; APPLICANT: Greider, Carol W.
 ; APPLICANT: Le, Siyuan
 ; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
 ; FILE REFERENCE: 07265/157001
 ; CURRENT APPLICATION NUMBER: US/09/286,959B
 ; CURRENT FILING DATE: 1999-04-06
 ; PRIOR APPLICATION NUMBER: 60/080,783
 ; PRIOR FILING DATE: 1998-04-06
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 26
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 ; US-09-286-959B-4

Query Match 73.3%; Score 22; DB 4; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
 DB 5 GCTCTAGATGAACGGTGAAG 26

Search completed: June 23, 2003, 10:17:06
 Job time : 46.9721 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 199.363 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-8

Perfect score: 30
Sequence: 1 GCTCTAGTAATGACGCTGGAAGCGCGCAGG 30

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
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- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	100.0	30	AAV63649	Antisense oligonuc
2	30	100.0	30	AAV41175	RNA component of h
3	30	100.0	30	AAZ23631	Human clone 28-1 t
4	30	100.0	30	AA509476	Antisense oligonuc
5	30	100.0	30	AA515928	Human telomerase p
6	30	100.0	30	ABA91517	Oligonucleotide us
7	23	76.7	27	AAV41193	RNA component of h
8	23	76.7	27	ABA95497	Human telomerase R
9	22	73.3	25	AAZ08704	Human telomerase R

10	22	73.3	26	17	AAT10304	RNA component of h	
11	22	73.3	26	17	AAT10299	RNA component of h	
12	22	73.3	26	17	AAT11044	Primer for product	
13	22	73.3	26	18	AAT58811	Human telomerase p	
14	22	73.3	26	19	AAV19489	Human hTR gene RT-	
15	22	73.3	26	19	AAV17033	Telomerase PCR pri	
16	22	73.3	26	20	AAV90788	Human telomerase R	
17	22	73.3	26	20	AAV77402	Human telomerase R	
18	22	73.3	26	20	AAV01542	PCR primer for Hum	
19	22	73.3	26	21	AAA88250	Human telomerase R	
20	22	73.3	26	24	ABK48024	Human telomerase-a	
21	22	73.3	26	24	ABD24246	Human telomerase (
22	19	63.3	19	19	AAV41176	RNA component of h	
23	15	50.0	15	19	AAV41177	RNA component of h	
24	15	50.0	15	23	AAV15927	Human telomerase p	
25	15	50.0	15	23	AAV15931	Human telomerase p	
26	15	50.0	15	23	AAV15932	Human telomerase p	
27	14	46.7	27	18	AAV97049	Sense primer for h	
28	13	43.3	13	23	AAV15921	Human telomerase p	
29	13	43.3	13	23	AAV15922	Human telomerase p	
30	13	43.3	13	23	AAV15923	Human telomerase p	
31	13	43.3	13	23	AAV15924	Human telomerase p	
32	13	43.3	13	23	AAV15925	Human telomerase p	
33	13	43.3	13	23	AAV15926	Human telomerase p	
34	13	43.3	13	23	AAV15930	Human telomerase p	
35	13	43.3	28	24	ABA04366	CRT C-domain-green	
36	13	43.3	32	21	AAA46113	Human GPCR TDAG8(I	
c	37	13	43.3	46	22	AAV11788	PCR primer #1 used
38	12	40.0	17	22	AAV57369	Murine Cdc25A intr	
39	12	40.0	24	22	AAV62045	Soybean 318013 reg	
c	40	12	40.0	24	ABQ03136	Oligonucleotide ad	
c	41	12	40.0	24	ABQ03136	Oligonucleotide ad	
42	12	40.0	24	24	ABQ10149	Oligonucleotide ad	
43	12	40.0	26	17	AAV29258	C. difficile toxin	
44	12	40.0	26	19	AAV30567	Clostridium diffic	
45	12	40.0	26	21	ABK09963	Novel recombinant	

ALIGNMENTS

RESULT 1		
ID	AAV63649	standard; DNA; 30 BP.
AC	XX	
AC	XX	AAV63649;
DT	15-FEB-1999	(first entry)
XX		
DE	Antisense oligonucleotide 14 for human telomerase RNA component.	
XX		
KW	Human; telomerase RNA component; anticancer therapy; purification;	
KW	assay; vaccine; cancer; antisense oligonucleotide; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1
FT		/tag= a
FT		/note= "biotinylated"
XX		
PN	W09845450-A1.	
XX		
PD	15-OCT-1998.	
XX		
XX	04-APR-1997;	97WO-US06012.
PR	04-APR-1997;	97WO-US06012.
XX		
FA	(GERO-) GERON CORP.	
PI	Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;	

ALIGNMENTS

RESULT 1	AAV63649	AAV63649 standard; DNA; 30 BP.
ID	AAV63649	standard; DNA; 30 BP.
AC	AAV63649;	
XX		
DT	15-FEB-1999	(first entry)
DE	Antisense oligonucleotide 14 for human telomerase RNA component.	
XX		
KW	Human; telomerase RNA component; anticancer therapy; purification; assay; vaccine; cancer; antisense oligonucleotide; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	modified_base	1
FT		/*tag= a
FT		/note= "biotinylated"
XX		
PN	WO9845450-A1.	
XX		
PD	15-OCT-1998.	
XX		
PF	04-APR-1997; 97WO-US06012.	
XX		
PR	04-APR-1997; 97WO-US06012.	
XX		
PA	(GERO-) GERON CORP.	
XX		
PI	Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;	

PI Vasserot AP, Weinrich SL;

XX WPI; 1998-594485/50.

XX Purification of telomerase on affinity material - useful for, e.g.

PT diagnosis and treatment of cancer

XX Disclosure; Page 24; 76pp; English.

XX The present sequence represents an antisense oligonucleotide
CC directed against the human telomerase RNA component gene sequences.
CC The oligonucleotide can be used as an affinity agent in the methods of
CC the invention, which are used to purify human telomerase. The methods
CC involve the use of several sequential steps, including the use of two
CC matrices that bind molecules bearing negative charges, a matrix that
CC binds molecules bearing positive charges, an affinity purification step
CC and a size separation. Telomerase is a particular target of anticancer
CC therapies, and is useful in assays for characterizing (pre)cancerous
CC cells. Telomerase can also be used to screen for specific modulators,
CC for biochemical analysis of its activity, and in preparation of
CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
CC are used in vaccines, and for treating over expression of telomerase,
CC particularly in cancer.

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 Other;

Query Match 100.0%; Score 30; DB 19; Length 30;
Best Local Similarity 100.0%; Fred. No. 7.6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGAATGACGGTGGAGCGGCAGG 30

Db 1 GCTTAGAATGACGGTGGAGCGGCAGG 30

RESULT 2

AAV41175
ID AAV41175 standard; DNA; 30 BP.

AC AAV41175;

DT 08-OCT-1998 (first entry)

XX RNA component of human telomerase (hTR) antisense oligo 21.

XX RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilization; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.

XX Synthetic.

OS Homo sapiens.

PN WO9828442-A1.

XX 02-JUL-1998.

XX 19-DEC-1997; 97WO-US23619.

XX 20-DEC-1996; 96US-0770565.

XX 20-DEC-1996; 96US-0770564.

XX (GERO-) GERON CORP.

XX Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

XX WPI; 1998-377670/32.

XX New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contraception, immuno-suppression or treating infection

XX Claim 11; Page 65; 80pp; English.

XX

CC Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridize to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridize to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilization, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
CC parasites or fungi.

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 Other;

Query Match 100.0%; Score 30; DB 19; Length 30;

Best Local Similarity 100.0%; Fred. No. 7.6e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGAATGACGGTGGAGCGGCAGG 30

Db 1 GCTTAGAATGACGGTGGAGCGGCAGG 30

RESULT 3

AAZ23631
ID AAZ23631 standard; DNA; 30 BP.

XX AAZ23631;

DT 07-JAN-2000 (first entry)

XX Human clone 28-1 telomerase oligonucleotide oligo-14.

XX Telomerase; human; immune response; cancer; vaccine; treatment;
KW disease; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT modified_base 1
FT /tag= a
FT /note= "5'-biotinylated guanosine"

XX US95968506-A.

XX 19-OCT-1999.

XX 04-APR-1997; 97US-0833377.

XX 04-AUG-1995; 95US-0510736.

XX (GERO-) GERON CORP.

XX Atkinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;

XX Vasserot AP;

XX WPI; 1999-590379/50.

XX Compositions comprising human telomerase, useful for treating diseases
PT associated with overexpression of telomerase e.g. cancer -

PS Disclosure; Column 45-46; 34pp; English.

CC This invention describes a novel composition comprising human telomerase having at least 2000-fold (preferably at least 6000-fold) increased relative purity compared with crude extract of cells from adenovirus-transformed kidney cell line. The composition is useful for eliciting an immune response in animals and may therefore be used as a vaccine for treating diseases associated with the overexpression of telomerase e.g. cancer. AA23626-Z23637 represent oligonucleotides used in the isolation of human clone 28-1 which contains a fragment of the human telomerase described in the method of the invention.

XX

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 20; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCGCAGG 30
|||||
Db 1 GCTCTAGATGAACGGTGGAGCGGCGCAGG 30

RESULT 4

AAS09476

ID AAS09476 standard; DNA; 30 BP.

XX

AC AAS09476;

XX

DT 24-OCT-2001 (first entry)

XX

DE Antisense oligonucleotide for human telomerase, Oligo 14.

XX

KW Human; Telomerase; vaccine; antibody; cancer; BP2H;
KW nucleolin; antisense oligonucleotide; Oligo 14; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT modified_base 1

FT /*tag= a

FT /mod_base= G

FT /note= "G is biotinylated"

XX

PN US6261556-B1.

XX

PD 17-JUL-2001.

XX

PF 18-OCT-1999; 99US-0420056.

XX

PR 04-APR-1997; 97US-0833377.

PR 04-AUG-1995; 95US-0510736.

XX

PA (GERO-) GERON CORP.

XX

PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;
PI Kealey JT;

XX

PI WPI; 2001-450477/48.

DR

XX

PT Purified human telomerase, useful for inducing immune response in animals, comprises several thousand folds increased purity compared with cytoplasmic crude cell preparations -

PT

XX

PS Disclosure; Column 18; 29pp; English.

XX

CC The sequence represents a biotinylated antisense oligonucleotide used in the purification of human telomerase. The invention relates to a purified human telomerase core enzyme protein comprising 2000-fold increased purity compared with a crude extract of cells from adenovirus-transformed kidney cell line (293 cells) and when associated with telomerase RNA component has DNA polymerase activity and a molecular weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful

CC

CC for inducing a humoral or cell-mediated immune response in an animal.

CC Purified telomerase or immunogenic fragments are useful as vaccines for treating diseases associated with over-expression of telomerase, such as cancer and for producing antibodies that recognize telomerase, which are useful as affinity agents in isolating the proteins and for detecting the presence of proteins in a sample, such as cell or tissue. Identification of telomerase aids in diagnosis of cancer or pre-cancerous states.

CC Telomerase and/or telomerase associated proteins are also useful for screening compounds to identify agents that alter the association of telomerase-associated proteins, such as nucleolin or BP2H with telomerase.

XX

SQ Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 22; Length 30;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGGAGCGGCGCAGG 30
|||||
Db 1 GCTCTAGATGAACGGTGGAGCGGCGCAGG 30

RESULT 5

AAS15928

ID AAS15928 standard; DNA; 30 BP.

XX

AC AAS15928;

XX

DT 27-FEB-2002 (first entry)

XX

DE Human telomerase polynucleotide inhibitor #9.

XX

KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
KW fertility; inflammatory condition; tumour; cancer; veterinary;
KW immunosuppression; telomerase inhibitor; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified_base 1..30

FT /*tag= a

FT /mod_base= OTHER

FT /note= "N3'-P5' phosphoramidate linkages"

XX

PN WO200174136-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US10476.

XX

PR 31-MAR-2000; 2000US-0540119.

XX

PA (GERO-) GERON CORP.

XX

PI Gryaznov SM, Pruzan R, Weinrich SL;
PI WPI; 2001-656955/75.

DR

XX

PT New polynucleotide useful for inhibiting telomerase activity in cells, or for treating telomerase-mediated condition or disease, such as cancers, tumours, Hodgkin's disease, or inflammatory conditions -

PT

XX

PS Example 3; Page 32; 48pp; English.

XX

CC The invention relates to polynucleotide inhibitors (I) and methods for inhibiting telomerase activity. (I) are useful in inhibiting telomerase activity and proliferation of a telomerase positive cell, and in manufacturing a medicament for inhibiting telomerase activity in a cell and in treating telomerase-mediated condition or disease, such as adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,

CC Hodgkin's disease, fertility and inflammatory conditions. (1) are also
 CC useful in treating a tumour or in manufacturing a medicament for the
 CC treatment of tumour. The polynucleotide inhibitors may also be used in
 CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
 CC activity in cells in vivo is useful in prophylactic and therapeutic
 CC methods of treating cancer and other disorders involving inappropriate
 CC expression of telomerase, and in treating veterinary proliferative
 CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
 CC for immunosuppression and for selectively down-regulating specific
 CC branches of the immune system. The present sequence represents
 CC human telomerase polynucleotide inhibitor #9, as described in the
 CC method of the invention.

CC Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 7.6e-08;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGGGAGCGGCAGG 30
 DB 1 GCTCTAGATGACGGTGGGAGCGGCAGG 30

RESULT 6

ID ABA91517 standard; DNA; 30 BP.

AC ABA91517;

DT 18-APR-2002 (first entry)

DE Oligonucleotide used in gold nanoparticle complex.

KW Silver staining; signal detection; nanoparticle; diagnosis;
 KW screening; ss.

OS Synthetic.

Key Location/Qualifiers

FT modified_base 1..30
 FT /*tag= a
 FT /note= "phosphoramidate linkage"

PN WO200204681-A2.

PD 17-JAN-2002.

PF 11-JUL-2001; 2001WO-US21846.

PR 11-JUL-2000; 2000US-217782P.

PA (NANO-) NANOSPHERE INC.

PI Letsinger RL, Garimella V;

PS WPI; 2002-164654/21.

PT Amplifying signal by contacting nanoparticles (N) having bound
 PT oligonucleotides to silver deposited on substrate to form N-silver
 PT sandwich that is contacted with silver, reducing agent to form
 PT silver-N-silver sandwich

PS Example 1; Page 12; 24pp; English.

CC The present sequence is that of an oligonucleotide prepared using
 CC phosphoramidite chemistry. A nanoparticle conjugate was prepared
 CC by joining the 5'-mercaptoalkyl oligonucleotide to gold
 CC nanoparticles. The nanoparticle conjugate was used to enhance
 CC the sandwich amplification of a silver signal on glass slides
 CC containing silver spots from oligonucleotide assays performed
 CC using silver staining. This illustrated the method of the
 CC invention, which is based on the discoveries that: (1) gold

CC nanoparticles coated with oligonucleotides bind to silver that has
 CC previously been deposited on gold nanoparticle-oligonucleotide
 CC conjugates immobilised by hybridisation on a glass substrate or
 CC plate; and (2) that the gold-nanoparticle-oligonucleotide-silver-gold
 CC oligonucleotide structures function as a catalyst for the further
 CC deposition of silver ions. The discoveries were applied to a method
 CC for amplifying signal by enhancing silver deposition in detecting
 CC systems where the formation of a silver spot serves as a reporter
 CC for the presence of a molecule, including proteins, nucleic acids
 CC and small molecules. The detecting systems include detection of
 CC molecules in situ (e.g. on cells or in a tissue sample) and assays
 CC where the target molecule is bound to a substrate or is captured by
 CC a capture molecule. The method has special utility in increasing
 CC the signal strength in diagnostic and screening applications
 CC involving detection of target molecules arrayed at discrete
 CC positions on a solid surface. It provides a means for greatly
 CC enhancing the sensitivity of tests carried out on microarrays or
 CC microchips. The method is simple, economical, and provides a large
 CC enhancement in signal and sensitivity.

CC Sequence 30 BP; 8 A; 5 C; 13 G; 4 T; 0 other;

Query Match 100.0%; Score 30; DB 24; Length 30;

Best Local Similarity 100.0%; Pred. No. 7.6e-08;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGACGGTGGGAGCGGCAGG 30

DB 1 GCTCTAGATGACGGTGGGAGCGGCAGG 30

RESULT 7

ID AAV41193 standard; DNA; 27 BP.

AC AAV41193;

DT 08-OCT-1998 (first entry)

DE RNA component of human telomerase (hTR) amplifying reverse primer.

KW RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; RT-PCR;
 KW primer; ss.

OS Synthetic.

OS Homo sapiens.

PN WO9828442-A1.

PD 02-JUL-1998.

PF 19-DEC-1997; 97WO-US23619.

PR 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

PA (GERO-) GERON CORP.

PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;

PS WPI; 1998-377670/32.

PT New polynucleotide(s) anti-sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection

PS Claim 65; Page 75; 80pp; English.

CC This primer is used for the RT-PCR amplification of an RNA component of
 CC human telomerase (hTR). This is used in the method of invention of

CC determining the amount of hTR in a sample. The method comprises
 CC amplifying a sequence of hTR and a control polynucleotide from a sample
 CC and determining an amount of amplified hTR and an amount of amplified
 CC control polynucleotide. The amount of amplified hTR is normalised with
 CC respect to the amount of amplified control polynucleotide to provide a
 CC normalised amount of hTR which provides a determination of the amount of
 CC hTR in the sample. The invention provides a determination of an RNA component
 CC of human telomerase in a sample. This is useful for diagnosing cancer
 CC (especially neuroblastoma, bladder, colon and prostate cancer), and
 CC providing prognosis for a cancer patient. The antisense oligonucleotides
 CC can be used for inhibiting telomerase activity in both cultured cells and
 CC in cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in anti-
 CC inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 CC
 SQ Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;

Query Match 76.7%; Score 23; DB 19; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGTAATGAACGGTGAAGG 23
 DB 5 GCTCTAGTAATGAACGGTGAAGG 27

RESULT 8
 ABA95497
 ID ABA95497 standard; DNA; 27 BP.
 XX
 AC ABA95497;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human telomerase RNA, hTR, antisense PCR primer.
 XX
 KW Human; telomerase RNA; PCR primer; cancer; breast; ovarian; stomach;
 KW colon; hTR; ss.
 XX
 OS Homo sapiens.
 XX
 PN EP1158055-A1.
 XX
 PD 28-NOV-2001.
 XX
 PF 26-MAY-2000; 2000EP-0111370.
 XX
 PR 26-MAY-2000; 2000EP-0111370.
 XX
 PA (CHEN/) CHEN X Q.
 PA (STROU/) STROU M.
 PA (ANKER/) ANKER P.
 XX
 PI Chen XQ, Stroun M, Anker P;
 XX
 DR WPI; 2002-099090/14.
 XX
 XX Accurate, reliable diagnosis and/or prognosis of cancer, e.g. breast
 PT cancer, by analyzing the RNA components of telomerase in plasma or
 PT serum -
 XX
 PS Example; Column 3; 6pp; French.

XX The present invention relates to a method for diagnosing and/or
 CC monitoring the evolution of cancers. The method comprises analysing
 CC enzyme telomerase RNA in blood plasma or serum. The method is typically
 CC used for diagnosing breast, ovarian, stomach or colon cancer and/or
 CC monitoring the evolution of the cancers after treatment by chemotherapy
 CC or operations. The present sequence is a PCR primer for human telomerase

CC RNA (hTR), which was used in the example from the present invention.
 SQ Sequence 27 BP; 7 A; 3 C; 10 G; 7 T; 0 other;
 XX
 Query Match 76.7%; Score 23; DB 24; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGTAATGAACGGTGAAGG 23
 DB 5 GCTCTAGTAATGAACGGTGAAGG 27

RESULT 9
 AAZ08704
 ID AAZ08704 standard; DNA; 25 BP.
 XX
 AC AAZ08704;
 XX
 DT 20-OCT-1999 (first entry)
 XX
 DE Human telomerase RNA template PCR primer R3C.
 XX
 KW Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
 KW telomeric repeat amplification protocol; detection; PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9941406-A1.
 XX
 PD 19-AUG-1999.
 XX
 PF 16-FEB-1999; 99WO-US03302.
 XX
 PR 16-FEB-1999; 98US-0074793.
 XX
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 XX
 PI Abruzzo LV, Highsmith B, Stamberg J, Strovel JW;
 XX
 DR WPI; 1999-508655/42.
 XX
 PT Detecting telomerase activity in non-cellular body fluid using a
 PT modified telomeric repeat amplification protocol
 XX
 PS Disclosure; Page 16; 32pp; English.
 XX
 CC A method has been developed for detecting telomerase activity in a
 CC non-cellular portion of body fluid from a cancer patient using a
 CC modified telomeric repeat amplification protocol (TRAP). A method for
 CC detecting cancer comprises: (a) removing the cellular portion of a body
 CC fluid specimen from the patient; (b) preparing a protein extract from
 CC the body fluid remainder; (c) assaying the extract for the presence and
 CC quantity of telomerase RNA or telomerase activity; and (d) comparing the
 CC results with normal levels, to determine the presence of cancer. The
 CC methods are used in cancer diagnosis and prognosis, and also to monitor
 CC cancer therapy effectiveness. Unlike prior art telomerase activity
 CC assays in cancer patients, the method allows noninvasive sample
 CC collection. The methods are also more reliable and less tumour specific
 CC than other methods which detect circulating tumour markers. The present
 CC sequence represents a human telomerase RNA template PCR primer used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
 XX
 Query Match 73.3%; Score 22; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGTAATGAACGGTGAAG 22
 DB 4 GCTCTAGTAATGAACGGTGAAG 25

```

XX DE RNA component of human telomerase nested PCR primer R3c.
XX DE
XX KW RNA component; human; telomerase; lung fibroblast; cell line WI-38;
XX KW recombinant production; synthesis; mutant; detection; mammalian;
XX KW identification; modulating agent; neoplastic condition;
XX KW transcriptional regulatory sequence; gene therapy; disease;
XX KW polymerase chain reaction; antisense plasmid; PCR primer; ss.
XX OS Synthetic.
XX PN WO9601835-A1.
XX PD 25-JAN-1996.
XX PF 06-JUL-1995; 95WO-US08530.
XX PR 07-JUN-1995; 95US-0482115.
XX PR 07-JUL-1994; 94US-0272102.
XX PR 27-OCT-1994; 94US-0330123.
XX PR 07-JUN-1995; 95US-0472802.
XX PA (GERO-) GERON CORP.
XX PI Andrews WH, Feng J, Funk W, Villeponteau B;
XX DR WPI; 1996-097581/10.
XX PT RNA component of mammalian telomerase, esp. human - useful in
XX PT identifying e.g. candidate telomerase-modulating agents
XX PS Example 10; Page 82; 114pp; English.
XX CC The present sequence, a nested PCR primer for the RNA component
XX CC of human telomerase (RCHT), was used in a 5' RACE procedure. The
XX CC RCHT can be used in the recombinant prodn. of an active telomerase
XX CC mol., capable of adding sequences to chromosomal DNA telomeres, and
XX CC in the synthesis of mutant sequences for the detection of mutant
XX CC mammalian telomerase RNA component polynucleotides. The RCHT may
XX CC also be used in the identification of telomerase modulating agents,
XX CC and in the detection of telomerase related, or neoplastic
XX CC conditions in a patient. Polynucleotides of at least 25
XX CC consecutive nucleotides identical, or complementary to the RCHT
XX CC sequence linked to heterologous transcriptional regulatory
XX CC sequences, can be used for the gene therapy of human diseases.
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 73.3%; Score 22; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGGAG 22
DB 5 GCTCTAGAATGACGGTGGGAG 26

RESULT 11
AAT10299
ID AAT10299 standard; DNA; 26 BP.
XX KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
XX KW plasmid; probe; primer; ribozyme; ss.
XX DT 09-SEP-1996 (first entry)

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XX DE RNA component of human telomerase antisense plasmid PCR primer R3c.
XX DE
XX KW RNA component; human; telomerase; lung fibroblast; cell line WI-38;
XX KW recombinant production; synthesis; mutant; detection; mammalian;
XX KW identification; modulating agent; neoplastic condition;
XX KW transcriptional regulatory sequence; gene therapy; disease;
XX KW polymerase chain reaction; antisense plasmid; PCR primer; ss.
XX OS Synthetic.
XX PN WO9601835-A1.
XX PD 25-JAN-1996.
XX PF 06-JUL-1995; 95WO-US08530.
XX PR 07-JUN-1995; 95US-0482115.
XX PR 07-JUL-1994; 94US-0272102.
XX PR 27-OCT-1994; 94US-0330123.
XX PR 07-JUN-1995; 95US-0472802.
XX PA (GERO-) GERON CORP.
XX PI Andrews WH, Feng J, Funk W, Villeponteau B;
XX DR WPI; 1996-097581/10.
XX PT RNA component of mammalian telomerase, esp. human - useful in
XX PT identifying e.g. candidate telomerase-modulating agents
XX PS Example 8; Page 80; 114pp; English.
XX CC The present sequence is a PCR primer for a RNA component of human
XX CC telomerase (RCHT), antisense plasmid. RCHT was derived from a
XX CC genomic DNA library obtd. from the human lung fibroblast cell line
XX CC WI-38. The RCHT can be used in the recombinant prodn. of an active
XX CC telomerase mol., capable of adding sequences to chromosomal DNA
XX CC telomeres, and in the synthesis of mutant sequences for the
XX CC detection of mutant mammalian telomerase RNA component
XX CC polynucleotides. The RCHT may also be used in the identification
XX CC of telomerase modulating agents, and in the detection of
XX CC telomerase related, or neoplastic conditions in a patient.
XX CC Polynucleotides of at least 25 consecutive nucleotides identical,
XX CC or complementary to the RCHT sequence linked to heterologous
XX CC transcriptional regulatory sequences, can be used for the gene
XX CC therapy of human diseases.
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;

Query Match 73.3%; Score 22; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATGACGGTGGGAG 22
DB 5 GCTCTAGAATGACGGTGGGAG 26

RESULT 12
AAT11044
ID AAT11044 standard; DNA; 26 BP.
XX KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
XX KW plasmid; probe; primer; ribozyme; ss.
XX DT 02-JUL-1996 (first entry)
XX DE Primer for production of telomerase antisense oligonucleotide.
XX KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
XX KW plasmid; probe; primer; ribozyme; ss.
XX OS Synthetic.

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XX PN WO9601614-A2.
XX XX
XX PD 25-JAN-1996.
XX XX
XX PF 07-JUL-1995; 95WO-US08620.
XX XX
XX PR 07-JUN-1995; 95US-0485778.
XX PR 07-JUL-1994; 94US-0272102.
XX PR 27-OCT-1994; 94US-0330123.
XX PR 13-FEB-1995; 95US-0387524.
XX XX
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX PA (GERO-) GERON CORP.
XX XX
XX PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
XX PI Marhuenda MA, Villeponteau B;
XX XX
XX DR WPI; 1996-097428/10.
XX XX
XX PT RNA components of (non)human mammalian telomerase(s) - useful in
XX PT studying cell senescence and immortalisation
XX XX
XX PS Example 8; Page 53; 85pp; English.
XX XX
XX CC The RNA components of (non) human mammalian telomerase(s) especially
XX CC from mouse, rat and chinese hamster are all claimed. Antisense
XX CC oligonucleotides can be used to block the activity of the
XX CC telomerase; probes and primers can be used in detection; vectors and
XX CC host cells transformed with the isolated telomerase genes can be
XX CC used for production of telomerases; RNA and DNA ribozymes and triplex
XX CC forming oligonucleotides directed against the telomerase genes can
XX CC be used therapeutically as can plasmids. A mouse which lacks the
XX CC telomerase gene (also claimed) can be used for study of telomere
XX CC regulation in vivo, and the role it plays in immortalisation.
XX CC Three primers (AAT11040, AAT11043, AAT11044) were used to produce
XX CC antisense oligonucleotides which were then used to produce antisense
XX CC expression plasmids. AAT11040 was used alongside both AAT11043 and
XX CC AAT11044 to produce two different antisense molecules.
XX XX
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
XX XX
XX Query Match 73.3%; Score 22; DB 17; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.003;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB |||||
5 GCTCTAGATGAACGGTGAAG 26

RESULT 13
AAT58811
ID AAT58811 standard; DNA; 26 BP.
XX AC
XX AC AAT58811;
XX XX
XX DT 20-NOV-1997 (first entry)
XX XX
XX DE Human telomerase PCR 3'-primer R3C.
XX XX
XX KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
XX KW protozoa; tumour; antibody; polymerase chain reaction; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9640868-A1.
XX XX
XX PD 19-DEC-1996.
XX XX
XX PF 06-JUN-1996; 96WO-US09517.
XX XX
XX PR 07-JUN-1995; 95US-0478352.

```

```

XX XX
XX PA (COLD-) COLD SPRING HARBOR LAB.
XX XX
XX PI Autexier C, Greider C;
XX XX
XX DR WPI; 1997-099928/09.
XX XX
XX PT DNA encoding essential RNA components of human telomerase - also
XX PT truncated or recombinant telomerase, useful for diagnosis and
XX PT treatment of cancer and infection by eukaryotic parasites
XX XX
XX PS Example 5; Page 32; 48pp; English.
XX XX
XX CC The present sequence represents PCR 3'-primer R3C used for
XX CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
XX CC hybridisation assays to detect or quantify telomerase activity in cells,
XX CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
XX CC (yeast and protozoa) or tumours. It is also useful as primers for
XX CC amplification assays. The truncated or recombinant vertebrate telomerase
XX CC is used therapeutically to increase telomerase activity (also as
XX CC as antisense molecules, are used to reduce such activity. Typical
XX CC applications are initiation/restoration of activity to cause senescence
XX CC or to prevent immortalisation of cells in tumours or parasites. The DNA
XX CC is also used to produce recombinant telomerase, which can then be used
XX CC conventionally to raise antibodies for diagnostic detection of
XX CC telomerase. Detecting telomerase allows early diagnosis of tumour or
XX CC infection, before clinical signs manifest. Telomerase inhibitors
XX CC directed against e.g. Trypanosoma should cause fewer side effects than
XX CC drugs currently used to treat such infections. The DNA encodes those
XX CC parts of hTR RNA essential for activity but are significantly shorter
XX CC than the endogenous RNA component.
XX XX
XX SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
XX XX
XX Query Match 73.3%; Score 22; DB 18; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 0.003;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATGAACGGTGAAG 22
DB |||||
5 GCTCTAGATGAACGGTGAAG 26

RESULT 14
AAV19489
ID AAV19489 standard; DNA; 26 BP.
XX AC
XX AC AAV19489;
XX XX
XX DT 28-AUG-1998 (first entry)
XX XX
XX DE Human hTR gene RT-PCR primer R3c.
XX XX
XX KW hTR gene; TPC2; TPC3; telomere length; telomerase; human; cancer;
XX KW gene therapy; diagnosis; PCR; primer; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9811204-A1.
XX XX
XX PD 19-MAR-1998.
XX XX
XX PF 13-SEP-1996; 96WO-US14679.
XX XX
XX PR 13-SEP-1996; 96WO-US14679.
XX XX
XX PA (GERO-) GERON CORP.
XX XX
XX PI Adams RR, Andrews WH, Feng J, Villeponteau B;
XX XX
XX DR WPI; 1998-207373/18.

```

XX Human TPC3 and TR genes - regulate telomere length or modulate
 PT telomerase activity
 XX
 PS Disclosure; Page 49; 86pp; English.
 XX
 CC Primers R3c and F3b (see AAV19488) were designed for the PCR
 CC amplification of the human telomerase hTR gene (see AAV19481). hTR
 CC mRNA levels were showed to correlate with telomerase activity
 CC levels in a variety of mortal and immortal cell lines. Methods of
 CC the invention allow detection and quantitation of TPC2 (see
 CC AAV19479), TPC3 (see AAV19480) and/or TPC2 gene products and can be
 CC used to detect immortal cells, especially telomerase positive
 CC cancer cells.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 73.3%; Score 22; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCTCTAGAATGACGGTGGGAAG 22
 Db 5 GCTCTAGAATGACGGTGGGAAG 26
 RESULT 15
 AAV17033
 ID AAV17033 standard; DNA; 26 BP.
 XX
 AC AAV17033;
 XX
 DT 13-AUG-1998 (first entry)
 XX
 DE Telomerase PCR primer R3c.
 XX
 KW Human; telomerase reverse transcriptase; hTERT; TRT; diagnosis;
 KW Prognosis; cell proliferation; cancer; ageing; ribonucleoprotein;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN GB2317891-A.
 XX
 PD 08-APR-1998.
 XX
 PF 01-OCT-1997; 97GB-0020890.
 XX
 PR 14-AUG-1997; 97US-0915503.
 PR 01-OCT-1996; 96US-0724643.
 PR 18-APR-1997; 97US-0844419.
 PR 25-APR-1997; 97US-0846017.
 PR 06-MAY-1997; 97US-0851843.
 PR 09-MAY-1997; 97US-0854050.
 PR 14-AUG-1997; 97US-0911312.
 PR 14-AUG-1997; 97US-0912951.
 XX
 PA (GERO-) GERON CORP.
 PA (UYTE-) UNIV TECHNOLOGY CORP.
 XX
 PI Andrews WH, Cech TR, Chapman KB, Harley C, Lingner J;
 PI Morin GB, Nakamura T, Harley CB;
 XX
 DR WPI; 1998-171633/16.
 XX
 PT Pure and recombinant human Telomerase Reverse Transcriptase and its
 PT variants - are useful in the diagnosis, prognosis and treatment of
 PT cell proliferation conditions especially cancer and ageing
 XX
 PS Example 2; Page 218; 387pp; English.
 XX
 CC The present sequence represents a PCR primer from the present invention

CC which describes human telomerase reverse transcriptase (hTERT). The
 CC present invention also describes the following methods: (A) determining
 CC whether a test compound is a modulator of hTERT, by detecting the change
 CC in hTERT recombinant protein or polynucleotide, on administration of the
 CC compound; (B) preparation of recombinant telomerase by contacting a
 CC protein preparation of hTERT with a telomerase RNA component; (C)
 CC detection of the hTERT RNA or protein in a sample by binding a relevant
 CC probe to the sample and detecting the complex formed or, in the case of
 CC RNA detection, amplifying the product and correlating the presence of
 CC complex or amplification product with presence of hTERT in the sample;
 CC and (D) increasing the proliferation of a vertebrate cell by increasing
 CC hTERT expression; and (E) the use of an agent that causes an increase in
 CC cell vertebrate cell proliferation to create a medicament that inhibits
 CC ageing. A protein preparation of hTERT and the polynucleotide encoding
 CC hTERT can be used in the manufacture of medicaments for inhibiting the
 CC effect of ageing or cancer. Inhibitors of telomerase activity can be
 CC used to treat conditions that are associated with high telomerase
 CC activity. A protein preparation of hTERT can also be used in the new
 CC methods.
 XX
 SQ Sequence 26 BP; 7 A; 3 C; 9 G; 7 T; 0 other;
 Query Match 73.3%; Score 22; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GCTCTAGAATGACGGTGGGAAG 22
 Db 5 GCTCTAGAATGACGGTGGGAAG 26
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GenCore version 5.1.6
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(without alignments)
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- 34: em_htg_pln:*
- 35: em_htg_rod:*
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	15	88.2	25	6	AR016058	Sequence
6	15	88.2	25	6	AR075530	Sequence
c 7	14	82.4	24	6	AX255631	Sequence
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c 9	12	70.6	18	6	AR192804	Sequence
c 10	12	70.6	18	6	AR192805	Sequence
c 11	12	70.6	22	6	AX092789	Sequence
12	12	70.6	47	6	AX146611	Sequence
13	12	70.6	50	6	AR079681	Sequence
14	12	70.6	50	6	AR079685	Sequence
15	12	70.6	50	6	AR081211	Sequence
16	12	70.6	50	6	AR081215	Sequence
17	12	70.6	50	6	AR141990	Sequence
18	12	70.6	50	6	AR141994	Sequence
19	12	70.6	50	6	AR170571	Sequence
20	12	70.6	50	6	AR170575	Sequence
c 21	12	70.6	50	6	AX146616	Sequence
22	11	64.7	12	6	A01745	DNA fragment
c 23	11	64.7	17	6	AR021242	Sequence
c 24	11	64.7	17	6	AR034106	Sequence
c 25	11	64.7	17	6	AR093907	Sequence
c 26	11	64.7	17	6	AR191738	Sequence
27	11	64.7	18	6	AX118331	Sequence
28	11	64.7	19	6	AX369321	Sequence
29	11	64.7	19	6	AX395172	Sequence
30	11	64.7	20	6	AR086198	Sequence
31	11	64.7	20	6	AR126692	Sequence
32	11	64.7	20	6	AR176764	Sequence
33	11	64.7	20	6	AX139028	Sequence
34	11	64.7	20	6	BD011428	Determina
c 35	11	64.7	21	6	AX477227	Sequence
36	11	64.7	22	6	AR016064	Sequence
37	11	64.7	22	6	AR075540	Sequence
38	11	64.7	22	6	AX105072	Sequence
c 39	11	64.7	27	6	AR069990	Sequence
40	11	64.7	27	6	AR189756	Sequence
c 41	11	64.7	30	6	AX233628	Sequence
42	11	64.7	31	6	AR195952	Sequence
c 43	11	64.7	31	6	BD002481	Gene comp
44	11	64.7	33	6	AR111921	Sequence
45	11	64.7	33	6	AR119977	Sequence

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR063838
Sequence 14 from patent US 5846723.
AR063838
AR063838.1 GI:5993146
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 17)
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 14 08-DEC-1998;
Location/Qualifiers

17 bp DNA linear PAT 29-SBP-1999

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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Keith W.N.
TITLES
Promoter regions of the mouse and human telomerase rna component
JOURNAL
Patent: WO 938964-A 20 05-AUG-1999;
KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
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/notes="primer"
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Best Local Similarity 100.0%; Score 17; DB 6; Length 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTGACA 17
Db 7 CGGGCCAGCAGCTGACA 23
RESULT 3
A84595
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Atkinson,E.M. and Kealey,J.T.
TITLES
PURIFIED TELOMERASE
JOURNAL
Patent: WO 9845450-A 5 15-OCT-1998;
GERON CORP (US)
FEATURES
source
1. 30
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"
modified_base
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/notes="N = BIOTINYLATED G"
/modified_bases=OTHER
6 a 6 c 7 g 10 t 1 others
BASE COUNT
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Query Match
Best Local Similarity 100.0%; Score 17; DB 6; Length 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20
RESULT 4
AR079892
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 30)
AUTHORS
Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vasserot,A.P.,
Przan,R.A. and Kealey,J.T.
TITLES
Purified telomerase
JOURNAL
Patent: US 5968506-A 5 19-OCT-1999;
FEATURES
source
1. 30
Location/Qualifiers
/organism="unknown"
6 a 6 c 7 g 10 t 1 others
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Score 17; DB 6; Length 30;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20
RESULT 5
AR016058
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS
Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLES
Assays for the DNA component of human telomerase
JOURNAL
Patent: US 5776679-A 26 07-JUL-1998;
FEATURES
source
1. 25
Location/Qualifiers
/organism="unknown"
8 a 8 c 6 g 3 t
BASE COUNT
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23
RESULT 6
AR075530
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 27)
AUTHORS
Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLES
Assays for the DNA component of human telomerase
JOURNAL
Patent: US 5776679-A 26 07-JUL-1998;
FEATURES
source
1. 27
Location/Qualifiers
/organism="unknown"
25 bp DNA
PAT 30-AUG-2000
Sequence
US 5958690.
AR075530
ACCESSION
AR075530.1
GI:10002278
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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 25)
AUTHORS     Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE       Mammalian telomerase
JOURNAL     Patent: US 5958680-A 27 28-SEP-1999;
FEATURES    Location/Qualifiers
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            /organism="unknown"
BASE COUNT  8 a      8 c      6 g      3 t
ORIGIN

Query Match      88.2%; Score 15; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3  GGCCAGCAGCTGACA 17
Db  9  GGCCAGCAGCTGACA 23

RESULT 7
AX255631/c
LOCUS       AX255631                24 bp    DNA        linear        PAT 10-OCT-2001
DEFINITION  Sequence 52 from Patent WO0170982.
ACCESSION   AX255631
VERSION     AX255631.1 GI:16074687
KEYWORDS    synthetic construct.
SOURCE      synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Beger,C., Barber,J. and Wong-Staal,P.
TITLE       Brca-1 regulators and methods of use
JOURNAL     Patent: WO 0170982-A 52 27-SEP-2001;
            Immusol Incorporated (US); Beger, Carmela (DE)
FEATURES    Location/Qualifiers
            1..24
            /organism="synthetic construct"
            /db_xref="taxon:32630"
            /notes="Primer"
BASE COUNT  2 a      8 c      7 g      7 t
ORIGIN

Query Match      82.4%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  CGGGCCAGCAGCTG 14
Db  23 CGGGCCAGCAGCTG 10

RESULT 8
AX009124
LOCUS       AX009124                17 bp    DNA        linear        PAT 06-SEP-2000
DEFINITION  Sequence 157 from Patent WO9963975.
ACCESSION   AX009124
VERSION     AX009124.1 GI:9996498
KEYWORDS    human.
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Brysch,W., Schlingensiepen,K.H. and Schlingensiepen,R.
TITLE       A method for stimulating the immune system
JOURNAL     Patent: WO 9963975-A 157 16-DEC-1999;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE); SCHLINGENSIEPEN KARL
            HERMANN (DE); SCHLINGENSIEPEN REIMAR (DE)
FEATURES    Location/Qualifiers

KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 8293 12-FEB-2002;
JOURNAL     Patent: US 6346398-A 8293 12-FEB-2002;
FEATURES    Location/Qualifiers
            1..18
            /organism="unknown"
BASE COUNT  3 a      6 c      6 g      3 t
ORIGIN

Query Match      70.6%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5  CCAGCAGCTGAC 16
Db  1  CCAGCAGCTGAC 12

RESULT 9
AR192804/c
LOCUS       AR192804                18 bp    DNA        linear        PAT 20-APR-2002
DEFINITION  Sequence 8292 from patent US 6346398.
ACCESSION   AR192804
VERSION     AR192804.1 GI:20238769
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 8292 12-FEB-2002;
JOURNAL     Patent: US 6346398-A 8292 12-FEB-2002;
FEATURES    Location/Qualifiers
            1..18
            /organism="unknown"
BASE COUNT  3 a      4 c      7 g      4 t
ORIGIN

Query Match      70.6%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5  CCAGCAGCTGAC 16
Db  15 CCAGCAGCTGAC 4

RESULT 10
AR192805/c
LOCUS       AR192805                18 bp    DNA        linear        PAT 20-APR-2002
DEFINITION  Sequence 8293 from patent US 6346398.
ACCESSION   AR192805
VERSION     AR192805.1 GI:20238770
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 18)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
            Patent: US 6346398-A 8293 12-FEB-2002;
JOURNAL     Patent: US 6346398-A 8293 12-FEB-2002;
FEATURES    Location/Qualifiers
            1..18
            /organism="unknown"
BASE COUNT  3 a      6 c      6 g      3 t
ORIGIN

Query Match      70.6%; Score 12; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  5  CCAGCAGCTGAC 16
Db  12 CCAGCAGCTGAC 1


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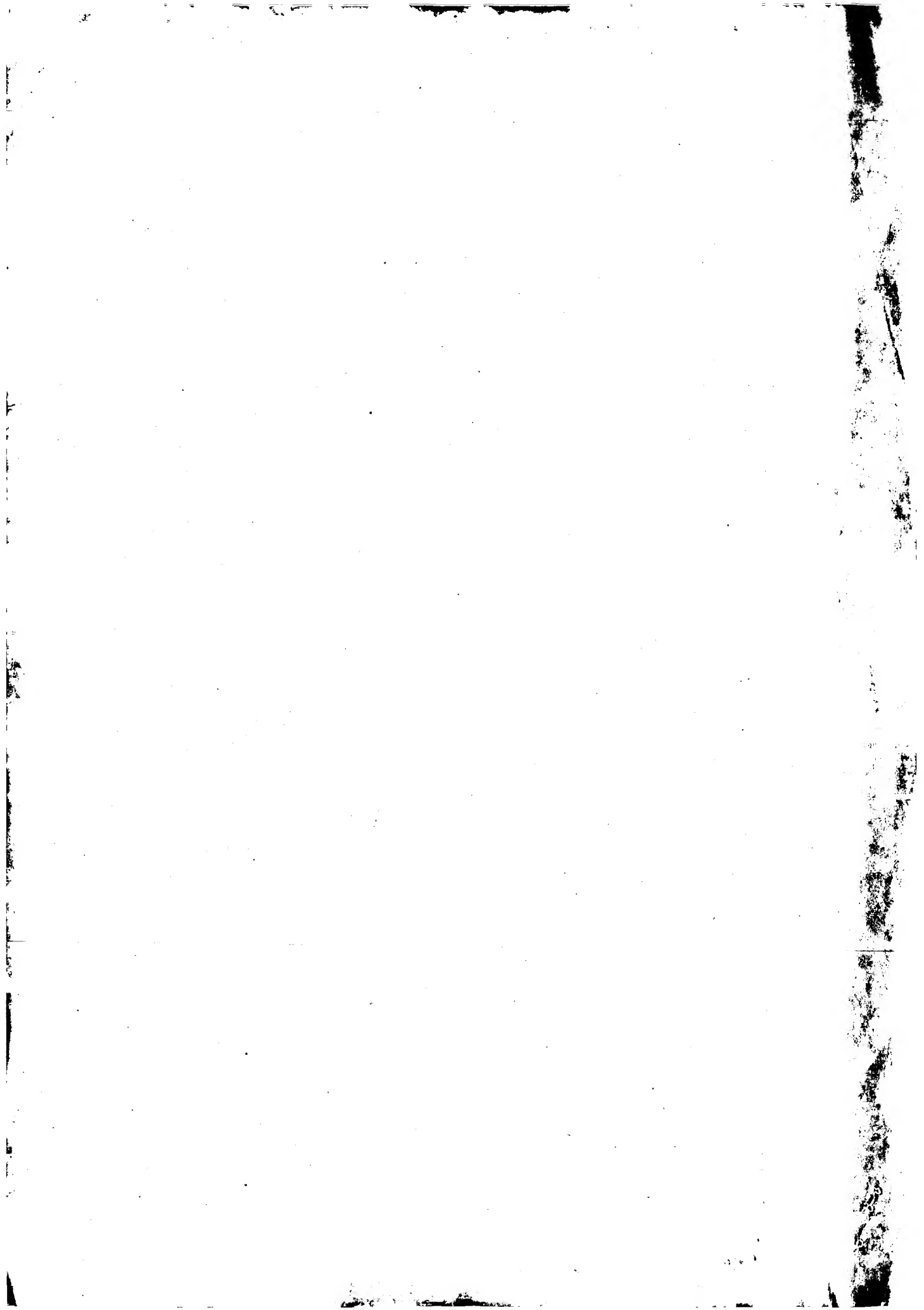
RESULT 11
AX092789/c
LOCUS AX092789 22 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 201 from Patent WO0115676.
ACCESSION AX092789
VERSION AX092789.1 GI:13444846
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.
TITLE Compositions and methods for modulating hdl cholesterol and triglyceride levels
JOURNAL Patent: WO 0115676-A 201 08-MAR-2001; Xenon Genetics Inc. (CA)
UNIVERSITY OF BRITISH COLUMBIA (CA);
LOCATION/Qualifiers
FEATURES
1..22
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/db_xref="taxon:9606"
BASE COUNT 3 a 4 c 9 g 6 t
ORIGIN
Query Match 70.6%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 12 CAGCAGCTGACA 1
RESULT 12
AX146611
LOCUS AX146611 47 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 73 from Patent WO0134654.
ACCESSION AX146611
VERSION AX146611.1 GI:14285004
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Strauch, K.
TITLE Hedgehog fusion proteins and uses
JOURNAL Patent: WO 0134654-A 73 17-MAY-2001;
BIOGEN, INC. (US)
LOCATION/Qualifiers
FEATURES
1..47
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 9 a 15 c 20 g 3 t
ORIGIN
Query Match 70.6%; Score 12; DB 6; Length 47;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 CCAGCAGCTGAC 16
Db 35 CCAGCAGCTGAC 46
RESULT 13
AR079681
LOCUS AR079681 50 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5965726.
ACCESSION AR079681
VERSION AR079681.1 GI:10006422

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Pavlakis, G.N. and Felber, B.K.
TITLE Method of eliminating inhibitory/ instability regions of mRNA
JOURNAL Patent: US 5965726-A 5 12-OCT-1999;
LOCATION/Qualifiers
FEATURES
1..50
/organism="unknown"
BASE COUNT 26 a 10 c 12 g 2 t
ORIGIN
Query Match 70.6%; Score 12; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46
RESULT 14
AR079685
LOCUS AR079685 50 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 9 from patent US 5965726.
ACCESSION AR079685
VERSION AR079685.1 GI:10006426
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Pavlakis, G.N. and Felber, B.K.
TITLE Method of eliminating inhibitory/ instability regions of mRNA
JOURNAL Patent: US 5965726-A 9 12-OCT-1999;
LOCATION/Qualifiers
FEATURES
1..50
/organism="unknown"
BASE COUNT 20 a 13 c 15 g 2 t
ORIGIN
Query Match 70.6%; Score 12; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46
RESULT 15
AR081211
LOCUS AR081211 50 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5972596.
ACCESSION AR081211
VERSION AR081211.1 GI:10007937
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Pavlakis, G.N. and Felber, B.K.
TITLE Nucleic acid constructs containing HIV genes with mutated inhibitory/instability regions and methods of using same
JOURNAL Patent: US 5972596-A 5 26-OCT-1999;
LOCATION/Qualifiers
FEATURES
1..50
/organism="unknown"
BASE COUNT 26 a 10 c 12 g 2 t
ORIGIN

Query Match 70.6%; Score 12; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred.No. 8.5e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
 |||||
 Db 35 CAGCAGCTGACA 46

Search completed: June 23, 2003, 06:34:27
 Job time : 200.163 secs



Query Match: 100.0%; Score 7; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 3.6e+07;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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DB 1 GCTTCAG 7

RESULT 2

US-08-235-503B-28
; Sequence 28, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovici, Berit
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1889
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-235-503B-28

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 1 GCTTCAG 7

RESULT 3

US-07-951-715A-49
; Sequence 49, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lytle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.

; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Desc = "Primer C1 - second half"
; HYPOTHETICAL: NO
US-07-951-715A-49

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 2 GCTTCAG 8

RESULT 4

US-08-459-448A-49
; Sequence 49, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lytle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 589336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
US-08-459-448A-49

Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 5
US-08-899-786-10/c
Sequence 10, Application US/08899786
Patent No. 6001572
GENERAL INFORMATION:
APPLICANT: Toothman, Penelope
TITLE OF INVENTION: Method of Identifying Aloe Using
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,786
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,611
FILING DATE: 26-JULY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: UNI.07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-899-786-10

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 7 GCTTCAG 1

RESULT 6
US-08-459-595A-49
Sequence 49, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
US-08-459-595A-49

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Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Fred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

```

```

RESULT 7
US-08-459-504B-49
; Sequence 49, Application US/08459504B
; Patent No. 6075185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
US-08-459-504B-49

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Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Fred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

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RESULT 8
US-08-459-444-49
; Sequence 49, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; TITLE OF INVENTION: NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-JUN-1995

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-08-459-444-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 9
US-09-424-518-1/C
Sequence 1, Application US/09424518
Patent No. 6260034
GENERAL INFORMATION:
APPLICANT: Bjorksten, Lennart
TITLE OF INVENTION: A Method and a System for Nucleic Acid Sequence Analysis
Patent No. 6260034
FILE REFERENCE: 45687-00004
CURRENT APPLICATION NUMBER: US/09/424,518
CURRENT FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: PCT/SE98/01005
PRIOR FILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 9702008-5
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-09-424-518-1

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
DB 8 GCTTCAG 2

RESULT 10
US-09-547-422-49
Sequence 49, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lunnis, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-547-422-49
Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
DB 2 GCTTCAG 8
RESULT 11
PCT-US95-05365-28
Sequence 28, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

```
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch; 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-592332-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-1249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PCT-US95-05265-28

Query Match 100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 1 GCTTCAG 7

RESULT 12
US-08-093-383-16
Sequence 16, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
APPLICANT: DeBoer, Herman A.
APPLICANT: Heyneker, Herbert H.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch; 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/519827
FILING DATE: 28-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988
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STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch; 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

Query Match 100.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 13
US-08-811-949-9
Sequence 9, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"
US-08-811-949-9

Query Match 100.0%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 14
US-09-281-418-93
; Sequence 93, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 93
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-93

Query Match 100.0%; Score 7; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 4 GCTTCAG 10

RESULT 15
US-09-404-430-3
; Sequence 3, Application US/09404430
; Patent No. 6350853
; GENERAL INFORMATION:
; APPLICANT: Neilsen, Peter
; APPLICANT: Knudsen, Helle
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Cellular Uptake
; FILE REFERENCE: ISIS4181
; CURRENT APPLICATION NUMBER: US/09/404,430
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US08/564,765
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6350853el Sequence
US-09-404-430-3

Query Match 100.0%; Score 7; DB 4; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 5 GCTTCAG 11

Search completed: June 25, 2003, 00:24:40
Job time : 10.6255 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 360.904 Seconds
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Title: US-08-770-564A-12
Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0
Total number of hits satisfying chosen parameters: 102860

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Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 21: em_gss_vrt:*
- 22: em_gss_fun:*
- 23: em_gss_man:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	7	100.0	19	AZ858978	AZ858978 2M0164E24
3	7	100.0	25	AU257776	AU257776 AU257776
4	7	100.0	25	BM399457	BM399457 5009-0-57
5	7	100.0	25	AZ310966	AZ310966 1M0026K08
6	7	100.0	27	H84968	H84968 ya89c08.r1

7	7	100.0	27	AZ320101	AZ320101 1M0040B04
8	7	100.0	27	TA80D02P	TA80D02P
9	7	100.0	28	AI429345	AI429345 mn95C09.x
10	7	100.0	28	AZ592130	AZ592130 1M0402J17
11	7	100.0	28	AZ603080	AZ603080 1M0422J09
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20	7	100.0	31	BM007283	BM007283 603615061
21	7	100.0	31	AZ628881	AZ628881 1M0481A19
22	7	100.0	32	BE547551	BE547551 601075188
23	7	100.0	32	BM051667	BM051667 603638419
24	7	100.0	32	AZ826678	AZ826678 2M0102F06
25	7	100.0	33	AV834163	AV834163 AV834163
26	7	100.0	33	BJ076555	BJ076555
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28	7	100.0	33	AZ785987	AZ785987 2M0030G18
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30	7	100.0	34	AV852639	AV852639
31	7	100.0	34	AW698792	AW698792 r378 non-
32	7	100.0	34	BF973182	BF973182 602241432
33	7	100.0	34	BG536263	BG536263 602565486
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36	7	100.0	34	BH864764	BH864764 SALK_0968
37	7	100.0	34	TA163C01P	TA163C01P
38	7	100.0	34	TA9H02P	TA9H02P
39	7	100.0	35	AZ471193	AZ471193 1M0285J12
40	7	100.0	36	BI766883	BI766883 603053118
41	7	100.0	36	AZ788319	AZ788319 2M0035N17
42	7	100.0	36	TA146G01Q	TA146G01Q
43	7	100.0	37	AI024153	AI024153 ov73b09.s
44	7	100.0	37	AI079739	AI079739 oy55f02.s
45	7	100.0	37	AA228354	AA228354 nc39c12.r

ALIGNMENTS

RESULT 1	AZ621656	19 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	1M0455C01F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0455C01 F, DNA sequence.				
ACCESSION	AZ621656				
VERSION	AZ621656.1	GI:11743846			
KEYWORDS	GSS.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00				

Plate: 0455 row: C column: 01
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0455C01"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 2 a 3 c 7 g 7 t

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
Db 9 GCTTCAG 15

RESULT 2

AZ858978/c
LOCUS 2M0164F24F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
DEFINITION clone UUGC2M0164F24 F, DNA sequence.
ACCESSION AZ858978
VERSION GSS.
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0164 row: F column: 24
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES

Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0164F24"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"

/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 4 a 3 c 7 g 5 t

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
Db 15 GCTTCAG 9

RESULT 3

AU257776/c
LOCUS AU257776 3'-directed mouse cDNA library Mus musculus cDNA clone
DEFINITION BED0011369 3', mRNA sequence.
ACCESSION AU257776
VERSION AU257776.1 GI:20322727
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Kato, K. and Matsuda, R.
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@nara.ac.jp
URL: http://love2.aist-nara.ac.jp/BED/index.html.

Location/Qualifiers
1..25
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0011369"

FEATURES

Location/Qualifiers
1..25
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="BED0011369"

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/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/notes="Vector: pGEM-T-easy"
5 t
BASE COUNT      12 a      5 c      3 g      5 t
ORIGIN

Query Match      100.0%; Score 7; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      22 GCTTCAG 16

RESULT 4
BM399457/c
LOCUS      25 bp mRNA linear EST 17-JAN-2002
DEFINITION      5009-0-57-H06.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM399457
VERSION      BM399457.1 GI:18199510
KEYWORDS      EST.
SOURCE      Tetrahymena thermophila.
ORGANISM      Tetrahymena thermophila.
REFERENCE      1 (bases 1 to 25)
AUTHORS      J. and Klobutcher, L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
    source
    1..25
    /organism="Tetrahymena thermophila"
    /strain="CU428.1"
    /db_xref="taxon:5911"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /notes="Vector: Bluescript2 SK-; Details on library
    preparation can be found in Chilcoat and Turkewitz (2001)
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
    4 t
BASE COUNT      6 a      6 c      9 g      4 t
ORIGIN

Query Match      100.0%; Score 7; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      10 GCTTCAG 4

RESULT 5
AZ310966
LOCUS      25 bp DNA linear GSS 29-SEP-2000
DEFINITION      IM0026K08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0026K08 F, DNA sequence.
ACCESSION      AZ310966
VERSION      AZ310966.1 GI:10353460
KEYWORDS      GSS.
SOURCE      house mouse.
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 25)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0026 row: K column: 08
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 25.

FEATURES
    Location/Qualifiers
    1..25
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC1M0026K08"
    /clone_lib="Mouse 10kb plasmid UUGC1M library"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
    /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (GI|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."
    5 a      4 c      6 g      10 t
BASE COUNT      5 a      4 c      6 g      10 t
ORIGIN

Query Match      100.0%; Score 7; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
      |||||
Db      4 GCTTCAG 10

RESULT 6
H84968/c
LOCUS      27 bp mRNA linear EST 14-NOV-1995
DEFINITION      y89c08.r1 Soares retina N2b5HR Homo sapiens cDNA clone
IMAGE:221966 5' similar to gb|U73048|HUMU3AAA Human U3 small
nuclear RNA (rRNA);, mRNA sequence.
ACCESSION      H84968
VERSION      H84968.1 GI:1064601
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```


Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and rh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1. .27
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="80d02" 7 g 9 t
 4 a 7 c 7 g 9 t

BASE COUNT
 4 a 7 c 7 g 9 t

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 |||||
 23 GCTTCAG 17

LOCUS
 AI429345/c 28 bp mRNA linear EST 09-MAR-1999
 mn95c09.x1 Stragatene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:551824.3; similar to TR:015157 O15157 DOLICHRON MONOPHOSPHATE
 MANNOSE SYNTHASE ;, mRNA sequence.

ACCESSION
 AI429345
 AI429345.1 GI:4275271

VERSION
 EST.

KEYWORDS
 house mouse.

SOURCE
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28

FEATURES
 source

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and rh@sanger.ac.uk
 Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
 Location/Qualifiers
 1. .27
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="80d02" 7 g 9 t
 4 a 7 c 7 g 9 t

BASE COUNT
 4 a 7 c 7 g 9 t

ORIGIN

Query Match 100.0%; Score 7; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 |||||
 23 GCTTCAG 17

LOCUS
 AI429345/c 28 bp mRNA linear EST 09-MAR-1999
 mn95c09.x1 Stragatene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:551824.3; similar to TR:015157 O15157 DOLICHRON MONOPHOSPHATE
 MANNOSE SYNTHASE ;, mRNA sequence.

ACCESSION
 AI429345
 AI429345.1 GI:4275271

VERSION
 EST.

KEYWORDS
 house mouse.

SOURCE
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person
 B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
 E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R. and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 Trace considered overall poor quality
 Possible reversed clone; similarity on wrong strand
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28

FEATURES
 source

/organism="Mus musculus"
 /strain="C57BL/6 x CBA"
 /db_xref="taxon:10090"
 /clone="IMAGE:551824"
 /clone.lib="Stragatene mouse lung 937302"
 /sex="female"
 /tissue_type="lung"
 /dev_stage="6-8 month old"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: lung; Vector: pBluescript SK-; Site 1: EcoRI
 ; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo
 dt. 6-8 month old female lung and 1.5 year old male lung
 were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP
 XR Vector; -5' adaptor sequence: 5' GAATTCGACGACG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
 7 a 5 c 5 g 11 t

BASE COUNT
 7 a 5 c 5 g 11 t

ORIGIN

Query Match 100.0%; Score 7; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.5e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 |||||
 18 GCTTCAG 12

LOCUS
 AZ592130 28 bp DNA linear GSS 13-DEC-2000
 IM0402J17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0402J17 R, DNA sequence.

ACCESSION
 AZ592130
 AZ592130.1 GI:11714320

VERSION
 GSS.

KEYWORDS
 house mouse.

SOURCE
 Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: rdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Place: 0402 row: J column: 17
 Seq primer: CACACAGGAACAGGTATGACC
 Class: plasmid ends
 High quality sequence stop: 28.
 Location/Qualifiers
 1. .28
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0402J17"
 /clone.lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /note="Vector: PWD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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BASE COUNT      9 a      6 c      4 g      9 t
ORIGIN
Query Match      100.0%; Score 7; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTCAG 7
        |||||
Db      13 GCTTCAG 7

```

```

RESULT 11
AZ603080/c
LOCUS
DEFINITION
1M0422J09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0422J09 F, DNA sequence.
ACCESSION
AZ603080
VERSION
GSS.
KEYWORDS
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 28)
REFERENCE
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.; 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0422 row: J column: 09
Seq primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 28.
Location/Qualifiers
1..28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0422J09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

BASE COUNT      5 a      9 c      6 g      8 t
ORIGIN
Query Match      100.0%; Score 7; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTTCAG 7
        |||||
Db      16 GCTTCAG 10

```

```

RESULT 12
T99092
LOCUS
DEFINITION
Y667f08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
IMAGE:122823 3' similar to gb:L27670 Human Landsteiner-Wiener blood
group glycoprotein (HUMAN);, mRNA sequence.
ACCESSION
T99092
VERSION
EST.
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 30)
REFERENCE
AUTHORS
Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman,
M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, B., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston,
R., Williamson, A., Wohlmann, F. and Wilson, R.
TITLE
The WashU-Merck EST Project
JOURNAL
Unpublished (1995)
COMMENT
Contact: Wilton RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1341
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 1341 Std Error: 0.00
Seq primer: -21m13
High quality sequence stop: 1.
Location/Qualifiers
1..30
/organism="Homo sapiens"
/db_xref="GDB:475368"
/db_xref="taxon:9606"
/clone="IMAGE:122823"
/clone_lib="Soares fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

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```

FEATURES
Source
1..28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0422J09"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA

```



```

RESULT 15
AL764630/c
LOCUS       AL764630             30 bp    DNA        linear    GSS 19-JUN-2002
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence GK-128H09-012669,
              genomic survey sequence.
ACCESSION   AL764630
VERSION     AL764630.1  GI:21517673
KEYWORDS    GSS.
SOURCE      thale cress.
ORGANISM    Arabidopsis thaliana
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
             Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE   1  Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.
AUTHORS     and Weishaar,B.
TITLE       A pipeline for automated high-throughput generation of FSTs
            (flanking sequence tags) from Arabidopsis thaliana T-DNA
            transformed lines
JOURNAL     unpublished
REFERENCE   2  Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weishaar,B.
AUTHORS     A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
            for flanking sequence tag based reverse genetics
JOURNAL     unpublished
REFERENCE   3  (bases 1 to 30)
AUTHORS     Li,Y., Strizhov,N., Rosso,M. and Weishaar,B.
JOURNAL     Direct Submission
            Submitted (17-JUN-2002) Weishaar B., Max-Planck-Institut fuer
            Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
            This sequence is recovered from the left border of the T-DNA. It
            indicates an insertion close to or within gene At3g62580. The
            sequences are generated at the MPI for plant breeding research in
            the context of the GABI-Kat project. GABI-Kat is part of the German
            plant genomics program designated 'GABI'. Information on line
            availability can be found at:
            http://www.mpiz-koeln.mpg.de/GABI-Kat/.
FEATURES             Location/Qualifiers
     source           1..30
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="GK-128H09-012669"
                     /clone_11b="Arabidopsis thaliana T-DNA insertion lines"
                     /notes="PCR was performed on DNA from Arabidopsis thaliana
                     plants (T1) which were transformed with the T-DNA from
                     vector pAC161. The lines contain one or more T-DNA from
                     insertions. The DNA fragment(s) resulting from the PCR
                     were directly sequenced to determine the genomic sequence
                     flanking the insertion. Sequences displaying significant
                     similarity to the A. thaliana nuclear genome sequences were
                     processed for submission. T-DNA derived sequences were
                     removed"
BASE COUNT      8 a      6 c      7 g      9 t
ORIGIN
Query Match      100.0%; Score 7; DB 17; Length 30;
Best Local Similarity 100.0%; Pred No. 3.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCTTCAG 7
        |||||
Db      28  GCTTCAG 22

Search completed: June 23, 2003, 10:10:32
Job time : 364.058 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 307.275 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*
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3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	7	100.0	10	9	US-10-329-465-53
C 2	7	100.0	10	10	US-10-293-222-131
C 3	7	100.0	11	9	US-10-314-322-34
C 4	7	100.0	12	9	US-10-240-580-38
C 5	7	100.0	13	9	US-10-106-799-13
C 6	7	100.0	13	9	US-10-106-799-14
C 7	7	100.0	13	9	US-10-146-505-84
C 8	7	100.0	14	9	US-10-303-778-13859
C 9	7	100.0	15	9	US-10-294-035-747
C 10	7	100.0	15	9	US-10-294-035-748
C 11	7	100.0	15	9	US-10-294-035-940
C 12	7	100.0	15	9	US-10-294-038-1008
C 13	7	100.0	15	9	US-10-294-038-2682
C 14	7	100.0	15	9	US-10-294-038-4251
C 15	7	100.0	15	9	US-10-287-822-1580
C 16	7	100.0	15	9	US-10-310-188-33324
C 17	7	100.0	15	9	US-10-310-188-72013
C 18	7	100.0	15	9	US-10-305-273-169
C 19	7	100.0	15	9	US-10-305-273-1191
C 20	7	100.0	15	9	US-10-305-275-550

C 21	7	100.0	15	9	US-10-316-956-1230	Sequence 1230, Ap
C 22	7	100.0	15	9	US-10-316-956-1239	Sequence 1239, Ap
C 23	7	100.0	15	9	US-10-316-956-1250	Sequence 1250, Ap
C 24	7	100.0	15	9	US-10-316-956-1251	Sequence 1251, Ap
C 25	7	100.0	15	9	US-10-316-956-1252	Sequence 1252, Ap
C 26	7	100.0	15	9	US-10-316-954-413	Sequence 413, App
C 27	7	100.0	15	9	US-10-316-954-1307	Sequence 1307, Ap
C 28	7	100.0	15	9	US-10-316-954-2852	Sequence 2852, Ap
C 29	7	100.0	15	9	US-10-316-954-2853	Sequence 2853, Ap
C 30	7	100.0	15	9	US-10-316-954-3393	Sequence 3393, Ap
C 31	7	100.0	15	9	US-10-316-954-4302	Sequence 4302, Ap
C 32	7	100.0	15	9	US-10-316-954-4303	Sequence 4303, Ap
C 33	7	100.0	15	9	US-10-321-854-1864	Sequence 1864, Ap
C 34	7	100.0	15	9	US-10-321-854-3261	Sequence 3261, Ap
C 35	7	100.0	15	9	US-10-310-157-1213	Sequence 1213, Ap
C 36	7	100.0	15	9	US-10-310-157-1214	Sequence 1214, Ap
C 37	7	100.0	15	9	US-10-310-157-3299	Sequence 3299, Ap
C 38	7	100.0	15	9	US-10-310-157-4486	Sequence 4486, Ap
C 39	7	100.0	15	9	US-10-310-157-5923	Sequence 5923, Ap
C 40	7	100.0	15	9	US-10-310-157-5935	Sequence 5935, Ap
C 41	7	100.0	15	9	US-10-310-157-6009	Sequence 6009, Ap
C 42	7	100.0	15	9	US-10-305-273A-169	Sequence 169, App
C 43	7	100.0	15	9	US-10-305-273A-1191	Sequence 1191, Ap
C 44	7	100.0	15	9	US-10-305-275A-550	Sequence 550, App
C 45	7	100.0	15	10	US-10-367-892-657	Sequence 657, App

ALIGNMENTS

RESULT 1
US-10-329-465-53/c
; Sequence 53, Application US/10329465
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN ML-
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-53

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
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Db 7 GCTTCAG 1

RESULT 2
US-10-293-222-131/c
; Sequence 131, Application US/10293222
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 131
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-131

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 10 GCTTCAG 4

RESULT 3

US-10-314-322-34/c
; Sequence 34, Application US/10314322

; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; FILE REFERENCE: 000486.00016
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US/10/314,322
; PRIOR FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; PRIOR APPLICATION NUMBER: US 09/249,155
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-314-322-34

Query Match 100.0%; Score 7; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 10 GCTTCAG 4

RESULT 4

US-10-240-580-38
; Sequence 38, Application US/10240580

; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: METHOD AND APPARATUS FOR MICROORGANISM DISCRIMINATION, METHOD OF
; TITLE OF INVENTION: DATABASE FOR MICROORGANISM DISCRIMINATION, AND MICROORGANISM DIS
; TITLE OF INVENTION: PROGRAM AND RECORDING MEDIUM ON WHICH SUCH PROGRAM IS RECORDED
; FILE REFERENCE: 9982-24
; CURRENT APPLICATION NUMBER: US/10/240,580
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/JP01/02516
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: JP 2000-99482
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent In version 3.1

; SEQ ID NO 38
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-240-580-38

Query Match 100.0%; Score 7; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 4 GCTTCAG 10

RESULT 5

US-10-106-799-13
; Sequence 13, Application US/10106799

; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
; FILE REFERENCE: US 673
; CURRENT APPLICATION NUMBER: US/10/106,799
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 13
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP34 arbitrary primer for differential display
US-10-106-799-13

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 3 GCTTCAG 9

RESULT 6

US-10-106-799-14
; Sequence 14, Application US/10106799

; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
; TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
; FILE REFERENCE: US 673
; CURRENT APPLICATION NUMBER: US/10/106,799
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 14
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: AP35 arbitrary primer for differential display
US-10-106-799-14

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 3 GCTTCAG 9

RESULT 7
US-10-146-505-84/c
; Sequence 84, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)-(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGACCTCTGTG is deleted
US-10-146-505-84

Query Match 100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 7 GCTTCAG 1
RESULT 8
US-10-303-778-13859/c
; Sequence 13859; Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13859
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-13859

Query Match 100.0%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 8 GCTTCAG 2

RESULT 9
US-10-294-035-747/c
; Sequence 747, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 747
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1041
US-10-294-035-747

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 12 GCTTCAG 6

RESULT 10
US-10-294-035-748/c
; Sequence 748, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 748
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1040
US-10-294-035-748

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
Db 12 GCTTCAG 6

RESULT 11
US-10-294-035-940/c
; Sequence 940, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 940
; LENGTH: 15
; TYPE: DNA

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; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (2080233)...(2080248)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 1297
US-10-294-035-940

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GCTTCAG 7
   |||||
Db 7 GCTTCAG 1

RESULT 12
US-10-294-038-1008
; Sequence 1008, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 1008
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (371601)...(371615)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 1249
US-10-294-038-1008

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
   |||||
Db 8 GCTTCAG 14

RESULT 13
US-10-294-038-2682
; Sequence 2682, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 2682
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1117875)...(1117888)
; OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectionObjectNumber = 3354
US-10-294-038-2682

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GCTTCAG 7
   |||||
Db 1 GCTTCAG 7
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RESULT 14
US-10-294-038-4251
; Sequence 4251, Application US/10294038
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,038
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 5372
; SOFTWARE: Proprietary
; SEQ ID NO 4251
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
; FEATURE:
; LOCATION: (1902455)...(1902469)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 5315
US-10-294-038-4251

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05; 0; Indels 0;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

QY 1 GCTTCAG 7
   |||||
Db 8 GCTTCAG 14

RESULT 15
US-10-287-822-1580/c
; Sequence 1580, Application US/10287822
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Synchocystis PCC6803 complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,822
; CURRENT FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 5726
; SOFTWARE: Proprietary
; SEQ ID NO 1580
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Synchocystis PCC6803 complete genome.
; FEATURE:
; LOCATION: (959678)...(959693)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 2089
US-10-287-822-1580

Query Match      100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 11 GCTTCAG 5

Search completed: June 23, 2003, 19:12:13
Job time : 307.275 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 587.108 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-12
Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0
Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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- 81: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:*
- 82: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:*
- 83: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:*
- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	7	100.0	11	US-08-770-564A-12
2	7	100.0	8	US-08-632-782-86
3	7	100.0	10	PCT-US00-04606-65
4	7	100.0	10	PCT-US01-10743A-43
5	7	100.0	10	PCT-US01-10743A-44
6	7	100.0	10	PCT-US01-18814-44
7	7	100.0	10	PCT-US01-18814-49
8	7	100.0	10	PCT-US01-21306-130
9	7	100.0	10	PCT-US01-23100-118
10	7	100.0	10	PCT-US01-29207-36
11	7	100.0	10	PCT-US01-42727-58
12	7	100.0	10	PCT-US02-24250-52
13	7	100.0	10	PCT-US97-13001-10
14	7	100.0	10	PCT-US99-13800-226
15	7	100.0	10	PCT-US99-13800-149
16	7	100.0	8	US-08-458-785-49
17	7	100.0	10	US-08-459-444-49
18	7	100.0	10	US-08-459-448-49
19	7	100.0	10	US-08-459-504-49
20	7	100.0	10	US-08-459-504A-49
21	7	100.0	10	US-08-459-595-49
Sequence 12, Appl				Sequence 86, Appl
Sequence 65, Appl				Sequence 43, Appl
Sequence 43, Appl				Sequence 44, Appl
Sequence 44, Appl				Sequence 49, Appl
Sequence 49, Appl				Sequence 118, App
Sequence 118, App				Sequence 149, App
Sequence 149, App				Sequence 49, Appl
Sequence 49, Appl				Sequence 49, Appl
Sequence 49, Appl				Sequence 49, Appl
Sequence 49, Appl				Sequence 49, Appl

Sequence 49, Appl
Sequence 369, Appl
Sequence 2641, AD
Sequence 2931, AD
Sequence 4373, AD
Sequence 8177, AD
Sequence 8178, AD
Sequence 1613, AD
Sequence 1701, AD
Sequence 4067, AD
Sequence 4990, AD
Sequence 61, Appl
Sequence 49, Appl
Sequence 1449, AD
Sequence 81, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 3, Appl
Sequence 20, Appl
Sequence 3, Appl
Sequence 2823, AD
Sequence 7616, AD
Sequence 25, Appl

Sequence 49, Appl
Sequence 369, Appl
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Sequence 49, Appl
Sequence 1449, AD
Sequence 81, Appl
Sequence 34, Appl
Sequence 34, Appl
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Sequence 20, Appl
Sequence 3, Appl
Sequence 2823, AD
Sequence 7616, AD
Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-08-770-564A-12
; Sequence 12, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA

Sequence 49, Appl
Sequence 369, Appl
Sequence 2641, AD
Sequence 2931, AD
Sequence 4373, AD
Sequence 8177, AD
Sequence 8178, AD
Sequence 1613, AD
Sequence 1701, AD
Sequence 4067, AD
Sequence 4990, AD
Sequence 61, Appl
Sequence 49, Appl
Sequence 1449, AD
Sequence 81, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 3, Appl
Sequence 20, Appl
Sequence 3, Appl
Sequence 2823, AD
Sequence 7616, AD
Sequence 25, Appl

Query Match 100.0%; Score 7; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 7; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 49, Appl
Sequence 369, Appl
Sequence 2641, AD
Sequence 2931, AD
Sequence 4373, AD
Sequence 8177, AD
Sequence 8178, AD
Sequence 1613, AD
Sequence 1701, AD
Sequence 4067, AD
Sequence 4990, AD
Sequence 61, Appl
Sequence 49, Appl
Sequence 1449, AD
Sequence 81, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 3, Appl
Sequence 20, Appl
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Sequence 2823, AD
Sequence 7616, AD
Sequence 25, Appl

Sequence 49, Appl
Sequence 369, Appl
Sequence 2641, AD
Sequence 2931, AD
Sequence 4373, AD
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Sequence 1613, AD
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Sequence 4067, AD
Sequence 4990, AD
Sequence 61, Appl
Sequence 49, Appl
Sequence 1449, AD
Sequence 81, Appl
Sequence 34, Appl
Sequence 34, Appl
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Sequence 3, Appl
Sequence 2823, AD
Sequence 7616, AD
Sequence 25, Appl

US-08-770-564A-12
; Sequence 12, Application US/08632782
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/632,782
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

US-08-770-564A-12
; Sequence 12, Application US/08632782
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/632,782
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

Query Match 100.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 7; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.1e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-08-770-564A-12
; Sequence 12, Application US/08632782
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/632,782
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

US-08-770-564A-12
; Sequence 12, Application US/08632782
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/632,782
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

;; CURRENT APPLICATION NUMBER: PCT/US00/04606
;; CURRENT FILING DATE: 2000-02-23
;; EARLIER APPLICATION NUMBER: 60/121,314
;; EARLIER FILING DATE: 1999-02-23
;; NUMBER OF SEQ ID NOS: 113
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 65
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: HOMO SAPIENS
PCT-US00-04606-65

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Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 9 GCTTCAG 3

RESULT 4
PCT-US01-10743A-43/c
;; Sequence 43, Application PC/TUS0110743A
;; GENERAL INFORMATION:
;; APPLICANT: Genassance Pharmaceuticals, Inc.
;; APPLICANT: Chew, Anne
;; APPLICANT: Choi, Julie Y.
;; APPLICANT: Koshy, Beena
;; TITLE OF INVENTION: Haplotypes of the SCN2B Gene
;; FILE REFERENCE: MWH-0481PCT SCN2B
;; CURRENT APPLICATION NUMBER: PCT/US01/10743A
;; CURRENT FILING DATE: 2001-04-03
;; PRIOR APPLICATION NUMBER: 60/196,597
;; PRIOR FILING DATE: 2000-04-13
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 43
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapien
PCT-US01-10743A-43

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 7 GCTTCAG 1

RESULT 5
PCT-US01-10743A-44
;; Sequence 44, Application PC/TUS0110743A
;; GENERAL INFORMATION:
;; APPLICANT: Genassance Pharmaceuticals, Inc.
;; APPLICANT: Chew, Anne
;; APPLICANT: Choi, Julie Y.
;; APPLICANT: Koshy, Beena
;; TITLE OF INVENTION: Haplotypes of the SCN2B Gene
;; FILE REFERENCE: MWH-0481PCT SCN2B
;; CURRENT APPLICATION NUMBER: PCT/US01/10743A
;; CURRENT FILING DATE: 2001-04-03
;; PRIOR APPLICATION NUMBER: 60/196,597
;; PRIOR FILING DATE: 2000-04-13
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 44
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapien
PCT-US01-10743A-44

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
Db 3 GCTTCAG 9

RESULT 6
PCT-US01-18814-44/c
;; Sequence 44, Application PC/TUS0118814
;; GENERAL INFORMATION:
;; APPLICANT: Genassance Pharmaceuticals, Inc.
;; APPLICANT: Choi, Julie Y.
;; APPLICANT: Koshy, Beena
;; APPLICANT: Sanchis, Angela
;; APPLICANT: Sausker, Elizabeth Ann
;; TITLE OF INVENTION: HAPLOTYPES OF THE PHKG2 GENE
;; FILE REFERENCE: MWH-0770PCT PHKG2
;; CURRENT APPLICATION NUMBER: PCT/US01/18814
;; CURRENT FILING DATE: 2001-06-11
;; PRIOR APPLICATION NUMBER: 60/210,568
;; PRIOR FILING DATE: 2000-06-09
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 44
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
PCT-US01-18814-44

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
Db 10 GCTTCAG 4

RESULT 7
PCT-US01-18814-49
;; Sequence 49, Application PC/TUS0118814
;; GENERAL INFORMATION:
;; APPLICANT: Genassance Pharmaceuticals, Inc.
;; APPLICANT: Choi, Julie Y.
;; APPLICANT: Koshy, Beena
;; APPLICANT: Sanchis, Angela
;; APPLICANT: Sausker, Elizabeth Ann
;; TITLE OF INVENTION: HAPLOTYPES OF THE PHKG2 GENE
;; FILE REFERENCE: MWH-0770PCT PHKG2
;; CURRENT APPLICATION NUMBER: PCT/US01/18814
;; CURRENT FILING DATE: 2001-06-11
;; PRIOR APPLICATION NUMBER: 60/210,568
;; PRIOR FILING DATE: 2000-06-09
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 49
;; LENGTH: 10
;; TYPE: DNA
;; ORGANISM: Homo sapiens
PCT-US01-18814-49

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
Db 4 GCTTCAG 10

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RESULT 8
PCT-US01-21306-130
; Sequence 130, Application PC/TUS0121306
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshiy, Beena
; TITLE OF INVENTION: Haplotypes of the ETFB Gene
; FILE REFERENCE: MMH-0902PCT ETFB
; CURRENT APPLICATION NUMBER: PCT/US01/21306
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/215,984
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-21306-130

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 3 GCTTCAG 9

RESULT 9
PCT-US01-23100-118
; Sequence 118, Application PC/TUS0123100
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Duda, Amy
; APPLICANT: Koshiy, Beena
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: Haplotypes of the CHRNA1 Gene
; FILE REFERENCE: MMH-071PCT CHRNA1
; CURRENT APPLICATION NUMBER: PCT/US01/23100
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 60/219,538
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-23100-118

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 3 GCTTCAG 9

RESULT 10
PCT-US01-29207-36
; Sequence 36, Application PC/TUS0129207
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Koshiy, Beena
; APPLICANT: Sanchis, Angela
; APPLICANT: Tirrell, Charles
; TITLE OF INVENTION: Haplotypes of the GPR7 Gene
; FILE REFERENCE: MMH-1293PCT
; CURRENT APPLICATION NUMBER: PCT/US01/29207
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/232,900
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-29207-36

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 7 GCTTCAG 1

RESULT 11
PCT-US01-42727-58/c
; Sequence 58, Application PC/TUS0142727
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Allison E.
; APPLICANT: Chew, Anne
; APPLICANT: Han, Jin-Hua
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: HAPLOTYPES OF THE CYP27A1 GENE
; FILE REFERENCE: CYP27A1 MMH-1279PCT
; CURRENT APPLICATION NUMBER: PCT/US01/42727
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,942
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-42727-58

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 7 GCTTCAG 1

RESULT 12
PCT-US02-24250-52/c
; Sequence 52, Application PC/TUS0224250
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Drysdale, Connie M.
; APPLICANT: Hoffman, Michael
; APPLICANT: Judson, Richard S.
; APPLICANT: Maez, Winfried
; APPLICANT: Mandabalan, Krishnan
; APPLICANT: Stack, Catherine B.
; APPLICANT: Stephens, J. Claborn
; APPLICANT: Vanden Eng, Jodi
; APPLICANT: Winkelmann, Bernhard R.
; TITLE OF INVENTION: Association of Low Density Lipoprotein Receptor (LDLR) Gene Haplot;
; TITLE OF INVENTION: Therapeutic Response to Statins
; FILE REFERENCE: MMH-2889PCT LDLR
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; CURRENT APPLICATION NUMBER: PCT/US02/24250
 ; CURRENT FILING DATE: 2002-07-30
 ; PRIOR APPLICATION NUMBER: US 60/308,688
 ; PRIOR FILING DATE: 2001-07-30
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 52
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 PCT-US02-24250-52

Query Match 100.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 10 GCTTCAG 4

RESULT 13

PCT-US97-13001-10/c
 ; Sequence 10, Application PC/TUS9713001
 ; GENERAL INFORMATION:

; APPLICANT: Toothman, Penelope
 ; TITLE OF INVENTION: Method of Identifying Aloe Using
 ; NUMBER OF SEQUENCES: 32
 ; CORRESPONDENCE ADDRESS:

; ADDRESSES: Swanson & Bratschun, L.L.C.
 ; STREET: 8400 E. Prentice Avenue, Suite 200
 ; CITY: Englewood
 ; STATE: Colorado
 ; COUNTRY: USA
 ; ZIP: 80111

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
 ; COMPUTER: IBM pc compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 8.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US97/13001
 ; FILING DATE:

; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/022,611
 ; FILING DATE: 26-JULY-1996
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson
 ; REGISTRATION NUMBER: 33,215
 ; REFERENCE/DOCKET NUMBER: UNI.07/PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 793-3333
 ; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE:

PCT-US97-13001-10

Query Match 100.0%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.7e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 7 GCTTCAG 1

RESULT 14

PCT-US99-13800-226/c
 ; Sequence 226, Application PC/TUS9913800
 ; GENERAL INFORMATION:
 ; APPLICANT: Genzyme Corporation
 ; APPLICANT: Roberts, Bruce L.
 ; APPLICANT: Shankara, Srinivas
 ; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
 ; FILE REFERENCE: 68126881206940
 ; CURRENT APPLICATION NUMBER: PCT/US99/13800
 ; CURRENT FILING DATE: 1999-06-18
 ; EARLIER APPLICATION NUMBER: 60/090,039
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,040
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,041
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,853
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,997
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,079
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,035
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,993
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,992
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,072
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,878
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,991
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,000
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,048
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,999
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,043
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,042
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,036
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,044
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,844
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,080
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,833
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/089,994
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,077
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,078
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,047
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,076
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/090,045
 ; EARLIER FILING DATE: 1998-06-19
 ; EARLIER APPLICATION NUMBER: 60/111,715
 ; EARLIER FILING DATE: 1998-12-08
 ; NUMBER OF SEQ ID NOS: 2138
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 226
 ; LENGTH: 10
 ; TYPE: DNA

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; ORGANISM: Homo sapiens
PCT-US99-13800-226
Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 9 GCTTCAG 3

RESULT 15
PCT-US99-13800-1449/c
; Sequence 1449, Application PC/TUS9913800
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce L.
; APPLICANT: Shankara, Srinivas
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: 68124881206940
; CURRENT APPLICATION NUMBER: PCT/US99/13800
; CURRENT FILING DATE: 1999-06-18
; EARLIER APPLICATION NUMBER: 60/090,039
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,040
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,041
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,853
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,997
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,079
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,035
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,993
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,992
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,072
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,878
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,991
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,000
; EARLIER FILING DATE: 1998-06-19
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; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,999
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; EARLIER APPLICATION NUMBER: 60/090,043
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; EARLIER APPLICATION NUMBER: 60/090,080
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/089,994
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; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,078
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/090,047
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,076
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,045
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/111,715
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 2138
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-13800-1449

Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 10 GCTTCAG 4

Search completed: June 23, 2003, 16:08:23
Job time : 588.185 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 56.251 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext_60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	10	9	US-09-988-462-49
2	7	100.0	10	10	US-09-816-763-61
3	7	100.0	10	12	US-10-033-145-226
4	7	100.0	10	12	US-10-033-145-1449
5	7	100.0	11	9	US-09-249-155-34
6	7	100.0	13	9	US-09-879-813-84
7	7	100.0	13	9	US-10-146-505-84
8	7	100.0	13	10	US-09-770-601-4
9	7	100.0	13	10	US-09-770-601-6
10	7	100.0	14	9	US-10-146-058-41
11	7	100.0	15	9	US-10-146-575-21
12	7	100.0	15	9	US-10-145-289-2
13	7	100.0	15	10	US-09-922-261-10
14	7	100.0	16	9	US-10-146-058-39
15	7	100.0	17	9	US-09-879-813-51
16	7	100.0	17	9	US-10-041-856-79
17	7	100.0	17	9	US-09-780-164-249
18	7	100.0	17	9	US-09-780-164-250
19	7	100.0	17	9	US-09-780-164-612

20	7	100.0	17	9	US-09-780-164-613	Sequence 613, App
21	7	100.0	17	9	US-09-780-164-738	Sequence 738, App
22	7	100.0	17	9	US-09-780-164-825	Sequence 825, App
23	7	100.0	17	9	US-09-780-164-928	Sequence 928, App
24	7	100.0	17	9	US-09-780-164-1066	Sequence 1066, App
25	7	100.0	17	9	US-10-029-677-6	Sequence 6, Appl
26	7	100.0	17	9	US-10-029-677-7	Sequence 7, Appl
27	7	100.0	17	9	US-10-060-895A-248	Sequence 248, App
28	7	100.0	17	9	US-10-060-895A-249	Sequence 249, App
29	7	100.0	17	9	US-10-060-895A-250	Sequence 250, App
30	7	100.0	17	9	US-10-060-895A-251	Sequence 251, App
31	7	100.0	17	9	US-10-060-895A-252	Sequence 252, App
32	7	100.0	17	9	US-10-060-895A-253	Sequence 253, App
33	7	100.0	17	9	US-10-060-895A-254	Sequence 254, App
34	7	100.0	17	9	US-10-060-895A-255	Sequence 255, App
35	7	100.0	17	9	US-10-060-895A-256	Sequence 256, App
36	7	100.0	17	9	US-10-060-895A-257	Sequence 257, App
37	7	100.0	17	9	US-10-060-895A-258	Sequence 258, App
38	7	100.0	17	9	US-10-060-998-1537	Sequence 1537, App
39	7	100.0	17	9	US-10-060-998-1538	Sequence 1538, App
40	7	100.0	17	9	US-10-060-998-1539	Sequence 1539, App
41	7	100.0	17	9	US-10-060-998-1540	Sequence 1540, App
42	7	100.0	17	9	US-10-060-998-1541	Sequence 1541, App
43	7	100.0	17	9	US-10-060-998-1542	Sequence 1542, App
44	7	100.0	17	9	US-10-060-998-1543	Sequence 1543, App
45	7	100.0	17	9	US-10-060-998-1544	Sequence 1544, App

ALIGNMENTS

RESULT 1

US-09-988-462-49
; Sequence 49, Application US/09988462
; Publication NO. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

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; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: 8-188051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-988-462-49

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 2
US-09-816-763-61
; Sequence 61, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
US-09-816-763-61

Query Match 100.0%; Score 7; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 1 GCTTCAG 7

RESULT 3
US-10-033-145-226/c
; Sequence 226, Application US/10033145
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
```

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; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-226

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 9 GCTTCAG 3

RESULT 4
US-10-033-145-1449/c
; Sequence 1449, Application US/10033145
; Patent No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1449

Query Match 100.0%; Score 7; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 10 GCTTCAG 4

RESULT 5
US-09-249-155-34/c
; Sequence 34, Application US/09249155
; Publication No. US20030037345A1
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155
; CURRENT FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: 60/074,737
; EARLIER FILING DATE: 1998-02-13
; EARLIER APPLICATION NUMBER: 60/097,937
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/102,051
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 34
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155-34

Query Match      100.0%; Score 7; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.8e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 10 GCTTCAG 4

RESULT 6
US-09-879-813-84/c
; Sequence 84, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (8)..(8)
; OTHER INFORMATION: F220
; OTHER INFORMATION: The sequence TGAGCTCTGTG is deleted
US-09-879-813-84

Query Match      100.0%; Score 7; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
    |||||
Db 7 GCTTCAG 1

RESULT 8
US-09-770-601-4
; Sequence 4, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/127,276
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: 60/054,730
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for PCR
US-09-770-601-4

Query Match      100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
    |||||
Db 7 GCTTCAG 13

RESULT 9
US-09-770-601-6/c
; Sequence 6, Application US/09770601
; Patent No. US20020104110A1
; GENERAL INFORMATION:
; APPLICANT: Lipes, Myra A.
; APPLICANT: Chen, Qian
; TITLE OF INVENTION: IMMUNOLOGICALLY PRIVILEGED CELLS AND
; FILE REFERENCE: 10276-015002
; CURRENT APPLICATION NUMBER: US/09/770,601
; CURRENT FILING DATE: 2001-01-26
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;; PRIOR APPLICATION NUMBER: 09/127,276
;; PRIOR FILING DATE: 1998-07-30
;; PRIOR APPLICATION NUMBER: 60/054,730
;; PRIOR FILING DATE: 1997-08-05
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 13
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: primer for PCR
US-09-770-601-6

Query Match 100.0%; Score 7; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.7e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 GCTTCAG 7
Db 7 GCTTCAG 1

RESULT 10
US-10-146-058-41/c
;; Sequence 41, Application US/10146058
;; Publication No. US20030040499A1
;; GENERAL INFORMATION:
;; APPLICANT: Schlingensiefen, Georg-Ferdinand
;; APPLICANT: Brysch, Wolfgang
;; APPLICANT: Schlingensiefen, Karl-Hermann
;; APPLICANT: Schlingensiefen, Reimar
;; APPLICANT: Bogdahn, Ulrich
;; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
;; NUMBER OF SEQUENCES: 137
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jacobson, Price, Holman & Stern
;; STREET: 400 Seventh St. N.W.
;; CITY: Washington D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/146,058
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/535,249
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93 107 089.0
;; FILING DATE: 30-APR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: EP 93 107 849.7
;; FILING DATE: 13-MAY-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Player, William E.
;; REGISTRATION NUMBER: 31,409
;; REFERENCE/DOCKET NUMBER: 10577/P58418
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)539-6666
;; TELEFAX: (202)393-5350
;; TELEX: RCA 248593 IDEA UR
;; INFORMATION FOR SEQ ID NO: 41:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 14 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: unknown

;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
;; ANTI-SENSE: YES
US-10-146-058-41
Query Match 100.0%; Score 7; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.7e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 GCTTCAG 7
Db 11 GCTTCAG 5

RESULT 11
US-10-146-575-21/c
;; Sequence 21, Application US/10146575
;; Publication No. US20030059800A1
;; GENERAL INFORMATION:
;; APPLICANT: Lichter, Jay
;; APPLICANT: Guido, Marco
;; TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
;; FILE REFERENCE: SEQ-12P
;; CURRENT APPLICATION NUMBER: US/10/146,575
;; PRIOR FILING DATE: 2002-05-14
;; PRIOR APPLICATION NUMBER: US/09/144,367
;; PRIOR FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 58
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 21
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: H. sapiens
US-10-146-575-21

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e+04; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

Qy 1 GCTTCAG 7
Db 8 GCTTCAG 2

RESULT 12
US-10-145-289-2
;; Sequence 2, Application US/10145289
;; Publication No. US20030077812A1
;; GENERAL INFORMATION:
;; APPLICANT: James G. McArthur
;; APPLICANT: Dale John Talbot
;; APPLICANT: Andrew D. Simmons
;; APPLICANT: Ryan McGuinness
;; APPLICANT: Michael Kelly
;; APPLICANT: Lisa V. Tsui
;; APPLICANT: Thomas Dull
;; TITLE OF INVENTION: LENTIVIRAL VECTORS ENCODING CLOTTING
;; FILE REFERENCE: 131.2USU1
;; CURRENT APPLICATION NUMBER: US/10/145,289
;; PRIOR FILING DATE: 2002-05-14
;; PRIOR APPLICATION NUMBER: 60/291,083
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 15
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: primer
US-10-145-289-2

Query Match 100.0%; Score 7; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 9 GCTTCAG 15

RESULT 13
US-09-922-261-10/c
; Sequence 10, Application US/09922261
; Patent No. US20020111471A1
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/922,261
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US/09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-922-261-10

Query Match 100.0%; Score 7; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 11 GCTTCAG 5

RESULT 14
US-10-146-058-39/c
; Sequence 39, Application US/10146058
; Publication No. US2003004099A1
; GENERAL INFORMATION:
; APPLICANT: Schlingsiepen, Georg-Ferdinand
; APPLICANT: Brysch, Wolfgang
; APPLICANT: Schlingsiepen, Karl-Hermann
; APPLICANT: Schlingsiepen, Reimar
; APPLICANT: Bogdahn, Ulrich
; TITLE OF INVENTION: Antisense-oligonucleotides for the treatment of
; TITLE OF INVENTION: immuno-suppressive effect of transforming-growth-factor beta
; NUMBER OF SEQUENCES: 137
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/146,058
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/535,249
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 089.0
; FILING DATE: 30-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93 107 849.7
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-10-146-058-39

Query Match 100.0%; Score 7; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 6.7e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 7 GCTTCAG 1

RESULT 15
US-09-879-813-51/c
; Sequence 51, Application US/09879813
; Patent No. US20020155453A1
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005
; CURRENT APPLICATION NUMBER: US/09/879,813
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 51
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(12)
; OTHER INFORMATION: D3
; OTHER INFORMATION: The sequence GACCC between positions 7 and 12 replace the sequence
; OTHER INFORMATION: e AGGACTGT
US-09-879-813-51

Query Match 100.0%; Score 7; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||

Fri Jun 27 07:41:14 2003

us-08-770-564a-12.oligo.rnpb

Page 6

Db 17 GCTTCAG 11

Search completed: June 23, 2003, 20:01:33
Job time : 56.251 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 10.9602 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	8	3 US-08-859-954-86	Sequence 86, Appl
2	7	100.0	10	1 US-08-235-503B-28	Sequence 28, Appl
3	7	100.0	10	1 US-07-951-715A-49	Sequence 49, Appl
4	7	100.0	10	2 US-08-459-448A-49	Sequence 49, Appl
5	7	100.0	10	3 US-08-899-786-10	Sequence 10, Appl
6	7	100.0	10	3 US-08-459-595A-49	Sequence 49, Appl
7	7	100.0	10	3 US-08-459-504B-49	Sequence 49, Appl
8	7	100.0	10	3 US-08-459-444-49	Sequence 49, Appl
9	7	100.0	10	4 US-09-424-518-1	Sequence 1, Appl
10	7	100.0	10	4 US-09-547-422-49	Sequence 49, Appl
11	7	100.0	10	5 PCT-US95-05265-28	Sequence 28, Appl
12	7	100.0	11	1 US-08-093-383-16	Sequence 16, Appl
13	7	100.0	11	2 US-08-811-949-9	Sequence 9, Appl
14	7	100.0	12	4 US-09-281-418-93	Sequence 93, Appl
15	7	100.0	12	4 US-09-404-430-3	Sequence 3, Appl
16	7	100.0	13	1 US-08-254-811D-10	Sequence 10, Appl
17	7	100.0	13	4 US-08-981-988A-39	Sequence 39, Appl
18	7	100.0	13	6 5182195-35	Patent No. 5182195
19	7	100.0	14	1 US-08-332-747-4	Sequence 4, Appl
20	7	100.0	14	1 US-08-332-747-12	Sequence 12, Appl
21	7	100.0	14	3 US-08-904-871-14	Sequence 14, Appl
22	7	100.0	14	4 US-08-535-249-41	Sequence 41, Appl
23	7	100.0	15	1 US-08-365-189-10	Sequence 10, Appl
24	7	100.0	15	1 US-08-311-760A-72	Sequence 72, Appl
25	7	100.0	15	1 US-08-311-760A-233	Sequence 233, Appl
26	7	100.0	15	1 US-08-363-240A-610	Sequence 610, Appl
27	7	100.0	15	1 US-08-471-033-34	Sequence 34, Appl

Query Match 100.0%; Score 7; DB 3; Length 8;

ALIGNMENTS

RESULT 1
US-08-859-954-86
; Sequence 86, Application US/08859954
; Patent No. 6083695
; GENERAL INFORMATION:
; APPLICANT: Hardin, Susan H.
; APPLICANT: Homayouni, Ramin
; APPLICANT: Hardin, Paul E.
; TITLE OF INVENTION: Design and Optimized Primer Library for
; TITLE OF INVENTION: Gene Sequencing and Method Thereof
; NUMBER OF SEQUENCES: 566
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 1301 McKinney, Suite 5100
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77010-3095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/859,954
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/632,782
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul, Thomas D.
; REGISTRATION NUMBER: 32,714
; REFERENCE/DOCKET NUMBER: D-5900
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713/651-5325
; TELEFAX: 713/651-5246
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ANTI-SENSE: YES

US-08-859-954-86

Query Match 100.0%; Score 7; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 3.6e+07;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 1 GCTTCAG 7

RESULT 2

US-08-235-503B-28
; Sequence 28, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,503B
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oeman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1389
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 28:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-235-503B-28

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 1 GCTTCAG 7

RESULT 3

US-07-951-715A-49
; Sequence 49, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Sptuill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
US-07-951-715A-49
Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 4
US-08-459-448A-49
; Sequence 49, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
US-08-459-448A-49

Query Match 100.0%; Score 7; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 5
US-08-899-786-10/c
Sequence 10, Application US/08899786
Patent No. 6001572
GENERAL INFORMATION:
APPLICANT: Toothman, Penelope
TITLE OF INVENTION: Method of Identifying Aloe Using
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,786
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,611
FILING DATE: 26-JULY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: UNI.07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-899-786-10

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 7 GCTTCAG 1

RESULT 6
US-08-459-595A-49
Sequence 49, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/459,595A
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; US-08-459-595A-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 7
US-08-459-504B-49
; Sequence 49, Application US/08459504B
; Patent No. 6073185
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/459,504B
; APPLICATION NUMBER: US/08/459,504B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer C1 - second half"
; HYPOTHETICAL: NO
; US-08-459-504B-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 8
US-08-459-444-49
; Sequence 49, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-JUN-1995

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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-08-459-444-49

Query Match 100.0%; Score 7; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 9
US-09-424-518-1/C
Sequence 1, Application US/09424518
Patent No. 6260034
GENERAL INFORMATION:
APPLICANT: Bjorkesten, Lennart
TITLE OF INVENTION: A Method and a System for Nucleic Acid Sequence Analysis
Patent No. 6260034
FILE REFERENCE: 45687-00004
CURRENT APPLICATION NUMBER: US/09/424,518
CURRENT FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: PCT/SE98/01005
PRIOR FILING DATE: 1998-05-27
PRIOR APPLICATION NUMBER: 9702008-5
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
US-09-424-518-1

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 8 GCTTCAG 2

RESULT 10
US-09-547-422-49
Sequence 49, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.

Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "primer C1 - second half"
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-09-547-422-49

Query Match 100.0%; Score 7; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
DB 2 GCTTCAG 8

RESULT 11
PCT-US95-05265-28
Sequence 28, Application PC/TUS9505265
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05265
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/235,503
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
PCT-US95-05265-28

Query Match 100.0%; Score 7; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 1 GCTTCAG 7

RESULT 12
US-08-093-383-16
Sequence 16, Application US/08093383
Patent No. 5489529
GENERAL INFORMATION:
APPLICANT: DeBoer, Herman A.
APPLICANT: Heyneker, Herbert L.
APPLICANT: Seeburg, Peter H.
TITLE OF INVENTION: DNA for Expression of Bovine Growth Hormone
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,383
FILING DATE: 14-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/619827
FILING DATE: 28-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/198824
FILING DATE: 05-APR-1988

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/632361
FILING DATE: 19-JUL-1984
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/303687
FILING DATE: 18-SEP-1981
ATTORNEY/AGENT INFORMATION:
NAME: Johnston, Sean A.
REGISTRATION NUMBER: P35,910
REFERENCE/DOCKET NUMBER: 46C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-093-383-16

Query Match 100.0%; Score 7; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 2 GCTTCAG 8

RESULT 13
US-08-811-949-9
Sequence 9, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE FLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "SYNTHETIC OLIGONUCLEOTIDE"
US-08-811-949-9

Query Match 100.0%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||
Db 2 GCTTCAG 8

RESULT 14

US-09-281-418-93
; Sequence 93, Application US/09281418
; Patent No. 6287769
; GENERAL INFORMATION:
; APPLICANT: Inoue, Takakazu
; TITLE OF INVENTION: Method of Amplifying DNA Fragment, Apparatus for Amplifying DNA F
; TITLE OF INVENTION: agment, Method of Assaying Microorganisms, Method of Analyzing Mi
; TITLE OF INVENTION: nisms and Method of Assaying Contaminant
; FILE REFERENCE: 9982-7
; CURRENT APPLICATION NUMBER: US/09/281,418
; CURRENT FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: JP/1998/87651
; EARLIER FILING DATE: 1998-03-31
; EARLIER APPLICATION NUMBER: JP/1999/69694
; EARLIER FILING DATE: 1999-03-16
; NUMBER OF SEQ ID NOS: 216
; SEQ ID NO 93
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-281-418-93

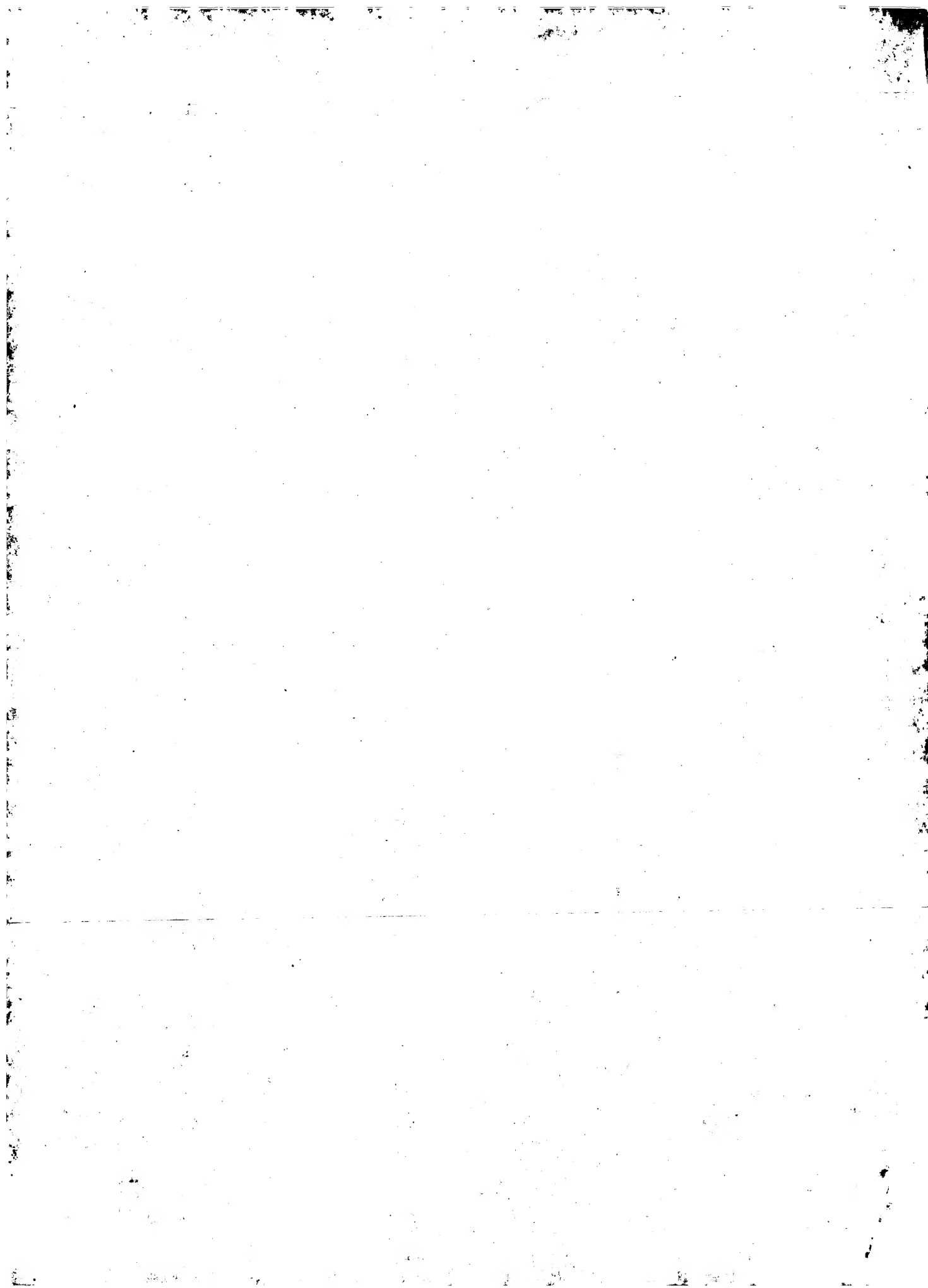
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QY 1 GCTTCAG 7
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Db 4 GCTTCAG 10

RESULT 15

US-09-404-430-3
; Sequence 3, Application US/09404430
; Patent No. 6350853
; GENERAL INFORMATION:
; APPLICANT: Neilsen, Peter
; APPLICANT: Knudsen, Helle
; TITLE OF INVENTION: Conjugated Peptide Nucleic Acids Having Enhanced
; TITLE OF INVENTION: Cellular Uptake
; FILE REFERENCE: ISIS4181
; CURRENT APPLICATION NUMBER: US/09/404,430
; CURRENT FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US08/564,765
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6350853el Sequence
US-09-404-430-3

Query Match 100.0%; Score 7; DB 4; Length 12;



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 46.5179 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
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Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	7	100.0	8	17	AAT09466
3	7	100.0	8	21	AAAB0773
4	7	100.0	10	19	AAV20924
5	7	100.0	10	21	AAAB0773
6	7	100.0	10	21	AAAB0773
7	7	100.0	10	21	AAZ77798
8	7	100.0	10	21	AAZ79021
9	7	100.0	10	21	AAZ82243
	7	100.0	10	21	AAZ83879

c 11	7	100.0	10	21	AAZ85548
c 12	7	100.0	10	22	AAF33630
c 13	7	100.0	10	22	AAF35902
c 14	7	100.0	10	22	AAF36192
c 15	7	100.0	10	22	AAF37634
c 16	7	100.0	10	22	AAF41438
c 17	7	100.0	10	22	AAF41439
c 18	7	100.0	10	24	ABK81943
c 19	7	100.0	10	24	ABA98387
c 20	7	100.0	10	24	ABA98387
c 21	7	100.0	10	24	ABK70549
c 22	7	100.0	10	24	ABL52257
c 23	7	100.0	10	24	ABL52262
c 24	7	100.0	10	24	ABK54423
c 25	7	100.0	10	24	ABK23504
c 26	7	100.0	10	24	ABL39540
c 27	7	100.0	11	20	ABZ18724
c 28	7	100.0	11	24	ABQ87385
c 29	7	100.0	11	24	ABZ18724
c 30	7	100.0	12	20	AAZ41732
c 31	7	100.0	12	21	AAA49912
c 32	7	100.0	12	22	AAI99755
c 33	7	100.0	12	22	AAI99755
c 34	7	100.0	12	22	AAI99755
c 35	7	100.0	13	17	AAT12072
c 36	7	100.0	13	20	AAI99755
c 37	7	100.0	13	21	AAI99755
c 38	7	100.0	13	21	AAI99755
c 39	7	100.0	14	15	AAQ78392
c 40	7	100.0	14	21	AAI99755
c 41	7	100.0	14	21	AAI99755
c 42	7	100.0	15	16	AAQ90627
c 43	7	100.0	15	17	AAI99755
c 44	7	100.0	15	17	AAI99755
c 45	7	100.0	15	17	AAI99755

ALIGNMENTS

RESULT 1
AAT09588
ID AAT09588 standard; DNA; 8 BP.
AC AAT09588;
XX
XX
DT 25-JUN-1996 (first entry)
DE 3'-primer used for characterisation of human biological samples.
DE 3'-primer; human; protein coding region; PCR primer kit;
KW characterisation; biological samples; PCR amplification; indexing;
KW identification; cloning; analysis; genes; genome mapping;
KW disease diagnosis; ss.
OS Synthetic.
XX
XX WO9531574-A1.
XX
PD 23-NOV-1995.
XX
PF 12-MAY-1995; 95WO-US06032.
XX
PR 16-MAY-1994; 94US-0242887.
XX
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
XX
PI Lopez-Nieto CE, Nigam SK;
XX
DR WPI; 1996-010958/01.
XX
PT Characterisation of nucleotide sequences using primer pairs - by PCR

Metastatic breast
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Yeast NORF gene SA
Human CYP27A1 gene
SCN2B gene polymor
SCN2B gene polymor
Human G protein-co
Human PHK2 prefer
Human PHK2 prefer
Human ISL1 gene AS
Transcript tag DNA
Human ETEB primer-
Murine C57BL/6 SAG
Human skin stress/
Human bax CCGGG m
Microbe detection
Organic material d
Pig costimulatory
Microbial SSC-PCR
Oligonucleotide de
Primer used to ill
PCR primer, B13, u
PCR primer H-AP34.
TdT-expressing Ram
Human p-Liv PCR pr
Antisense oligonuc
Oestrogen receptor
Oestrogen receptor
GnRH(His5, Trp7, Tyr
Mouse B7-2 hamsterh
Mouse B7-1 hamsterh
Mouse B7-1 hamsterh

PT amplification and indexing of amplification prods. w.r.t. primers
 PT used for genome mapping and disease diagnosis
 PS Disclosure, Page 19; 72pp; English.
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
 CC target human protein coding regions, together comprise a PCR primer
 CC kit with 1361 possible primer pairs. The kit is used in a new method
 CC for the characterisation of nucleic acid sequences obtd. from human
 CC biological samples, which comprises PCR amplification and indexing of
 CC the prods. w.r.t the primer pair that hybridised to its delineating
 CC subsequences. The method may be used in the identification, cloning
 CC and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis.
 XX
 SQ Sequence 8 BP; 1 A; 3 C; 2 G; 2 T; 0 other;
 Query Match 100.0%; Score 7; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 DB 1 GCTTCAG 7
 RESULT 2
 AAT09466/c
 ID AAT09466 standard; DNA; 8 BP.
 XX
 AC AAT09466;
 XX
 DT 21-JUN-1996 (first entry)
 DE
 DE 5'-primer used for characterisation of human biological samples.
 XX
 XX 5'-primer; human; protein coding region; PCR primer kit;
 KW Characterisation; Biological samples; PCR amplification; indexing;
 KW identification; cloning; analysis; genes; genome mapping;
 KW disease diagnosis; ss.
 XX
 OS Synthetic.
 XX
 XX WO9531574-A1.
 PN
 XX
 XX 23-NOV-1995.
 PD
 XX
 PF 12-MAY-1995; 95WO-US06032.
 XX
 PR 16-MAY-1994; 94US-0242887.
 XX
 XX (BGHM) BRIGHAM & WOMENS HOSPITAL.
 XX
 XX Lopez-Nieto CE, Nigam SK;
 PI
 PI WPI; 1996-010958/01.
 DR
 XX
 PT Characterisation of nucleotide sequences using primer pairs - by PCR
 PT amplification and indexing of amplification prods. w.r.t. primers
 PT used for genome mapping and disease diagnosis
 PS
 PS Claim 5; Page 44; 72pp; English.
 XX
 CC The 5'-primers AAT09358-508, and the 3'-primers AAT09509-659, which
 CC target human protein coding regions, together comprise a PCR primer
 CC kit with 1361 possible primer pairs. The kit is used in a new method
 CC for the characterisation of nucleic acid sequences obtd. from human
 CC biological samples, which comprises PCR amplification and indexing of
 CC the prods. w.r.t the primer pair that hybridised to its delineating
 CC subsequences. The method may be used in the identification, cloning
 CC and analysis of genes, e.g. in genome mapping, and disease
 CC diagnosis.
 XX

SQ Sequence 8 BP; 2 A; 2 C; 3 G; 1 T; 0 other;
 Query Match 100.0%; Score 7; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 DB 8 GCTTCAG 2
 RESULT 3
 AAA80773
 ID AAA80773 standard; DNA; 8 BP.
 XX
 AC AAA80773;
 XX
 DT 24-NOV-2000 (first entry)
 DE A. thaliana primer walking octamer SEQ ID NO: 86.
 DE
 DE Primer walking; octamer; primer; DNA sequencing; PCR; ss.
 KW Arabidopsis thaliana.
 OS
 OS US6083695-A.
 PN
 XX
 PD 04-JUL-2000.
 XX
 PF 21-MAY-1997; 97US-0859954.
 XX
 PR 15-APR-1996; 96US-0632782.
 XX
 XX (UVHO-) UNIV HOUSTON.
 PA (HARD/) HARDIN S H.
 XX
 PI Hardin PE, Hardin SH, Homayouni R;
 XX
 DR WPI; 2000-474852/41.
 XX
 PT Sequencing an unknown DNA molecule for the polymerase chain reaction
 PT and other primer processes comprises primer walking of octamer
 PT oligonucleotides -
 PT
 XX
 XX Example 8; Column 67-68; 161pp; English.
 PS
 CC This invention describes a novel method for sequencing an unknown DNA
 CC molecule which comprises selecting a library primer from an octamer
 CC oligonucleotide library consisting of 48 8-bp sequences and
 CC corresponding complementary sequences, where the library primer is
 CC complementary to a known sequence adjacent to the unknown sequence or
 CC is complementary to a sequence in a known extension product. The method
 CC is useful for DNA nucleotide sequencing, in PCR, and in other processes
 CC which make use of primers. The octamers are used to identify coding
 CC sequences. Primer walking using the octamer libraries is advantageous
 CC over other sequencing methods because it does not require multiple
 CC cloning steps nor subsequent template preparations, and it is a
 CC directed and methodical approach. AAA80698-A81253 represent the octamer
 CC primers used in the primer walking method of the invention.
 XX
 SQ Sequence 8 BP; 2 A; 2 C; 2 G; 2 T; 0 other;
 Query Match 100.0%; Score 7; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.6e+08;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 DB 1 GCTTCAG 7
 RESULT 4
 AAV20924/c

ID AAV20924 standard; DNA; 10 BP.
 XX
 AC AAV20924;
 XX
 DT 07-JUL-1998 (first entry)
 XX
 DE Aloc specific universal PCR primer OPAB-10.
 XX
 KW Aloc; detection; identification; PCR primer; antioxidant;
 KW differentiation; anti-tumour; anti-diabetic; tyrosine inhibiting; ss.
 XX
 OS Synthetic.
 OS Aloc sp.
 XX
 PN WO9804741-A1.
 XX
 PD 05-FEB-1998.
 XX
 PF 24-JUL-1997; 97WO-US13001.
 XX
 PR 26-JUL-1996; 96US-0022611.
 XX
 PA (UNIV-) UNIVERA PHARM INC.
 XX
 PI Toothman P;
 XX
 DR WPI; 1998-159152/14.
 XX
 PT Detection and assay of Aloe - by extraction of DNA from a sample and
 PT amplification by polymerase chain reaction using primers specific
 PT for Aloe.
 XX
 PS Claim 3; Page 15; 37pp; English.
 XX
 CC The present sequence represents an Aloe specific universal PCR primer
 CC from the present invention. The present invention describes a method for
 CC identifying Aloe using polymerase chain reaction (PCR). The method
 CC comprises: (a) extracting DNA from a sample containing Aloe; (b)
 CC amplifying the DNA using PCR, and (c) comparing the sequence of the
 CC amplified DNA obtained from PCR with the sequence of DNA obtained from
 CC a known sample of Aloe. Also described are: (1) a nucleotide sequence
 CC comprising sequences given in the specification or a fragment; (2) a
 CC method for differentiating between different species of Aloe comprising:
 CC (a) extracting DNA from an unknown sample containing Aloe, and (b)
 CC amplifying the DNA by PCR using primers specific for a particular
 CC species of Aloe, and (3) a method for determining the amount of Aloe
 CC present in a mixture comprising: (a) extracting DNA from an unknown
 CC sample with internal controls for recovery of DNA, and (b) simultaneous
 CC amplification of DNA with primers specific to a particular Aloe species
 CC and amplification of non-homologous DNA added to a sample to internally
 CC quantify the amplification. The methods can be used for detecting and
 CC assaying Aloe in samples and for differentiating between different
 CC species of Aloe. The Aloe compounds have diverse biological activities,
 CC including anti-tumour activity, anti-acid activity, anti-diabetic
 CC activity, tyrosine inhibiting activity and antioxidant activity.
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;
 Query Match 100.0%; Score 7; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 Db 7 GCTTCAG 1
 RESULT 5
 AAA95165/c
 ID AAA95165 standard; DNA; 10 BP.
 XX
 AC AAA95165;
 XX

DT 12-JAN-2001 (first entry)
 XX
 DE Primer #12 for detection of TNFR1 polymorphism by primer extension.
 XX
 KW TNFR1; tumour necrosis factor receptor; polymorphism; human;
 KW tumour; cancer; apoptosis; bacterial infection; primer;
 KW primer extension; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200050436-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 23-FEB-2000; 2000WO-US04606.
 XX
 PR 23-FEB-1999; 99US-0121314.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA (NAND/) NANDABALAN K.
 PA (SCHU/) SCHULZ V P.
 PA (STEP/) STEPHENS J C.
 PA (CHEW/) CHEW A.
 XX
 PI Nandabalan K, Schulz VP, Stephens JC, Chew A;
 XX
 DR WPI; 2000-543909/49.
 XX
 PT Polynucleotides comprising polymorphic variants of a reference sequence
 PT for tumour necrosis factor receptor 1 (TNFR1), useful for studying the
 PT biological function of TNFR1 and identifying drugs targeting the
 PT protein for treating disorders -
 XX
 PS Claim 15; Page 21; 79pp; English.
 XX
 CC The present invention relates to polymorphic variants of the tumour
 CC necrosis factor receptor 1 (TNFR1) gene. The sequence of the gene is
 CC given in AAA95102, AAA95103 and AAA95104. The polymorphisms were
 CC identified by amplifying and sequencing regions of the gene. Twelve
 CC polymorphic loci were discovered. Of these twelve polymorphisms, four can
 CC cause a change in the TNFR1 protein. The present sequence is the
 CC terminal sequence of a primer used for detection of a TNFR1 gene
 CC polymorphism by primer extension. The TNFR1 polymorphisms may be useful
 CC for studying the biological function of TNFR1 as well as for
 CC identifying drugs targeting the protein for treatment of disorders
 CC related to its abnormal expression or function such as tumours,
 CC apoptosis related disorders and bacterial infection.
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;
 Query Match 100.0%; Score 7; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 Db 9 GCTTCAG 3
 RESULT 6
 AAZ77798/c
 ID AAZ77798 standard; DNA; 10 BP.
 XX
 AC AAZ77798;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:226.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX OS Homo sapiens.
 XX PN WO9965924-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US13800.
 XX PR 19-JUN-1998; 98US-0089833.
 XX PR 19-JUN-1998; 98US-0089844.
 XX PR 19-JUN-1998; 98US-0089853.
 XX PR 19-JUN-1998; 98US-0089878.
 XX PR 19-JUN-1998; 98US-0089991.
 XX PR 19-JUN-1998; 98US-0089992.
 XX PR 19-JUN-1998; 98US-0089993.
 XX PR 19-JUN-1998; 98US-0089994.
 XX PR 19-JUN-1998; 98US-0089997.
 XX PR 19-JUN-1998; 98US-0089999.
 XX PR 19-JUN-1998; 98US-0090000.
 XX PR 19-JUN-1998; 98US-0090036.
 XX PR 19-JUN-1998; 98US-0090039.
 XX PR 19-JUN-1998; 98US-0090040.
 XX PR 19-JUN-1998; 98US-0090041.
 XX PR 19-JUN-1998; 98US-0090042.
 XX PR 19-JUN-1998; 98US-0090043.
 XX PR 19-JUN-1998; 98US-0090044.
 XX PR 19-JUN-1998; 98US-0090045.
 XX PR 19-JUN-1998; 98US-0090047.
 XX PR 19-JUN-1998; 98US-0090048.
 XX PR 19-JUN-1998; 98US-0090072.
 XX PR 19-JUN-1998; 98US-0090076.
 XX PR 19-JUN-1998; 98US-0090077.
 XX PR 19-JUN-1998; 98US-0090078.
 XX PR 19-JUN-1998; 98US-0090079.
 XX PR 08-DEC-1998; 98US-0111715.
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX PI Roberts BL, Shankara S;
 XX WPI; 2000-106077/09.
 XX Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer -
 XX Claim 1; Page 70; 130pp; English.
 XX Sequences AA27573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding or immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that can lyse the tumour cells; immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (TILs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal

CC expression of these genes. Detection of the dendritic cell
 CC differentially expressed genes, or of their encoded proteins, can be used
 CC to identify cells as belonging to the monocyte lineage. Cells containing
 CC these genes can be used in active immunotherapy (or to stimulate
 CC production of a population of antigen-specific effector cells) and
 CC vectors containing them are used in gene therapy. Co-administration of
 CC tumour antigens and APC-associated costimulatory factors ensures adequate
 CC antigen presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells.
 XX Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 other;
 SQ Query Match 100.0%; Score 7; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.6e+04; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 GCCTCAG 7
 DB 9 GCCTCAG 3
 RESULT 7
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 ID AA279021 standard; DNA; 10 BP.
 XX AC AA279021;
 XX DT 10-APR-2000 (first entry)
 XX DE Human dendritic cell SAGE tag, SEQ ID NO.1449.
 XX KW SAGE tag; serial analysis of gene expression, antigen-presenting cell;
 XX KW APC, monocyte-derived dendritic cell; differential gene expression;
 XX KW immunostimulatory cofactor; costimulatory factor; CTL; anticancer; ss.
 XX KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy;
 XX OS Homo sapiens.
 XX PN WO9965924-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US13800.
 XX PR 19-JUN-1998; 98US-0089833.
 XX PR 19-JUN-1998; 98US-0089844.
 XX PR 19-JUN-1998; 98US-0089853.
 XX PR 19-JUN-1998; 98US-0089878.
 XX PR 19-JUN-1998; 98US-0089991.
 XX PR 19-JUN-1998; 98US-0089992.
 XX PR 19-JUN-1998; 98US-0089993.
 XX PR 19-JUN-1998; 98US-0089994.
 XX PR 19-JUN-1998; 98US-0089997.
 XX PR 19-JUN-1998; 98US-0090000.
 XX PR 19-JUN-1998; 98US-0090035.
 XX PR 19-JUN-1998; 98US-0090036.
 XX PR 19-JUN-1998; 98US-0090039.
 XX PR 19-JUN-1998; 98US-0090040.
 XX PR 19-JUN-1998; 98US-0090041.
 XX PR 19-JUN-1998; 98US-0090042.
 XX PR 19-JUN-1998; 98US-0090043.
 XX PR 19-JUN-1998; 98US-0090044.
 XX PR 19-JUN-1998; 98US-0090045.
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 XX PR 19-JUN-1998; 98US-0090077.
 XX PR 19-JUN-1998; 98US-0090078.
 XX PR 19-JUN-1998; 98US-0090079.

```
PR 19-JUN-1998; 98US-0090080.
XX 08-DEC-1998; 98US-01111715.
XX (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
XX cells, useful in gene vaccines against cancer -
XX
XX Claim 1; Page 106; 130pp; English.
XX
XX Sequences AA277573-279709 represent SAGE (serial analysis of gene
XX expression) tags used to identify mRNA transcripts encoding
XX immunostimulatory cofactor proteins which are preferentially or
XX differentially expressed in monocyte-derived dendritic cells compared
XX with monocytes. Some of the transcripts correspond to known genes or
XX ESTs (expressed sequence tags) which were previously unknown to be
XX preferentially or differentially expressed in dendritic cells, while
XX other transcripts correspond to novel genes. Antigen-presenting cell
XX (APC)-associated costimulatory factors play an important role in the
XX activation of the cytotoxic immune response, particularly against tumour
XX cells. Tumour antigen presentation via the MHC (major histocompatibility
XX complex) and subsequent recognition by T-cell receptors is alone
XX insufficient to activate a robust cytotoxic immune response that can
XX lyse the tumour cells. Immunostimulatory cofactors also being required
XX for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX sequences identified using the SAGE tags have several potential uses.
XX They may be used in vaccines to induce an immune response, particularly
XX against a tumour antigen; to modulate the genotype of an APC; to screen
XX for agents that modulate expression of differentially expressed genes in
XX an APC; and as hybridisation probes/amplification primers for the
XX diagnosis, prognosis and monitoring of diseases related to abnormal
XX expression of these genes. Detection of the dendritic cell
XX differentially expressed genes, or of their encoded proteins, can be used
XX to identify cells as belonging to the monocyte lineage. Cells containing
XX these genes can be used in active immunotherapy (or to stimulate
XX production of a population of antigen-specific effector cells) and
XX vectors containing them are used in gene therapy. Co-administration of
XX tumour antigens and APC-associated costimulatory factors ensures adequate
XX antigen presentation to endogenous APCs and upregulates the APCs for the
XX presentation of co-stimulatory signals, migration to T cell-rich sites,
XX secretion of T cell growth factors and secretion of chemokines for
XX recruitment of immune effector cells.
XX
XX Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;
XX
XX Query Match 100.0%; Score 7; DB 21; Length 10;
XX Best Local Similarity 100.0%; Pred No. 9.6e+04;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTCAG 7
XX |||||
XX 10 GCTTCAG 4
XX
XX RESULT 8
XX AA282243/c
XX ID AA282243 standard; DNA; 10 BP.
XX AC AA282243;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #1477.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX non-metastatic breast tumour tissue; gene therapy; anticancer;
XX antimetastatic; vaccine; diagnosis; ss.
XX
```

```
XX OS Homo sapiens.
XX
XX PN WO9965928-A2.
XX
XX PD 23-DEC-1999.
XX
XX PF 18-JUN-1999; 99WO-US13647.
XX
XX PR 19-JUN-1998; 98US-0089853.
XX PR 19-JUN-1998; 98US-0089997.
XX PR 19-JUN-1998; 98US-0090039.
XX PR 19-JUN-1998; 98US-0090040.
XX PR 19-JUN-1998; 98US-0090041.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
XX Isolated polynucleotides differentially expressed between metastatic
XX and non-metastatic breast cancer cells, useful for diagnosis,
XX prevention and treatment of cancer -
XX
XX Claim 1; Page 98; 219pp; English.
XX
XX AA280767 to AA283941 represent tags corresponding to distinct
XX transcripts that are preferentially transcribed in the metastatic breast
XX tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
XX AA283942 to AA286677 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the primary or non-metastatic
XX breast tumour tissue (i.e. are downregulated in metastatic breast tumour
XX cells). These transcripts can be used for diagnosis, prognosis,
XX monitoring and treatment of breast cancer, particularly where metastatic.
XX Diagnosis is by standard immunoassays or hybridisation/amplification
XX reactions. Compounds that modulate expression of the transcripts are
XX potentially useful for treatment of (metastatic) breast cancer, while
XX promoters from the transcripts are used to direct expression, in selected
XX cell types, of e.g. therapeutic genes (also ribozymes or antisense
XX sequences), particularly an antigen-encoding sequence for use in gene or
XX cell-based vaccines. Polypeptides encoded by the transcripts are also
XX useful in vaccines; for diagnosing breast cancer and for raising
XX specific antibodies (Ab). Ab are used to detect the polypeptides or as
XX therapeutic agents. Host cells that produce the polypeptides can be used
XX to expand and isolate populations of educated, antigen-specific immune
XX effector cells, e.g. cytotoxic T lymphocytes, and these used for
XX adoptive immunotherapy.
XX
XX Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 other;
XX
XX Query Match 100.0%; Score 7; DB 21; Length 10;
XX Best Local Similarity 100.0%; Pred No. 9.6e+04;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GCTTCAG 7
XX |||||
XX 9 GCTTCAG 3
XX
XX Db
XX
XX RESULT 9
XX AA283879
XX ID AA283879 standard; DNA; 10 BP.
XX AC AA283879;
XX
XX 07-APR-2000 (first entry)
XX
XX Metastatic breast tumour cell upregulated transcript tag #3113.
XX
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
XX
```

KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US13647.
 XX 19-JUN-1998; 98US-0089853.
 XX 19-JUN-1998; 98US-0089897.
 XX 19-JUN-1998; 98US-0090039.
 XX 19-JUN-1998; 98US-0090040.
 XX 19-JUN-1998; 98US-0090041.
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX Claim 1; Page 142; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 XX Sequence 10 BP; 2 A; 2 C; 3 G; 3 T; 0 other;
 SQ Query Match 100.0%; Score 7; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 |||||
 Db 3 GCTTCAG 9

RESULT 10
 AAZ85548
 ID AAZ85548 standard; DNA; 10 BP.
 XX
 AC AAZ85548;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #4782.

XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US13647.
 XX 19-JUN-1998; 98US-0089853.
 XX 19-JUN-1998; 98US-0089897.
 XX 19-JUN-1998; 98US-0090039.
 XX 19-JUN-1998; 98US-0090040.
 XX 19-JUN-1998; 98US-0090041.
 XX (GENZ) GENZYME CORP.
 XX (ROBE/) ROBERTS B L.
 XX (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 XX WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic
 PT and non-metastatic breast cancer cells, useful for diagnosis,
 PT prevention and treatment of cancer -
 XX Claim 1; Page 186; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct
 CC transcripts that are preferentially transcribed in the metastatic breast
 CC tumour tissue (i.e. are upregulated in metastatic breast tumour cells).
 CC AAZ83942 to AAZ86677 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the primary or non-metastatic
 CC breast tumour tissue (i.e. are downregulated in metastatic breast tumour
 CC cells). These transcripts can be used for diagnosis, prognosis
 CC monitoring and treatment of breast cancer, particularly where metastatic.
 CC Diagnosis is by standard immunoassays or hybridisation/amplification
 CC reactions. Compounds that modulate expression of the transcripts are
 CC potentially useful for treatment of (metastatic) breast cancer, while
 CC promoters from the transcripts are used to direct expression, in selected
 CC cell types, of e.g. therapeutic genes (also ribozymes or antisense
 CC sequences), particularly an antigen-encoding sequence for use in gene or
 CC cell-based vaccines. Polypeptides encoded by the transcripts are also
 CC useful in vaccines; for diagnosing breast cancer and for raising
 CC specific antibodies (Ab). Ab are used to detect the polypeptides or as
 CC therapeutic agents. Host cells that produce the polypeptides can be used
 CC to expand and isolate populations of educated, antigen-specific immune
 CC effector cells, e.g. cytotoxic T lymphocytes, and these used for
 CC adoptive immunotherapy.
 XX Sequence 10 BP; 1 A; 2 C; 4 G; 3 T; 0 other;
 SQ Query Match 100.0%; Score 7; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.6e+04;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 |||||
 Db 1 GCTTCAG 7

RESULT 11
 AAF33630/C
 ID AAF33630 standard; DNA; 10 BP.
 XX
 AC AAF33630;
 XX
 DT 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:369.
DE
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Claim 1; Page 388; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
XX invention.
XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTCAG 7
DB 7 GCTTCAG 1
RESULT 12
AAF35902/c
ID AAF35902 standard; DNA; 10 BP.

XX AAF35902;
AC
XX 23-MAR-2001 (first entry)
DT
XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2641.
DE
XX
KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
XX WO200077214-A2.
XX
XX 21-DEC-2000.
XX
XX 14-JUN-2000; 2000WO-US16223.
XX
XX 16-JUN-1999; 99US-0335032.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 94; 419pp; English.
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present
XX invention.
XX Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 other;
SQ
Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GCTTCAG 7
DB 7 GCTTCAG 1

RESULT 13
AAF36192 ID AAF36192 standard; DNA; 10 BP.
XX AC AAF36192;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:2931.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US16223.
XX PR 16-JUN-1999; 99US-0335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis
XX PT of gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle -
XX PS Example; Page 104; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a
XX CC yeast cell; and (b) monitoring expression of a NORF gene whose
XX CC expression varies as in M1, where a test substance which modifies the
XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method
XX CC (M3) for identifying human genes which are involved in cell cycle
XX CC progression comprising contacting human DNA with a probe which comprises
XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
XX CC member of a class of drugs having a characteristic effect on gene
XX CC expression in a yeast cell comprising contacting a yeast cell with a
XX CC candidate drug and monitoring expression in the yeast cell of at least 1
XX CC NORF gene whose expression is affected by the class of drugs. The NORF
XX CC genes may be used to study, monitor and affect phases of the cell cycle,
XX CC the differentially expressed genes may be used as markers of phases of
XX CC the cell cycle. The methods may be used to identify candidate drugs which
XX CC affect the cell cycle and for identification of antifungal drugs.
XX CC AAF3268 to AAF4064 represent SAGE tags used in the exemplification of
XX CC the present invention. AAF3262 to AAF3267 represent linkers and PCR
XX CC primers used in the SAGE method, in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 BP; 3 A; 2 C; 2 G; 3 T; 0 other;
Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. NO. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTTCAG 7
DB |||||
4 GCTTCAG 10
RESULT 14
AAF37634/C
ID AAF37634 standard; DNA; 10 BP.
XX AC AAF37634;
XX DT 23-MAR-2001 (first entry)
XX DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:4373.
XX KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
XX KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
XX KW serial analysis of gene expression; antifungal; tag; identification;
XX KW linker; PCR primer; ds.
XX OS Saccharomyces cerevisiae.
XX PN WO200077214-A2.
XX PD 21-DEC-2000.
XX PF 14-JUN-2000; 2000WO-US16223.
XX PR 16-JUN-1999; 99US-0335032.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Velculescu V, Vogelstein B, Kinzler K;
XX DR WPI; 2001-061874/07.
XX PT Yeast gene coding sequences comprising NORF genes with serial analysis
XX PT of gene expression (SAGE) tags, useful for studying, monitoring and
XX PT affecting phases of the cell cycle -
XX PS Example; Page 156; 419pp; English.
XX CC The present invention describes an isolated DNA molecule comprising a
XX CC coding sequence of a yeast gene selected from a group of 745 NORF (not
XX CC previously assigned open reading frame; or nonannotated ORF) genes
XX CC comprising a SAGE (serial analysis of gene expression) tag. Also
XX CC described are: (1) a method (M1) of using NORF genes to affect the cell
XX CC cycle comprising administering a NORF gene whose expression varies by at
XX CC least 10% between any two phases of the cell cycle selected from log
XX CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
XX CC antifungal drugs comprising: (a) contacting a test substance with a
XX CC yeast cell; and (b) monitoring expression of a NORF gene whose
XX CC expression varies as in M1, where a test substance which modifies the
XX CC expression of the yeast gene is a candidate antifungal drug; (3) a method
XX CC (M3) for identifying human genes which are involved in cell cycle
XX CC progression comprising contacting human DNA with a probe which comprises
XX CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
XX CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
XX CC member of a class of drugs having a characteristic effect on gene
XX CC expression in a yeast cell comprising contacting a yeast cell with a
XX CC candidate drug and monitoring expression in the yeast cell of at least 1
XX CC NORF gene whose expression is affected by the class of drugs. The NORF
XX CC genes may be used to study, monitor and affect phases of the cell cycle,
XX CC the differentially expressed genes may be used as markers of phases of
XX CC the cell cycle. The methods may be used to identify candidate drugs which
XX CC affect the cell cycle and for identification of antifungal drugs.
XX CC AAF3268 to AAF4064 represent SAGE tags used in the exemplification of
XX CC the present invention. AAF3262 to AAF3267 represent linkers and PCR
XX CC primers used in the SAGE method, in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 BP; 3 A; 2 C; 3 G; 2 T; 0 other;

Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

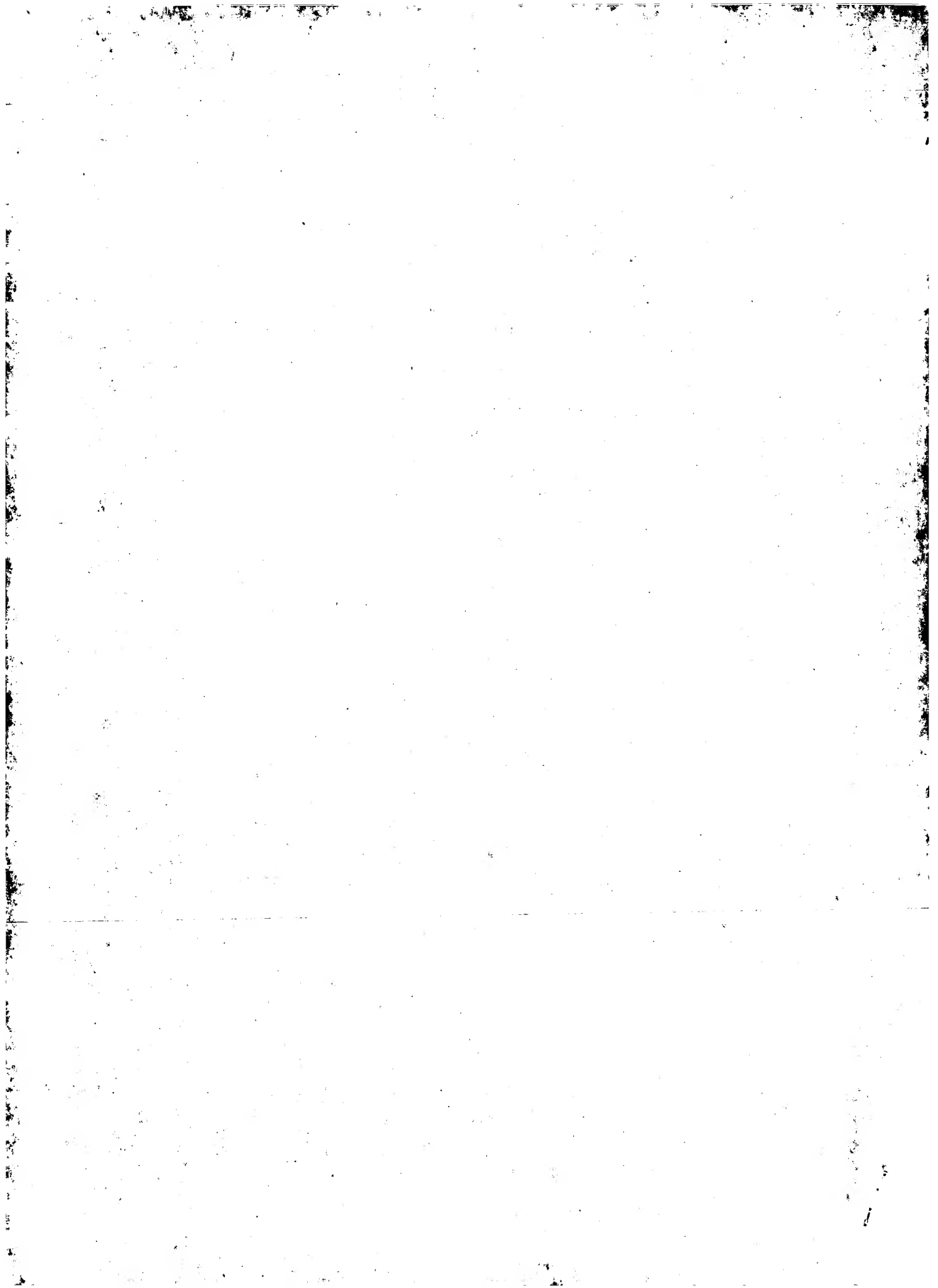
QY 1 GCTTCAG 7
Db 9 GCTTCAG 3

RESULT 15
AAF41438/c
ID AAF41438 standard; DNA; 10 BP.
XX AAF41438;
AC AAF41438;
XX 23-MAR-2001 (first entry)
DT Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8177.
DE
XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
XX Saccharomyces cerevisiae.
OS
XX WO200077214-A2.
FN
XX 21-DEC-2000.
PD
XX 14-JUN-2000; 2000WO-US16223.
PF
XX 16-JUN-1999; 99US-0335032.
PR
XX (UYJO) UNIV JOHNS HOPKINS.
PA
XX Velculescu V, Vogelstein B, Kinzler K;
PI
XX WPI; 2001-061874/07.
DR
XX
XX
XX Yeast gene coding sequences comprising NORF genes with serial analysis
PT of gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle -
XX
XX Example; Page 292; 419pp; English.
PS
XX
XX The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a
CC yeast cell; and (b) monitoring expression of a NORF gene whose
CC expression varies as in M1, where a test substance which modifies the
CC expression of the yeast gene is a candidate antifungal drug; (3) a method
CC (M3) for identifying human genes which are involved in cell cycle
CC progression comprising contacting human DNA with a probe which comprises
CC at least 10 contiguous nucleotides of a NORF gene whose expression varies
CC as in M1; and (4) a method (M4) for identifying a candidate drug as a
CC member of a class of drugs having a characteristic effect on gene
CC expression in a yeast cell comprising contacting a yeast cell with a
CC candidate drug and monitoring expression in the yeast cell of at least 1
CC NORF gene whose expression is affected by the class of drugs. The NORF
CC genes may be used to study, monitor and affect phases of the cell cycle,
CC the differentially expressed genes may be used as markers of phases of
CC the cell cycle. The methods may be used to identify candidate drugs which
CC affect the cell cycle and for identification of antifungal drugs.
CC AAF33268 to AAF44064 represent SAGE tags used in the exemplification of
CC the present invention. AAF33262 to AAF33267 represent linkers and PCR
CC primers used in the SAGE method, in the exemplification of the present

CC invention.
XX
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 other;
Query Match 100.0%; Score 7; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
Db 7 GCTTCAG 1

Search completed: June 23, 2003, 05:43:40
Job time : 47.8256 secs



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 81.4064 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-12
Perfect score: 7
Sequence: 1 GCTTCAG 7

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 2: gb.htg.*
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- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.mam.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7	100.0	10	6	AR029539	AR029539 Sequence
2	7	100.0	10	6	AR093732	AR093732 Sequence
3	7	100.0	10	6	AR098492	AR098492 Sequence
4	7	100.0	10	6	AR162919	AR162919 Sequence
5	7	100.0	10	6	AX301417	AX301417 Sequence
6	7	100.0	10	6	AX377325	AX377325 Sequence
7	7	100.0	10	6	AX441418	AX441418 Sequence
8	7	100.0	10	6	AX453914	AX453914 Sequence
9	7	100.0	10	6	I41452	I41452 Sequence 49
10	7	100.0	10	6	A27401	A27401 Oligonucleo
11	7	100.0	10	6	AR059962	AR059962 Sequence
12	7	100.0	10	6	AX339224	AX339224 Sequence
13	7	100.0	10	6	AX471563	AX471563 Sequence
14	7	100.0	10	6	HSOLIGON	A22481 oligonucleo
15	7	100.0	10	6	I17488	I17488 Sequence 16
16	7	100.0	10	6	AR167729	AR167729 Sequence
17	7	100.0	10	6	AR195296	AR195296 Sequence
18	7	100.0	10	6	AX027028	AX027028 Sequence
19	7	100.0	10	6	E29613	E29613 Method for
20	7	100.0	10	6	E38719	E38719 Method and
21	7	100.0	10	6	E64145	E64145 Method for
22	7	100.0	10	9	S57113S2	S57114 NF-kappa B
23	7	100.0	10	6	A11076	A11076 Oligonucleo
24	7	100.0	10	6	A59446	A59446 Sequence 39
25	7	100.0	10	6	AR013809	AR013809 Sequence
26	7	100.0	10	6	AR182199	AR182199 Sequence
27	7	100.0	10	6	AX003113	AX003113 Sequence
28	7	100.0	10	6	AX146661	AX146661 Sequence
29	7	100.0	10	6	A40504	A40504 Sequence 41
30	7	100.0	10	6	A44356	A44356 Sequence 4
31	7	100.0	10	6	A89031	A89031 Sequence 11
32	7	100.0	10	6	AX316400	AX316400 Sequence
33	7	100.0	10	6	BD005920	BD005920 Phytoflu
34	7	100.0	10	6	I95576	I95576 Sequence 4
35	7	100.0	10	6	I95584	I95584 Sequence 12
36	7	100.0	10	6	A04761	A04761 Oligonucleo
37	7	100.0	10	6	A11089	A11089 Oligonucleo
38	7	100.0	10	6	A11280	A11280 oligonucleo
39	7	100.0	10	6	A35086	A35086 Synthetic I
40	7	100.0	10	6	A64168	A64168 Sequence 34
41	7	100.0	10	6	A68354	A68354 Sequence 34
42	7	100.0	10	6	A88036	A88036 Sequence 18
43	7	100.0	10	6	A90003	A90003 Sequence 18
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45	7	100.0	10	6	AR036402	AR036402 Sequence

ALIGNMENTS

RESULT 1	AR029539	AR029539	10 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	Sequence 49 from patent US 5859336.					
DEFINITION	Sequence 49 from patent US 5859336.					
ACCESSION	AR029539					
VERSION	AR029539.1	GI:5941512				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 10)					
AUTHORS	Koziel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.I., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.					
TITLE	Synthetic DNA sequence having enhanced activity in maize					

JOURNAL Patent: US 5859336-A 49 12-JAN-1999;
 FEATURES Location/Qualifiers
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 /organism="unknown"

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Query Match 100.0%; Score 7; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 2 GCTTCAG 8

RESULT 2
 AR093732/c
 LOCUS AR093732 10 bp DNA linear PAT 08-SEP-2000
 DEFINITION Sequence 10 from patent US 6001572.
 ACCESSION AR093732
 VERSION AR093732.1 GI:10020481
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Toothman,P.
 TITLE Method of identifying Aloo using PCR
 JOURNAL Patent: US 6001572-A 10 14-DEC-1999;
 FEATURES Location/Qualifiers
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 /organism="unknown"

BASE COUNT 3 a 3 c 3 g 1 t
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
 AR098492
 LOCUS AR098492 10 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 49 from patent US 6075185.
 ACCESSION AR098492
 VERSION AR098492.1 GI:12807749
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Kozel,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V.,
 Wright,M.S., Lains,K.L., Rothstein,S.J., Bowman,C.G., Dawson,J.L.,
 Dunder,E.M., Pace,G.M., and Suttie,J.L.
 TITLE Synthetic DNA sequence having enhanced insecticidal activity in
 maize

JOURNAL Patent: US 6075185-A 49 13-JUN-2000;
 FEATURES Location/Qualifiers
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 /organism="unknown"

BASE COUNT 1 a 3 c 3 g 3 t
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Qy 1 GCTTCAG 7

Db 2 GCTTCAG 8

RESULT 4
 AR162919/c
 LOCUS AR162919 10 bp DNA linear PAT 17-OCT-2001
 DEFINITION Sequence 1 from patent US 6260034.
 ACCESSION AR162919
 VERSION AR162919.1 GI:16230279
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 10)
 AUTHORS Bjorksten,L.
 TITLE Method and a system for nucleic acid sequence analysis
 JOURNAL Patent: US 6260034-A 1 10-JUL-2001;
 FEATURES Location/Qualifiers
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 /organism="unknown"

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RESULT 5
 AX301417/c
 LOCUS AX301417 10 bp DNA linear PAT 30-NOV-2001
 DEFINITION Sequence 131 from Patent WO0185941.
 ACCESSION AX301417
 VERSION AX301417.1 GI:17382500
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Versteeg,R. and Caron,H.N.
 TITLE Myc targets
 JOURNAL Patent: WO 0185941-A 131 15-NOV-2001;
 Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:9606"

BASE COUNT 3 a 3 g 2 t
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Qy 1 GCTTCAG 7
 Db 10 GCTTCAG 4

RESULT 6
 AX377325/c
 LOCUS AX377325 10 bp DNA linear PAT 18-MAR-2002
 DEFINITION Sequence 63 from Patent WO0212498.
 ACCESSION AX377325
 VERSION AX377325.1 GI:19573612
 KEYWORDS
 SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Klien,S.E., Koshy,B. and Tanguay,D.A.
TITLE Haplotypes of the isl1 gene
JOURNAL Patent: WO 0212498-A 63 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)

FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606" 2 t

BASE COUNT 2 a 3 c 3 g 2 t
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Query Match 100.0%; Score 7; DB 6; Length 10;
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Db 9 GCTTCAG 3

RESULT 7
AX441418
LOCUS AX441418 10 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 49 from Patent EP1209237.
ACCESSION AX441418
VERSION AX441418.1 GI:21690399
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.
and Rothstein,S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1209237-A 49 29-MAY-2002;
Syngenta Participations AG (CH)

FEATURES
source 1..10
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer c1 - second half" 3 t

BASE COUNT 1 a 3 c 3 g 3 t
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Query Match 100.0%; Score 7; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 2 GCTTCAG 8

RESULT 8
AX453914
LOCUS AX453914 10 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 49 from Patent EP1213356.
ACCESSION AX453914
VERSION AX453914.1 GI:21713572
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.
and Rothstein,S.J.

TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1213356-A 49 12-JUN-2002;
Syngenta Participations AG (CH)

FEATURES
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BASE COUNT 1 a 3 c 3 g 3 t
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QY 1 GCTTCAG 7
|||||
Db 2 GCTTCAG 8

RESULT 9
I41452
LOCUS I41452 10 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 49 from patent US 5625136.
ACCESSION I41452
VERSION I41452.1 GI:2082042
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Koziel,M.G., Desai,N.M., Lewis,K.S., Kramer,V.C., Warren,G.W.,
Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L.,
Rothstein,S.J., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M.
and Suttie,J.B.
TITLE Synthetic DNA sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: US 5625136-A 49 29-APR-1997;
Syngenta Participations AG (CH)

FEATURES
source 1..10
Location/Qualifiers
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BASE COUNT 1 a 3 c 3 g 3 t
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QY 1 GCTTCAG 7
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Db 2 GCTTCAG 8

RESULT 10
A27401
LOCUS A27401 11 bp DNA linear PAT 09-JUL-2002
DEFINITION Oligonucleotide HP10.
ACCESSION A27401
VERSION A27401.1 GI:21727210
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1 (bases 1 to 11)
AUTHORS Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and
Kobayashi,M.
TITLE New tissue plasminogen activator
JOURNAL Patent: EP 0302456-A 1 08-FEB-1989;
FUJISAWA PHARMACEUTICAL CO., LTD

FEATURES
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Location/Qualifiers
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
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Db 2 GCTTCAG 8

RESULT 11
LOCUS      AR059962      11 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 9 from patent US 5840533.
ACCESSION      AR059962
VERSION      AR059962.1 GI:5986412
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Niwa,M., Saito,Y., Sasaki,H., Hayashi,M., Notani,J. and Kobayashi,M.
TITLE      Tissue plasminogen activator
JOURNAL      Patent: US 5840533-A 9 24-NOV-1998;
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
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Db 2 GCTTCAG 8

RESULT 12
LOCUS      AX339224      11 bp      DNA      linear      PAT 10-JAN-2002
DEFINITION      Sequence 18 from Patent WO0196602.
ACCESSION      AX339224
VERSION      AX339224.1 GI:18135485
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Yang,A.L. and Festing,M.
TITLE      Methods and materials to determine the p53 status of a sample by determining the binding of p53 to a vector
JOURNAL      Patent: WO 0196602-A 18 20-DEC-2001;
MEDICAL RESEARCH COUNCIL (GB)
FEATURES
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Qy 1 GCTTCAG 7
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Db 2 GCTTCAG 8

RESULT 13
LOCUS      AX471563      11 bp      DNA      linear      PAT 09-AUG-2002
DEFINITION      Sequence 1140 from Patent WO02053773.
ACCESSION      AX471563
VERSION      AX471563.1 GI:22206688
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
REFERENCE      1
AUTHORS      Hofmann,K., Conradt,M. and Petersohn,D.
TITLE      Method for determining skin stress or skin ageing in vitro
JOURNAL      Patent: WO 02053773-A 1140 11-JUL-2002;
HENKEL KGAA (DE)
FEATURES
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Db 9 GCTTCAG 3

RESULT 14
LOCUS      HSOLIGON      11 bp      DNA      linear      PAT 02-MAR-1995
DEFINITION      oligonucleotide.
ACCESSION      A22481
VERSION      A22481.1 GI:833691
KEYWORDS
SOURCE      synthetic construct.
ORGANISM      artificial sequences.
REFERENCE      1 (bases 1 to 11)
AUTHORS      Brownlee,G.G. and Choo,K.H.
TITLE      Molecular cloning of the gene for human anti-haemophilic factor IX
JOURNAL      Patent: EP 0107278-A 16 02-MAY-1984;
NATIONAL RESEARCH DEVELOPMENT CORPORATION
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
    |||||
Db 2 GCTTCAG 8

RESULT 15
LOCUS      IL17488      11 bp      DNA      linear      PAT 07-OCT-1996
DEFINITION      Sequence 16 from patent US 5485529.
ACCESSION      IL17488
VERSION      IL17488.1 GI:1597843
KEYWORDS

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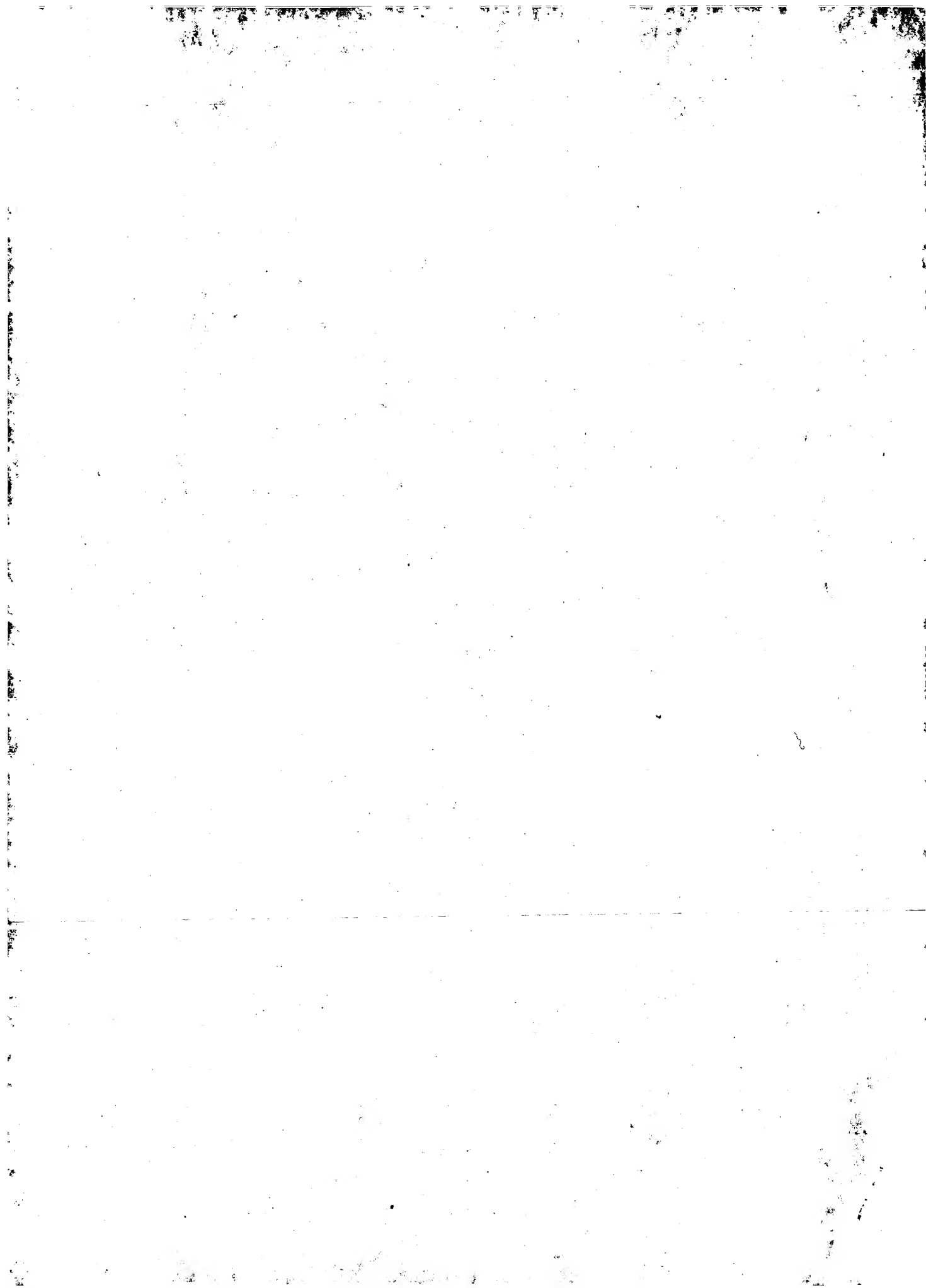
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ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      de Boer H.A., Heyneker, H.L. and Seeburg, P.H.
TITLE        DNA for expression of bovine growth hormone
JOURNAL      Patent: US 5489529-A 16 06-FEB-1996;
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GCTTCAG 7
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Db   2 GCTTCAG 8

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Job time : 84.8679 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 477.769 Seconds
(without alignments)
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Title: US-08-770-564A-13

Perfect score: 20
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Listing first 45 summaries

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- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 5	15.4	77.0	18	9	US-10-310-188-7112
C 6	15.4	77.0	25	12	US-60-427-808-774039
C 7	15.2	76.0	25	9	US-10-355-577-692202
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C 9	15.2	76.0	25	12	US-60-427-836-660522
C 10	15.2	76.0	27	9	US-10-310-695-12
C 11	15	75.0	25	9	US-10-355-577-635066
C 12	14.8	74.0	25	12	US-60-427-836-281208
C 13	14.8	74.0	25	12	US-60-427-836-561672
C 14	14.4	72.0	18	9	US-10-310-188-64233
C 15	14.4	72.0	25	9	US-10-355-577-85332
C 16	14.2	71.0	25	7	US-09-954-445A-48478
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C 19	14.2	71.0	25	12	US-60-427-836-242577
C 20	14.2	71.0	25	12	US-60-427-836-563632

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C 23	14	70.0	25	12	US-60-427-808-982397
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C 25	13.8	69.0	25	9	US-10-355-577-252936
C 26	13.8	69.0	25	9	US-10-355-577-288031
C 27	13.8	69.0	25	12	US-60-427-808-325661
C 28	13.8	69.0	25	12	US-60-427-808-339209
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C 30	13.8	69.0	25	12	US-60-427-808-743293
C 31	13.8	69.0	25	12	US-60-427-808-762708
C 32	13.8	69.0	25	12	US-60-427-808-762709
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C 34	13.8	69.0	25	12	US-60-427-836-132474
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C 43	13.6	68.0	25	12	US-60-417-190-112706
C 44	13.6	68.0	25	12	US-60-427-808-108802
C 45	13.6	68.0	25	12	US-60-427-808-115814

ALIGNMENTS

RESULT 1

PCT-US03-04088-15/c
; Sequence 15, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribosome Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-15

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TTTTGTGCTCTAGA 20
DB 19 TTTTGTGCTCTAGA 2

RESULT 2
PCT-US03-04088-279
; Sequence 279, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-279

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 38.9%; Pred. No. 1.2e+03;
Matches 7; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTAGA 20
DB 1 UUUUUUUUUUUUUUUU 18

RESULT 3
US-09-690-885-5/c
; Sequence 5, Application US/09690885
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO, HARUMI
; APPLICANT: OSHIMA, ATSUSHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/690,885
FILING DATE: 18-Oct-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1422-0319P
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-690-885-5

Query Match 90.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTCTAGA 20
DB 21 TTTTGTGCTCTCTAGA 4

RESULT 4
US-60-427-836-561675
; Sequence 561675, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 561675
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-561675

Query Match 82.0%; Score 16.4; DB 12; Length 25;
Best Local Similarity 94.4%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTCTAGA 20
DB 6 TTTTGTGCTCTCTAGA 23

RESULT 5
US-10-310-188-7112
; Sequence 7112, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN:
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7112
; LENGTH: 18
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-7112

Query Match      77.0%; Score 15.4; DB 9; Length 18;
Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19
   ||||| ||||| |||||
Db 1 TTTTGTGTTGCTCTAG 17

RESULT 6
US-60-427-808-774039
; Sequence 774039, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 774039
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-774039

Query Match      77.0%; Score 15.4; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 1.2e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCT 17
   ||||| ||||| |||||
Db 4 CATTGTTGTTGCTCT 20

RESULT 7
US-10-355-577-692202
; Sequence 692202, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-692202

Query Match      76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 6 CATTGTTGTTGCTCAG 25

RESULT 8
US-60-427-808-799814
; Sequence 799814, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
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; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 799814
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-799814

Query Match      76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 4 CTTTCTGTTGTTGCTCTAGA 23

RESULT 9
US-60-427-836-660522
; Sequence 660522, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 660522
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-660522

Query Match      76.0%; Score 15.2; DB 12; Length 25;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 6 CATTGTTGTTGCCNAGA 25

RESULT 10
US-10-310-695-12/c
; Sequence 12, Application US/10310695
; GENERAL INFORMATION:
; APPLICANT: DROGE, PETER
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
; FILE REFERENCE: DEB:019US
; CURRENT APPLICATION NUMBER: US/10/310,695
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-310-695-12

Query Match      76.0%; Score 15.2; DB 9; Length 27;
Best Local Similarity 85.0%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
   ||||| ||||| |||||
Db 25 CATTATTGATTCTCTAGA 6
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```
RESULT 11
US-10-355-577-635066
; Sequence 635066 Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-635066

Query Match 75.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGCTCTAGA 18
DB 4 TTTTGTGCTCTAGA 18

RESULT 12
US-60-427-836-281208
; Sequence 281208 Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 281208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-281208

Query Match 74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGCTCTAGA 20
DB 5 TTTTGTGCTCTAGA 22

RESULT 13
US-60-427-836-561672
; Sequence 561672 Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 561672
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-561672

Query Match 74.0%; Score 14.8; DB 12; Length 25;
Best Local Similarity 88.9%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
US-10-310-188-64233
; Sequence 64233 Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATICAALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64233
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64233

Query Match 72.0%; Score 14.4; DB 9; Length 18;
Best Local Similarity 93.8%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16
DB 3 CCTTTTGTGTTGCTC 18

RESULT 15
US-10-355-577-85332
; Sequence 85332 Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 85332
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-85332

Query Match 72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16
DB 5 CATTGTTGTTGCTC 20

Search completed: June 26, 2003, 04:15:22
Job time : 479.077 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-08-770-564A-13

Perfect score: 20

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Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

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SUMMARIES

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2	20	100.0	20	11	US-08-770-564A-13
3	20	100.0	30	9	US-08-521-634-10
4	19	95.0	20	21	US-09-540-119B-16
5	17	85.0	22	22	US-09-587-662A-5
6	16	80.0	22	13	US-08-973-589-18
7	16	80.0	25	36	US-09-954-427-58350
8	16	80.0	25	67	US-60-233-166-58350
9	15.2	76.0	25	79	US-60-353-987-692202
10	15	75.0	25	36	US-09-954-427-58351
11	15	75.0	25	67	US-60-233-166-58351
12	15	75.0	25	79	US-60-353-987-635066
13	14.8	74.0	41	36	US-09-953-138-241
14	14.4	72.0	25	36	US-09-956-584-317896
15	14.4	72.0	25	36	US-09-956-584-450073
16	14.4	72.0	25	36	US-09-956-584-450078
17	14.4	72.0	25	36	US-09-956-584-450079
18	14.4	72.0	25	36	US-09-956-584-450083
19	14.4	72.0	25	36	US-09-956-584-450085
20	14.4	72.0	25	67	US-60-234-017-323013
21	14.4	72.0	25	67	US-60-234-017-452894

C	22	14.4	72.0	25	67	US-60-234-017-452000
C	23	14.4	72.0	25	67	US-60-234-017-452001
C	24	14.4	72.0	25	67	US-60-234-017-452005
C	25	14.4	72.0	25	67	US-60-234-017-452007
C	26	14.4	72.0	25	67	US-60-234-017-452008
C	27	14.4	72.0	25	67	US-60-234-017-452009
C	28	14.4	72.0	25	67	US-60-234-017-452010
C	29	14.4	72.0	25	67	US-60-234-017-452011
C	30	14.4	72.0	25	67	US-60-234-017-452012
C	31	14.4	72.0	25	67	US-60-234-017-452013
C	32	14.4	72.0	25	67	US-60-234-017-452014
C	33	14.4	72.0	25	67	US-60-234-017-452015
C	34	14.4	72.0	25	67	US-60-234-017-452016
C	35	14.4	72.0	25	67	US-60-234-017-452017
C	36	14.4	72.0	25	67	US-60-234-017-452018
C	37	14.4	72.0	25	67	US-60-234-017-452019
C	38	14.4	72.0	25	67	US-60-234-017-452020
C	39	14.4	72.0	25	67	US-60-234-017-452021
C	40	14.4	72.0	25	67	US-60-234-017-452022
C	41	14.4	72.0	25	67	US-60-234-017-452023
C	42	14.4	72.0	25	67	US-60-234-017-452024
C	43	14.4	72.0	25	67	US-60-234-017-452025
C	44	14.4	72.0	25	67	US-60-234-017-452026
C	45	13.8	69.0	25	18	US-09-428-78-7670

ALIGNMENTS

RESULT 1
PCr-US97-23619-13
Sequence 13, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
Sequence 13, Application PC/TUS9723619
RNA Component of Telomerase
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

```

; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note="oligo 20/21"
PCT-US97-23619-13

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 1 CATTGTTGTTGCTCTAGA 20
DB 1 CATTGTTGTTGCTCTAGA 20

RESULT 2
US-08-770-564A-13
; Sequence 13: Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Prusan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944.
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-13

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 1 CATTGTTGTTGCTCTAGA 20
DB 1 CATTGTTGTTGCTCTAGA 20

RESULT 3
US-08-521-634-10/c

```

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; Sequence 10, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
; US-08-521-634-10

Query Match      100.0%; Score 20; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTCTTTGTTGCTCTAGA 20
Db      28 CATTCTTTGTTGCTCTAGA 9

RESULT 4
US-09-540-1198-16
; Sequence 16, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
```

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-1198-16

Query Match      95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTCTTTGTTGCTCTAG 19
Db      2 CATTCTTTGTTGCTCTAG 20

RESULT 5
US-09-587-662A-5
; Sequence 5, Application US/09587662A
; GENERAL INFORMATION:
; APPLICANT: Au, Jessie L.-S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING DRUG ACTIVITY
; TITLE OF INVENTION: THROUGH TELOMERE DAMAGE
; FILE REFERENCE: JAG-004
; CURRENT APPLICATION NUMBER: US/09/587,662A
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/137,549
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-587-662A-5

Query Match      85.0%; Score 17; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTCTTTGTTGCTCT 17
Db      8 CATTCTTTGTTGCTCT 24

RESULT 6
US-08-973-589-18
; Sequence 18, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; TITLE OF INVENTION: TELOMERASE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-08-973-589-18
```

Query Match 80.0%; Score 16; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 1 CATTGTTGTTGCTC 16
DB 7 CATTGTTGTTGCTC 22

RESULT 7
US-09-954-427-58350/c
; Sequence 58350, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-09-954-427-58350

Query Match 80.0%; Score 16; DB 16; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTAG 19
DB 25 TTTTGTGTTGCTCTAG 10

RESULT 8
US-60-233-166-58350/c
; Sequence 58350, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-60-233-166-58350

Query Match 80.0%; Score 16; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+04; Indels 0;
Matches 16; Conservative 0; Mismatches 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTAG 19
DB 25 TTTTGTGTTGCTCTAG 10

RESULT 9
US-60-353-987-692202
; Sequence 692202, Application US/60353987

GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 692202
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-692202

Query Match 76.0%; Score 15.2; DB 79; Length 25;
Best Local Similarity 85.0%; Pred. No. 2.6e+04; Indels 0;
Matches 17; Conservative 0; Mismatches 3; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
DB 6 CATTGTTGTTGCTCTAGA 25

RESULT 10
US-09-954-427-58351/c
; Sequence 58351, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-09-954-427-58351

Query Match 75.0%; Score 15; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04; Indels 0;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 5 TTTTGTGTTGCTCTAG 19
DB 25 TTTTGTGTTGCTCTAG 11

RESULT 11
US-60-233-166-58351/c
; Sequence 58351, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-60-233-166-58351

Query Match 75.0%; Score 15; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTTTGTGCTCTAG 19
| | | | |
Db 25 TTTTGTGCTCTAG 11

RESULT 12
US-60-353-987-635066
; Sequence 635066, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-60-353-987-635066

Query Match 75.0%; Score 15; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGCTCTA 18
| | | | |
Db 4 TTTTGTGCTCTA 18

RESULT 13
US-09-953-198-241
; Sequence 241, Application US/09953198
; GENERAL INFORMATION:
; APPLICANT: COMPUEN LTD
; TITLE OF INVENTION: DATA BASE OF SNP
; FILE REFERENCE: 1351253
; CURRENT APPLICATION NUMBER: US/09/953,198
; CURRENT FILING DATE: 2001-08-12
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-953-198-241

Query Match 74.0%; Score 14.8; DB 36; Length 41;
Best Local Similarity 88.9%; Pred. No. 4.1e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATTTTGTGCTCTAG 19
| | | | |
Db 2 ATTTTGTGCTCTAG 19

RESULT 14
US-09-956-584-317896
; Sequence 317896, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 317896
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-317896

Query Match 72.0%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTTTGTGCTCT 17
| | | | |
Db 1 ATTTTGTGCTCT 16

RESULT 15
US-09-956-584-450073/c
; Sequence 450073, Application US/09956584
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Mus Musculus
; FILE REFERENCE: 3115.1
; CURRENT APPLICATION NUMBER: US/09/956,584
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/234,017
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 605887
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 450073
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-956-584-450073

Query Match 72.0%; Score 14.4; DB 36; Length 25;
Best Local Similarity 93.8%; Pred. No. 5.6e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATTTTGTGCTCT 17
| | | | |
Db 24 ATTTTGTGCTCT 9

Search completed: June 25, 2003, 06:20:29
Job time : 1698.67 secs

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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 60.7968 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTTCCTTCTCTAGTA 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.2	71.0	21	9	US-10-032-924-8
C 2	14.2	71.0	40	10	US-09-765-272-253
C 3	14.2	71.0	42	9	US-09-769-787-375
C 4	13.6	68.0	20	9	US-09-971-894-8
C 5	13.4	67.0	26	10	US-09-815-171A-27
C 6	13.4	67.0	30	7	US-08-978-635-38
C 7	13.4	67.0	30	7	US-08-978-636-29
C 8	13.4	67.0	30	8	US-08-978-633-38
C 9	13.4	67.0	30	8	US-08-978-634-38
C 10	13.4	67.0	30	8	US-08-978-637-38
C 11	13.4	67.0	30	8	US-08-978-632-38
C 12	13.2	66.0	21	9	US-09-997-868-13
C 13	13.2	66.0	40	9	US-10-093-355-6
C 14	12.8	64.0	25	9	US-10-215-112-870
C 15	12.8	64.0	29	9	US-09-863-040-49
C 16	12.6	63.0	25	9	US-10-098-263B-32778
C 17	12.6	63.0	36	9	US-10-091-135-32
C 18	12.6	63.0	45	10	US-09-922-261-124
C 19	12.4	62.0	25	9	US-10-098-263B-67431

ALIGNMENTS

RESULT 1

US-10-032-924-8/c

; Sequence 8, Application US/10032924

; Publication No. US20030022190A1

; GENERAL INFORMATION:

; APPLICANT: Shipman, Robert

; Leushner, James M.

; Dunn, James M.

; TITLE OF INVENTION: METHOD AND REAGENTS FOR TESTING FOR

; MUTATIONS IN THE BRCA1 GENE

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Oppedahl & Larson

; STREET: 1992 Commerce Street Suite 309

; CITY: Yorktown

; STATE: NY

; COUNTRY: US

; ZIP: 10598

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage

; OPERATING SYSTEM: MS DOS

; SOFTWARE: Word Perfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/032,924

; FILING DATE: 26-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/649,950

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Larson, Marina T.

; REGISTRATION NUMBER: 32,038

; REFERENCE/DOCKET NUMBER: VGEN.P-028-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (914) 245-3252

; TELEFAX: (914) 962-4330

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: nucleic acid

Sequence 109459,
Sequence 116952,
Sequence 133, App
Sequence 370, App
Sequence 285, App
Sequence 15, Appl
Sequence 19, Appl
Sequence 18, Appl
Sequence 204, App
Sequence 1024, Ap
Sequence 16847, A
Sequence 72375, A
Sequence 9, Appli
Sequence 45, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 10137, A
Sequence 312, App
Sequence 23, Appl
Sequence 19, Appl
Sequence 5, Appli
Sequence 7, Appli
Sequence 5, Appli

20 12.4 62.0 25 9 US-10-098-263B-109459
21 12.4 62.0 25 9 US-10-098-263B-116952
22 12.4 62.0 26 10 US-09-426-548-1133
23 12.4 62.0 33 10 US-09-765-272-370
24 12.4 62.0 38 9 US-10-085-906-285
25 12.4 62.0 40 9 US-10-084-553-15
26 12.4 62.0 40 9 US-10-084-553-19
27 12.4 62.0 43 9 US-10-084-553-18
28 12.2 61.0 20 9 US-10-067-125-204
29 12.2 61.0 23 10 US-09-263-959-1024
30 12.2 61.0 25 9 US-10-098-263B-16847
31 12.2 61.0 25 9 US-10-098-263B-72375
32 12.2 61.0 29 9 US-09-841-513-9
33 12.2 61.0 29 9 US-10-038-718-9
34 12.2 61.0 32 9 US-10-045-631A-45
35 12.2 61.0 39 9 US-09-846-430A-4
36 12.2 61.0 48 9 US-10-179-046-4
37 12 60.0 20 10 US-09-839-136-7
38 12 60.0 25 9 US-10-098-263B-10137
39 12 60.0 26 9 US-10-044-692-312
40 12 60.0 26 9 US-10-044-539-312
41 12 60.0 26 10 US-09-057-351-23
42 12 60.0 27 9 US-10-199-024-19
43 12 60.0 30 9 US-10-263-766-5
44 12 60.0 30 9 US-10-263-766-7
45 12 60.0 30 10 US-09-272-162-5

RESULT 5
US-09-815-171A-27
; Sequence 27, Application US/09815171A
; Patent No. US20020064780A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Zichi, Dominic
; APPLICANT: Jenison, Robert D
; APPLICANT: Schneider, Daniel J
; TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
; TITLE OF INVENTION: Nucleic Acid Ligands
; FILE REFERENCE: SML.03
; CURRENT APPLICATION NUMBER: US/09/815,171A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/616,284
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/356,233
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/232,946
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 08/792,075
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: 09/143,190
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 08/469,609
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-815-171A-27

Query Match 67.0%; Score 13.4; DB 10; Length 26;
Best Local Similarity 93.3%; Pred. No. 7.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TTTTGTGTCCT 17
|||||
Db 3 TTTTGTGTCCT 17

RESULT 6
US-08-978-635-38/c
; Sequence 38, Application US/08978635A
; Publication No. US20030087434A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Stavrianopoulos, Jannis G.
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dekai
; APPLICANT: Kelker, No. US20030087434A1man E.
; APPLICANT: Engelhardt, Dean L.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; TITLE OF INVENTION: COMPOSITIONS FOR THERAPEUTIC AND DIAGNOSTIC USE
; FILE REFERENCE: ENZ-53D4.032499
; CURRENT APPLICATION NUMBER: US/08/978,635A
; CURRENT FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: oligo
US-08-978-635-38

Query Match 67.0%; Score 13.4; DB 7; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
Db 17 TTTGTTAGCTCTAGA 3

RESULT 7
US-08-978-636-29/c
; Sequence 29, Application US/08978636
; Publication No. US20030104620A1
; GENERAL INFORMATION:
; APPLICANT: ELAZAR RABBANI
; APPLICANT: JANNIS G. STAVRIANOPOULOS
; APPLICANT: JAMES J. DONEGAN
; APPLICANT: DAKAI LIU
; APPLICANT: NORMAN E. KELKER
; APPLICANT: DEAN L. ENGELHARDT
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING
; TITLE OF INVENTION: AND/OR PROPERTY EXHIBITING COMPOSITIONS FOR
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ENZO THERAPEUTICS, INC.
; STREET: C/O ENZO BIOCHEM, INC.
; STREET: 527 MADISON AVENUE,
; CITY: 9TH FLOOR
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Micro Floppy Disk. 1.44 KB
; MEDIUM TYPE: STORAGE
; COMPUTER: IBM PC/XT/AT, IBM PS/2 OR COMPATIBLES
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: MICROSOFT WORD - ASCII TEXT (DOS)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,636
; FILING DATE: 25-NOVEMBER-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: FEDUS, RONALD C.
; REGISTRATION NUMBER: 32,567
; REFERENCE/DOCKET NUMBER: ENZ-53 (D3)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 583-0100
; TELEFAX: (212) 583-0150
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "oligonucleotide"
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: TER-1
US-08-978-636-29

Query Match 67.0%; Score 13.4; DB 7; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
Db 17 TTTGTTAGCTCTAGA 3

RESULT 8
US-08-978-633-38/c
; Sequence 38, Application US/08978633
; Patent No. US20010006814A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Stavrianopoulos, Jannis G.
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dakai
; APPLICANT: Kelker, No. US20010006814Alman E.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; FILE REFERENCE: ENZ-53 (D1).081299
; CURRENT APPLICATION NUMBER: US/08/978,633
; CURRENT FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo
US-08-978-633-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
DB 17 TTTGTTAGCTCTAGA 3

RESULT 9
US-08-978-634-38/c
; Sequence 38, Application US/08978634A
; Patent No. US20010006815A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Stavrianopoulos, Jannis G.
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dakai
; APPLICANT: Kelker, No. US20010006815Alman E.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; FILE REFERENCE: ENZ-53 (D2).081299
; CURRENT APPLICATION NUMBER: US/08/978,634A
; CURRENT FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo
US-08-978-634-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
DB 17 TTTGTTAGCTCTAGA 3

RESULT 10

US-08-978-637-38/c
; Sequence 38, Application US/08978637A
; Patent No. US20010006816A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Stavrianopoulos, Jannis G.
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dakai
; APPLICANT: Kelker, No. US20010006816Alman E.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; FILE REFERENCE: ENZ-53 (U5).081299
; CURRENT APPLICATION NUMBER: US/08/978,637A
; CURRENT FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo
US-08-978-637-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
DB 17 TTTGTTAGCTCTAGA 3

RESULT 11
US-08-978-632-38/c
; Sequence 38, Application US/08978632A
; Patent No. US20010007767A1
; GENERAL INFORMATION:
; APPLICANT: Rabbani, Elazar
; APPLICANT: Stavrianopoulos, Jannis G.
; APPLICANT: Donegan, James J.
; APPLICANT: Liu, Dakai
; APPLICANT: Kelker, No. US20010007767Alman E.
; APPLICANT: Engelhardt, Dean L.
; TITLE OF INVENTION: NOVEL PROPERTY EFFECTING AND/OR PROPERTY EXHIBITING
; FILE REFERENCE: ENZ-53 (C)Sequence.073099
; CURRENT APPLICATION NUMBER: US/08/978,632A
; CURRENT FILING DATE: 1997-11-25
; EARLIER APPLICATION NUMBER: 08/574,443
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligo
US-08-978-632-38

Query Match 67.0%; Score 13.4; DB 8; Length 30;
Best Local Similarity 93.3%; Pred. No. 7.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTTGTTGCTCTAGA 20
|||||
DB 17 TTTGTTAGCTCTAGA 3

RESULT 12
US-09-997-868-13/c

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; Sequence 13, Application US/09997868
; Publication No. US20030031654A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.,
; Groskreutz, Debyra J.
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
; Polypeptide Synthesis
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,868
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/887265
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/803631
; FILING DATE: 06-DEC-1992
; APPLICATION NUMBER: PCT/US92/10621
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0748P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
;
US-09-997-868-13

Query Match 66.0%; Score 13.2; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 9.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
Db 21 TTGCTCTTTGCTCTAGA 4

RESULT 13
US-10-093-365-6/c
; Sequence 6, Application US/10093365
; Publication No. US2003009962A1
; GENERAL INFORMATION:
; APPLICANT: Scherthaner, Johann
; APPLICANT: Piche, Caroline
; APPLICANT: Robert, Laurian
; TITLE OF INVENTION: Methods to Isolate Gene Coding and Flanking DNA
; FILE REFERENCE: 0811.1200001
; CURRENT APPLICATION NUMBER: US/10/093,365
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: US 60/274,239
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
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; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificial DNA Sequence
US-10-093-365-6

Query Match 66.0%; Score 13.2; DB 9; Length 40;
Best Local Similarity 83.3%; Pred. No. 9.9e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
Db 24 TTTTGTGTTTCTCTAGA 7

RESULT 14
US-10-215-112-870
; Sequence 870, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mitmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 870
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-870

Query Match 64.0%; Score 12.8; DB 9; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGCTCT 17
Db 10 ACTTTTGTGTTGCTCT 25

RESULT 15
US-09-863-040-49/c
; Sequence 49, Application US/09863040
; Patent No. US20020155517A1
; GENERAL INFORMATION:
; APPLICANT: Rupp, Steffan
; APPLICANT: Robertson, Laura
; APPLICANT: Summers, Eric F.
; APPLICANT: Hecht, Peter
; APPLICANT: Roberts, Radclyffe
; APPLICANT: Madhani, Hiren
; APPLICANT: Styles, Cora Ann
; APPLICANT: Lo, Hsiu-Jung
; APPLICANT: Sherman, Amir
; APPLICANT: Cali, Brian
; APPLICANT: Fink, Gerald R.
; TITLE OF INVENTION: Regulation of Fungal Gene Expression
; FILE REFERENCE: 109772.152
; CURRENT APPLICATION NUMBER: US/09/863,040
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/066,129
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: US 60/066,308
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/066,462
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: US 60/078,610
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; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/094,523
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: #6K primer
US-09-863-040-49

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Query Match      64.0%; Score 12.8; DB 9; Length 29;
Best Local Similarity 87.5%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      4 TTTTGTCTCTCTAG 19
Db      19 TTTTCTTGTCTGAG 4

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Search completed: June 25, 2003, 22:25:09
Job time : 61.7968 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 30.3586 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-13
Perfect score: 20
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	US-08-770-565-13
C 2	18	90.0	28	1	US-08-318-867A-19
C 3	18	90.0	28	4	US-08-352-089A-5
C 4	14.2	71.0	21	4	US-08-649-950-8
C 5	14.2	71.0	40	3	US-08-961-083-253
C 6	13.8	69.0	27	2	US-08-766-439-17
C 7	13.8	69.0	30	2	US-08-766-439-89
C 8	13.8	69.0	30	2	US-08-766-439-91
C 9	13.6	68.0	20	4	US-09-472-035A-8
C 10	13.6	68.0	29	1	US-08-153-071-17
C 11	13.6	68.0	29	1	US-08-609-271-24
C 12	13.6	68.0	29	2	US-08-438-511-17
C 13	13.6	68.0	29	3	US-08-487-431-20
C 14	13.6	68.0	29	3	US-08-188-374-24
C 15	13.4	67.0	20	1	US-08-403-866-16
C 16	13.2	66.0	21	4	US-08-026-143B-13
C 17	13.2	66.0	21	5	PCT-US92-10621-13
C 18	13.2	66.0	21	5	PCT-US94-02233-13
C 19	13.2	66.0	30	1	US-07-862-831A-15
C 20	13.2	66.0	30	1	US-08-126-564A-15
C 21	13.2	66.0	30	5	PCT-US94-09143-15
C 22	13.2	66.0	36	2	US-08-928-692-33
C 23	13.2	66.0	36	4	US-09-339-972-33
C 24	13.2	66.0	38	1	US-08-510-215A-11
C 25	13.2	66.0	40	4	US-09-605-192-4
C 26	13.2	66.0	42	1	US-08-639-256-6
C 27	12.8	64.0	25	4	US-09-387-341-207

C 28	12.8	64.0	29	4	US-09-189-462-49	Sequence 49, Appl
C 29	12.8	64.0	33	1	US-08-741-881-110	Sequence 110, App
C 30	12.8	64.0	33	1	US-08-739-158-110	Sequence 110, App
C 31	12.8	64.0	33	2	US-08-739-167-110	Sequence 110, App
C 32	12.8	64.0	33	3	US-08-404-796-110	Sequence 110, App
C 33	12.8	64.0	33	3	US-08-931-869-110	Sequence 110, App
C 34	12.8	64.0	33	4	US-09-350-399-110	Sequence 110, App
C 35	12.8	64.0	33	4	US-09-236-140A-110	Sequence 110, App
C 36	12.8	64.0	37	2	US-08-702-572-11	Sequence 11, Appl
C 37	12.8	64.0	41	1	US-08-332-420-57	Sequence 57, Appl
C 38	12.8	64.0	45	4	US-09-387-341-192	Sequence 192, App
C 39	12.6	63.0	30	4	US-07-661-370-4	Sequence 4, Appl
C 40	12.6	63.0	35	1	US-07-958-133-3	Sequence 3, Appl
C 41	12.6	63.0	35	1	US-08-412-913-3	Sequence 3, Appl
C 42	12.6	63.0	45	4	US-09-461-697-124	Sequence 124, App
C 43	12.6	63.0	48	4	US-09-225-990-13	Sequence 13, Appl
C 44	12.6	63.0	48	4	US-09-225-990-14	Sequence 14, Appl
C 45	12.4	62.0	33	3	US-08-961-083-370	Sequence 370, App

ALIGNMENTS

RESULT 1
US-08-770-565-13
; Sequence 13, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-13

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20

```
Db      1 CATTTCCTGCTCTAGA 20
|||||
RESULT 2
US-08-318-867A-19/c
; Sequence 19, Application US/08318867A
; Patent No. 5714323
; GENERAL INFORMATION:
; APPLICANT: ATUSHI OHSHIMA
; APPLICANT: SUMIKO INOUE
; APPLICANT: MASAYORI INOUE
; TITLE OF INVENTION: OVER EXPRESSION OF SINGLE-STRANDED
; MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES, P.C.
; STREET: 230 S. 15th ST.
; CITY: PHILADELPHIA, PA.
; COUNTRY: U.S.A.
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,867A
; FILING DATE: MAY 4, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GERARD J. WEISER
; REFERENCE/DOCKET NUMBER: 377.6120P
; TELEPHONE: (215) 875-8383
; TELEFAX: (215) 875-8394
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-318-867A-19
Query Match          90.0%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTTTTCCTGCTCTAGA 20
|||||
Db      21 TTTTTCCTGCTCTAGA 4
|||||
RESULT 3
US-08-952-089A-5/c
; Sequence 5, Application US/08952089A
; Patent No. 6165749
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO, HARUMI
; APPLICANT: OSHIMA, ATSUSHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,089A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0319P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-952-089A-5
Query Match          90.0%; Score 18; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTTTTCCTGCTCTAGA 20
|||||
Db      21 TTTTTCCTGCTCTAGA 4
|||||
RESULT 4
US-08-649-950-8/c
; Sequence 8, Application US/08649950
; Patent No. 6403303
; GENERAL INFORMATION:
; APPLICANT: Shipman, Robert
; APPLICANT: Leushner, James
; APPLICANT: Dunn, James M.
; TITLE OF INVENTION: METHOD AND REAGENTS FOR TESTING FOR
; TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppedahl & Larson
; STREET: 1992 Commerce Street Suite 309
; CITY: Yorktown
; STATE: NY
; COUNTRY: US
; ZIP: 10598
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: word Perfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,950
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Larson, Marina T.
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-028-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
```

LENGTH: 21
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: human
FEATURE:
OTHER INFORMATION: amplification primer for BRCA1 gene
US-08-649-950-8

Query Match 71.0%; Score 14.2; DB 4; Length 21;
Best Local Similarity 84.2%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGCTCTAG 20
|||||
DB 20 ATTTGTGTTTCTGTAGA 2

RESULT 5
US-08-961-083-253/c
; Sequence 253, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-083-253

Query Match 71.0%; Score 14.2; DB 3; Length 40;
Best Local Similarity 84.2%; Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATTTTTGTGTTGCTCTAG 19
|||||
DB 33 CATTTTTGTGTTTCTGTG 15

RESULT 6
US-08-766-439-17
; Sequence 17, Application US/08766439
; Patent No. 5922538
; GENERAL INFORMATION:
; APPLICANT: HAZEL, JAMES WILLIAM
; APPLICANT: JENSEN, MARK ANTON
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR
; TITLE OF INVENTION: THE DETECTION OF LISTERIA
; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 INCH DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
; SOFTWARE: MICROSOFT WORD 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.439
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,228
; FILING DATE: NOVEMBER 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: MD-1065-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-766-439-17

Query Match 69.0%; Score 13.8; DB 2; Length 27;
Best Local Similarity 88.2%; Pred. No. 9.4e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAG 19
|||||
DB 4 TGTGTTGTTGCTCTAG 20

RESULT 7
US-08-766-439-89
; Sequence 89, Application US/08766439
; Patent No. 5922538
; GENERAL INFORMATION:
; APPLICANT: HAZEL, JAMES WILLIAM
; APPLICANT: JENSEN, MARK ANTON
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR
; TITLE OF INVENTION: THE DETECTION OF LISTERIA SPP.
; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.

```
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 INCH DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
; SOFTWARE: MICROSOFT WORD 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,439
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,228
; FILING DATE: NOVEMBER 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: MD-1065-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-766-439-89
;
; Query Match 69.0%; Score 13.8; DB 2; Length 30;
; Best Local Similarity 88.2%; Pred. No. 9.5e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 TTTTGTGTTGCTCTAG 19
; DB 4 TGTTGGTTTGCTCTAG 20
;
; RESULT 8
; US-08-766-439-91
; Sequence 91, Application US/08766439
; Patent No. 5922538
; GENERAL INFORMATION:
; APPLICANT: HAZEL, JAMES WILLIAM
; APPLICANT: JENSEN, MARK ANTON
; TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR
; TITLE OF INVENTION: THE DETECTION OF LISTERIA
; TITLE OF INVENTION: MONOCYTOGENES AND LISTERIA SPP.
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: U.S.A.
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.50 INCH DISKETTE
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
; SOFTWARE: MICROSOFT WORD 2.0C
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,439
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/745,228
; FILING DATE: NOVEMBER 8, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: MD-1065-A
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 302-892-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-766-439-91
;
; Query Match 69.0%; Score 13.8; DB 2; Length 30;
; Best Local Similarity 88.2%; Pred. No. 9.5e+02;
; Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 3 TTTTGTGTTGCTCTAG 19
; DB 4 TGTTGGTTTGCTCTAG 20
;
; RESULT 9
; US-09-472-035A-8/C
; Sequence 8, Application US/09472035A
; Patent No. 6322985
; GENERAL INFORMATION:
; APPLICANT: Yechezkel Kashi et al.
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND
; TITLE OF INVENTION: HYPERPOLYMORPHIC SIMPLE SEQUENCE REPEATS
; TITLE OF INVENTION: IN PROKARYOTE GENOMES AND USE OF SAME FOR
; TITLE OF INVENTION: PROKARYOTE CLASSIFICATION AND TYPING
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/472,035A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 74/77
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-5625553
; TELEFAX: 972-3-5625554
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-472-035A-8
;
; Query Match 68.0%; Score 13.6; DB 4; Length 20;
; Best Local Similarity 80.0%; Pred. No. 1.1e+03;
; Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 CATTTTTGTGTTGCTCTAGA 20
```

Db 20 CATTTGTCATTTGCTCTAGA 1
||||| || ||||| |||||

RESULT 10
US-08-153-071-17/c
; Sequence 17, Application US/08153071
; Patent No. 565869
; GENERAL INFORMATION:
; APPLICANT: Ryland, James R.
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Ernst, Ulrich P.
; APPLICANT: Houk, Daniel E.
; APPLICANT: Traylor, David W.
; APPLICANT: Williams, Lee R.
; APPLICANT: Mitchell, David J.
; APPLICANT: Chivers, Mark L.
; APPLICANT: Belval, Thomas K.
; TITLE OF INVENTION: Method for the Rapid Removal of
; TITLE OF INVENTION: Protoporphyrin IX from Protoporphyrin IX-Containing Solutions
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 5797 Central Avenue
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,071
; FILING DATE: No. 565869ember 15, 1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565869ak, Henry P.
; REGISTRATION NUMBER: 33200
; REFERENCE/DOCKET NUMBER: 120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3322
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: beta gene fragment
; HYPOTHETICAL: no
US-08-153-071-17

Query Match 68.0%; Score 13.6; DB 1; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATTTTTCATTTGCTCTAGA 20
||||| ||||| |||||

Db 26 CATATATTATTTCCCTCTAGA 7
||||| ||||| |||||

RESULT 11
US-08-609-271-24/c
; Sequence 24, Application US/08609271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izidor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; NUMBER OF SEQUENCES: 42

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Site FD-1
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,271
; FILING DATE: 28 February 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/188,374
; FILING DATE: 1/27/94
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5811264elli, Marianne F.
; REGISTRATION NUMBER: 38571
; NAME: Brown, Theresa A.
; REGISTRATION NUMBER: 32547
; REFERENCE/DOCKET NUMBER: 170/Div
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303-541-3324
; TELEFAX: 303-444-3013
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: beta gene fragment
; HYPOTHETICAL: no
US-08-609-271-24

Query Match 68.0%; Score 13.6; DB 1; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATTTTTCATTTGCTCTAGA 20
||||| ||||| |||||

Db 26 CATATATTATTTCCCTCTAGA 7
||||| ||||| |||||

RESULT 12
US-08-438-511-17/c
; Sequence 17, Application US/08438511
; Patent No. 5840851
; GENERAL INFORMATION:
; APPLICANT: Plomer, J. Jeffrey
; APPLICANT: Ryland, James R.
; APPLICANT: Matthews, Maura-Ann H.
; APPLICANT: Traylor, David W.
; APPLICANT: Milne, Erin E.
; APPLICANT: Durfee, Steven L.
; APPLICANT: Mathews, Antony J.
; APPLICANT: Neway, Justin O.
; TITLE OF INVENTION: Purification of Hemoglobin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.
; STREET: 2545 Central Avenue, Suite FDI
; CITY: Boulder
; STATE: Colorado
; ZIP: 80301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.0a
; CURRENT APPLICATION DATA:


```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,866
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30, 727
; REFERENCE/DOCKET NUMBER: 20747/30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1600
; TELEFAX: (716) 263-1487
; TELEX: 978450 (WUT)
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-403-866-16

```

```

Query Match      67.0%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4 TTTTGTGTTGCTCTA 18
        |||||
Db       6 TTTTGTGTTGCTCTA 20

```

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Search completed: June 25, 2003, 00:24:42
Job time : 32.3586 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 1031.16 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTCTTTGTTGCTCTAGA 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
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6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfum:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_nam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
c 1	13	65.0	37	17	BH790191
c 2	12	60.0	23	17	AZ488263
c 3	12	60.0	47	17	AL764740
c 4	12	60.0	50	9	AUI07157
c 5	11	55.0	19	17	AZ323986
c 6	11	55.0	23	17	AZ468097

7	11	55.0	23	17	AZ609822
8	11	55.0	24	17	AZ308225
c 9	11	55.0	24	17	AZ333171
10	11	55.0	25	10	AW245275
11	11	55.0	27	17	AZ591593
12	11	55.0	27	17	AZ807733
13	11	55.0	29	17	AZ827060
14	11	55.0	30	17	AZ808163
c 15	11	55.0	31	9	AA929219
c 16	11	55.0	31	14	R77576
c 17	11	55.0	33	10	BE267796
c 18	11	55.0	34	9	AA911862
19	11	55.0	34	17	AZ626219
20	11	55.0	35	9	AL641482
c 21	11	55.0	35	9	AU007015
c 22	11	55.0	35	9	AU007016
23	11	55.0	35	17	AZ785723
24	11	55.0	35	17	AZ788667
25	11	55.0	36	17	AZ446375
26	11	55.0	36	17	AZ512567
27	11	55.0	37	9	AA972505
28	11	55.0	39	14	C02027
29	11	55.0	40	9	AI118679
30	11	55.0	41	17	AZ793496
c 31	11	55.0	42	17	AZ807193
32	11	55.0	43	9	AI266869
c 33	11	55.0	45	12	BE896253
c 34	11	55.0	46	17	AZ345913
c 35	11	55.0	49	9	AZ267816
c 36	11	55.0	49	9	AI687910
37	11	55.0	50	9	AU105307
c 38	11	55.0	50	9	AA607953
39	10	50.0	17	10	AW247165
40	10	50.0	17	10	AW248574
c 41	10	50.0	19	9	AA934303
c 42	10	50.0	19	17	AZ650252
c 43	10	50.0	20	17	AZ579122
44	10	50.0	21	17	AZ308846
45	10	50.0	21	17	AZ627840

ALIGNMENTS

RESULT 1
BH790191/c 37 bp DNA linear GSS 02-APR-2002
LOCUS SALK_056569.17.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_056569.17.50.x, DNA sequence.
ACCESSION BH790191 GI:19883289
VERSION BH790191
KEYWORDS GSS,
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 37)
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckersalk.edu
This is single pass sequence recovered from the left border of

TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. 37
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_056569.17.50.x"
/notes="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

BASE COUNT 11 a 8 c 11 g 7 t
ORIGIN

Query Match 65.0%; Score 13; DB 17; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.2e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTTCCTC 16
|||||
Db 36 TTTTGTTCCTC 24
|||||

RESULT 2
AZ488263/c
LOCUS
DEFINITION
clone UUGC1M0318N21 F, DNA sequence.
ACCESSION
AZ488263
VERSION
GSS.
KEYWORDS
SOURCE
ORGANISM
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Irlam, H., Longacre, S., Mahmud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0318 row: N column: 21
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. 23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0318N21"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: FWD2nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor-mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 13 a 4 c 3 g 3 t
ORIGIN

Query Match 60.0%; Score 12; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTTCCTC 15
|||||
Db 20 TTTTGTTCCTC 9
|||||

RESULT 3
AL764740
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence GK-130E02-012667,
genomic survey sequence.
ACCESSION
AL764740
VERSION
AL764740.1 GI:21517783
KEYWORDS
GSS.
SOURCE
ORGANISM
Arabidopsis thaliana
thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.,
and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
2
Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
Unpublished
3 (bases 1 to 47)
Strizhov, N., Li, Y., Rosso, M. and Weisshaar, B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene At2g31610. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
Location/Qualifiers
1. 47
/organism="Arabidopsis thaliana"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-130E02-012667"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

BASE COUNT 10 a 5 c 10 g 22 t
 ORIGIN
 Query Match 60.0%; Score 12; DB 17; Length 47;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTT 12
 |||||
 Db 20 CATTGTTGTTT 31

RESULT 4
 AUI07157
 LOCUS
 DEFINITION AUI07157 Sugano Homo sapiens cDNA library EST 30-AUG-2001
 LNG02840, mRNA sequence.

ACCESSION AUI07157
 VERSION AUI07157.1 GI:13556678
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 50)

REFERENCE
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
 ENBO Rep. 2 (5), 388-393 (2001)
 21270072

COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano, S.
 Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="LNG02840"
 /clone_lib="Sugano Homo sapiens cDNA library"
 /note="Differential display comparison of untreated and dimethylformate treated U937 cells"
 BASE COUNT 7 a 10 c 8 g 25 t
 ORIGIN

Query Match 60.0%; Score 12; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ATTGTTGTTG 13
 |||||
 Db 1 ATTGTTGTTG 12

RESULT 5
 AZ323986
 LOCUS
 DEFINITION AZ323986 19 bp DNA linear GSS 29-SEP-2000
 IM0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0045P09 R, DNA sequence.
 ACCESSION AZ323986

VERSION AZ323986.1 GI:10379252
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE
 JOURNAL
 COMMENT

UNPUBLISHED (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0045 row: P column: 09

Seq primer: CACACAGGAACAGCTATGACC
 Class: plasmid ends

High quality sequence stop: 19.
 Location/Qualifiers

FEATURES

source
 1..19
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0045P09"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 0 a 2 c 3 g 14 t
 ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13
 |||||
 Db 5 TTTTGTGTTG 15

RESULT 6
 AZ468097
 LOCUS
 DEFINITION AZ468097 23 bp DNA linear GSS 04-OCT-2000
 IM0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0279K22 R, DNA sequence.
 ACCESSION AZ468097

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VERSION      AZ468097.1  GI:10626222
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
COMMENT      University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0279 row: K column: 22
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0279K22"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G114732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT   0 a 0 c 4 g 19 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
Db 3 TTTTGTGTTG 13

RESULT 7
AZ509822
LOCUS      23 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0434113R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0434J13 R, DNA sequence.
ACCESSION  AZ509822

VERSION      AZ609822.1  GI:11732012
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
JOURNAL      Contact: Robert B. Weiss
COMMENT      University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0434 row: J column: 13
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1. .23
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0434J13"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: pMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 Kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (G114732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT   0 a 0 c 6 g 17 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
Db 1 TTTTGTGTTG 11

RESULT 8
AZ308225
LOCUS      24 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M001E08F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M001E06 F, DNA sequence.
ACCESSION  AZ308225

```

```

VERSION      AZ308225.1  GI:10348004
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 24)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0011 row: E column: 06
              Seq primer: CGTGTAAACGACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 24.
FEATURES     Location/Qualifiers
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                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0011E06"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   1 a      0 c      4 g      19 t
ORIGIN
Query Match      55.0%; Score 11; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 TTTTGTGTTG 13
    |||||
Db   4 TTTTGTGTTG 14

RESULT 9
AZ333171/c
LOCUS
DEFINITION 24 bp DNA linear GSS 29-SEP-2000
ACCESSION  AZ333171
LOCUS
DEFINITION 1M0062B08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
              clone UUGC1M0062B08 F, DNA sequence.
ACCESSION  AZ333171

```

```

VERSION      AZ333171.1  GI:10397528
KEYWORDS     GSS.
SOURCE       house mouse.
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
              1 (bases 1 to 24)
              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
              M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
              and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0062 row: B column: 08
              Seq primer: CGTGTAAACGACGCGCCAGT
              Class: plasmid ends
              High quality sequence stop: 24.
FEATURES     Location/Qualifiers
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                /strain="C57BL/6J"
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                /clone="UUGC1M0062B08"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adapted DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adapted mouse DNA was annealed to
              adapted vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
BASE COUNT   16 a      4 c      1 g      3 t
ORIGIN
Query Match      55.0%; Score 11; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CATTGTTGTT 11
    |||||
Db   16 CATTGTTGTT 6

RESULT 10
AW245275
LOCUS
DEFINITION 2819996.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819996 3',
              mRNA sequence.
ACCESSION  AW245275

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VERSION  AW245275.1  GI:6588268
SOURCE    EST.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT  Unpublished (1999)
Other ESTs: 2819996.5prime
Contact: Robert Strausberg, Ph.D.
Email: cga@bte-mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing
Project Clone Distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNI at:
www.bio.llni.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 25 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L1CM3 row: A column: 21.
Location/Qualifiers
FEATURES             source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAG:2819996"
/clone_lib="NIH_MGC_7"
/tissue_type="small_cell carcinoma"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCGCGG(G) Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT  3 a 1 c 3 g 18 t
ORIGIN
Query Match 55.0%; Score 11; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 TTTTGTGTTG 13
Db  5 TTTTGTGTTG 15

RESULT 11
AZ591593
LOCUS  IM0401115R Mouse 10kb plasmid UGClM library Mus musculus genomic
DEFINITION clone UGClM0401115 R, DNA sequence.
ACCESSION AZ591593
VERSION  AZ591593.1 GI:11713783
KEYWORDS GSS.
SOURCE  house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

AW245275.1  GI:6588268
SOURCE    EST.
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE    NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL  National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT  Unpublished (1999)
Other ESTs: 2819996.5prime
Contact: Robert Strausberg, Ph.D.
Email: cga@bte-mail.nih.gov
Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNI) DNA Sequencing by: Berkeley MGC sequencing
Project Clone Distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNI at:
www.bio.llni.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 25 contiguous distinct peaks
following vector sequence. Polyadenylation: Based upon the presence
of a XhoI site followed by a run of 14 or more T residues at the
beginning of the sequence, this cDNA insert was polyadenylated.
Plate: L1CM3 row: A column: 21.
Location/Qualifiers
FEATURES             source
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAG:2819996"
/clone_lib="NIH_MGC_7"
/tissue_type="small_cell carcinoma"
/lab_hosts="DH10B (phage-resistant)"
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCGCGG(G) Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT  3 a 1 c 3 g 18 t
ORIGIN
Query Match 55.0%; Score 11; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 TTTTGTGTTG 13
Db  5 TTTTGTGTTG 15

RESULT 11
AZ591593
LOCUS  IM0401115R Mouse 10kb plasmid UGClM library Mus musculus genomic
DEFINITION clone UGClM0401115 R, DNA sequence.
ACCESSION AZ591593
VERSION  AZ591593.1 GI:11713783
KEYWORDS GSS.
SOURCE  house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0401 row: I column: 15
Seq primer: CACACAGGAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers
FEATURES             source
1..27
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGClM0401115"
/clone_lib="Mouse 10kb plasmid UGClM library"
/sex="Male"
/lab_hosts="B. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI:4732114) [gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
the adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT  1 a 0 c 6 g 20 t
ORIGIN
Query Match 55.0%; Score 11; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 TTTTGTGTTG 13
Db  1 TTTTGTGTTG 11

RESULT 12
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LOCUS  2M0070H16R Mouse 10kb plasmid UGClM library Mus musculus genomic
DEFINITION clone UGClM0070H16 R, DNA sequence.
ACCESSION AZ807733
VERSION  AZ807733.1 GI:12972374
KEYWORDS GSS.
SOURCE  house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

```

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE
JOURNAL
COMMENT

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0070 row: H column: 16

Seq primer: CACACAGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 27.

FEATURES
source

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    /clone="UUGC2M0070H16"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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BASE COUNT
ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13

Db 1 TTTTGTGTTG 11

RESULT 13

AZ827060

LOCUS

2M0103F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0103F17 F, DNA sequence.

DEFINITION

ACCESSION

AZ827060

VERSION

AZ827060.1 GI:12996968

KEYWORDS

GSS.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb

TITLE
JOURNAL
COMMENT

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0103 row: F column: 17

Seq primer: CGTTGTAACACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 29.

FEATURES
source

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1. .29
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    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone="UUGC2M0103F17"
    /sex="Male"
    /lab_host="E. Coli strain XL10-Gold, TI-resistant, P-"
    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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BASE COUNT
ORIGIN

Query Match 55.0%; Score 11; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTG 13

Db 5 TTTTGTGTTG 15

RESULT 14

AZ808163

LOCUS

2M0071N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0071N08 R, DNA sequence.

DEFINITION

ACCESSION

AZ808163

VERSION

AZ808163.1 GI:12973424

KEYWORDS

GSS.

SOURCE

ORGANISM

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 30)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 877.928 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTGTTTGTTCCTCTAGA 20

Scoring table:

Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Pending Patents_NA_New:*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
- 8: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 9: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 10: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
- 11: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*
- 13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	90.0	19	1	PCT-US03-04088-15
C 2	18	90.0	19	1	PCT-US03-04088-15
C 3	18	90.0	28	6	US-09-690-885-5
C 4	15	75.0	25	9	US-10-355-577-635066
C 5	14	70.0	18	9	US-10-310-188-64233
C 6	14	70.0	25	12	US-60-427-808-525499
C 7	14	70.0	22	12	US-60-427-808-982397
C 8	13	65.0	22	9	US-10-310-188-3317
C 9	13	65.0	25	9	US-10-355-577-14566
C 10	13	65.0	25	9	US-10-355-577-226117
C 11	13	65.0	25	9	US-10-355-577-949348
C 12	13	65.0	25	12	US-60-427-808-76032
C 13	13	65.0	25	12	US-60-427-808-523567
C 14	13	65.0	25	12	US-60-427-808-774039
C 15	13	65.0	25	12	US-60-427-836-281208
C 16	13	65.0	25	12	US-60-427-836-392577
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C 18	13	65.0	25	13	US-60-469-545-142606
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C 20	12	60.0	18	9	US-10-310-188-84760

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C 22	12	60.0	25	1	PCT-US02-10873A-373	Sequence 373, App
C 23	12	60.0	25	9	US-10-355-577-226115	Sequence 226115,
C 24	12	60.0	25	9	US-10-355-577-231716	Sequence 231716,
C 25	12	60.0	25	9	US-10-355-577-300369	Sequence 300369,
C 26	12	60.0	25	9	US-10-355-577-486926	Sequence 486926,
C 27	12	60.0	25	9	US-10-355-577-578563	Sequence 578563,
C 28	12	60.0	25	9	US-10-355-577-583938	Sequence 583938,
C 29	12	60.0	25	9	US-10-355-577-710151	Sequence 710151,
C 30	12	60.0	25	9	US-10-355-577-923328	Sequence 923328,
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C 32	12	60.0	25	9	US-10-355-577-970825	Sequence 970825,
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C 34	12	60.0	25	12	US-60-417-190-101304	Sequence 101304,
C 35	12	60.0	25	12	US-60-417-190-101305	Sequence 101305,
C 36	12	60.0	25	12	US-60-417-190-101306	Sequence 101306,
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C 38	12	60.0	25	12	US-60-417-190-101311	Sequence 101311,
C 39	12	60.0	25	12	US-60-417-190-101312	Sequence 101312,
C 40	12	60.0	25	12	US-60-417-190-101313	Sequence 101313,
C 41	12	60.0	25	12	US-60-417-190-101314	Sequence 101314,
C 42	12	60.0	25	12	US-60-427-808-47418	Sequence 47418, A
C 43	12	60.0	25	12	US-60-427-808-83312	Sequence 83312, A
C 44	12	60.0	25	12	US-60-427-808-137138	Sequence 137138,
C 45	12	60.0	25	12	US-60-427-808-148620	Sequence 148620,

ALIGNMENTS

RESULT 1

PCT-US03-04088-15/C
; Sequence 15, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-15

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 TTTTGTGTTGCTCTAGA 20
DB 19 TTTTGTGTTGCTCTAGA 2

RESULT 2
PCT-US03-04088-279
; Sequence 279, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR FILING DATE: 2002-07-17
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2002-03-11
; PRIOR FILING DATE: 2002-06-06
; PRIOR FILING DATE: 2002-08-29
; PRIOR FILING DATE: 2002-09-05
; PRIOR FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-279

Query Match 90.0%; Score 18; DB 1; Length 19;
Best Local Similarity 38.9%; Pred. No. 30;
Matches 7; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
DB 1 UUUUUUUUUCUUA 18

RESULT 3
US-09-690-885-5/c
; Sequence 5, Application US/09690885
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; UENO, HARUMI
; OSHISHI
; KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/690,885
; FILING DATE: 18-Oct-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0319P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-690-885-5

Query Match 90.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
DB 21 TTTTGTGTTGCTCTAGA 4

RESULT 4
US-10-355-577-635066
; Sequence 635066, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-635066

Query Match 75.0%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGTTGCTCTA 18
DB 4 TTTTGTGTTGCTCTA 18

RESULT 5
US-10-310-188-64233
; Sequence 64233, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GEN-
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 64233
; LENGTH: 18
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-64233

Query Match      70.0%; Score 14; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTC 16
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Db 5 TTTTGTGTTGCTC 18
   |||||

RESULT 6
US-60-427-808-525499
; Sequence 525499, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 525499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-525499

Query Match      70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTTTGTGTTGCTCA 18
   |||||
Db 3 TTTTGTGTTGCTCA 16
   |||||

RESULT 7
US-60-427-808-982397
; Sequence 982397, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 982397
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-982397

Query Match      70.0%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTTTGTGTTGCTCT 17
   |||||
Db 1 TTTTGTGTTGCTCT 14
   |||||

RESULT 8
US-10-310-188-3317
; Sequence 3317, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENE
; FILE REFERENCE: 47487

; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3317
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-3317

Query Match      65.0%; Score 13; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCT 15
   |||||
Db 4 TTTTGTGTTGCT 16
   |||||

RESULT 9
US-10-355-577-14566
; Sequence 14566, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 14566
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-14566

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTTTGTGTTGCTCT 17
   |||||
Db 10 TTTTGTGTTGCTCT 22
   |||||

RESULT 10
US-10-355-577-226117/C
; Sequence 226117, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-U133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 226117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-226117

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTGC 14
   |||||
Db 25 ATTTTGTGTTGC 13
   |||||

RESULT 11
US-10-355-577-949348/c
```

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; Sequence 949348, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 949348
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-949348

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TGTTCCTCTAGA 20
DB      25 TGTTCCTCTAGA 13

RESULT 12
US-60-427-808-76032
; Sequence 76032, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76032
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-76032

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTTCCTCTTG 13
DB      10 CATTTCCTCTTG 22

RESULT 13
US-60-427-808-523567
; Sequence 523567, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 523567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-523567

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TGTTCCTCTAG 19
DB      7 TGTTCCTCTAG 19

; Sequence 949348, Application US/10355577
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI33
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/10/355,577
; CURRENT FILING DATE: 2003-01-31
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 949348
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-355-577-949348

Query Match      65.0%; Score 13; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 TGTTCCTCTAGA 20
DB      25 TGTTCCTCTAGA 13

RESULT 12
US-60-427-808-76032
; Sequence 76032, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 76032
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-76032

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTTCCTCTTG 13
DB      10 CATTTCCTCTTG 22

RESULT 13
US-60-427-808-523567
; Sequence 523567, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 523567
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-523567

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 TGTTCCTCTAG 19
DB      7 TGTTCCTCTAG 19

; Sequence 774039, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 774039
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-774039

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CATTTCCTCTTG 13
DB      4 CATTTCCTCTTG 16

RESULT 15
US-60-427-836-281208
; Sequence 281208, Application US/60427836
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527
; CURRENT APPLICATION NUMBER: US/60/427,836
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 281208
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-60-427-836-281208

Query Match      65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 TTTTGTCTCTCT 17
DB      7 TTTTGTCTCTCT 19

Search completed: June 23, 2003, 19:12:14
Job time : 878.928 secs
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1677.45 Seconds
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299.770 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	11	US-08-770-564A-13
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4	19	95.0	20	21	US-09-540-119B-16
5	17	85.0	22	22	US-09-587-662A-5
6	16	80.0	24	13	US-08-973-589-18
c 7	16	80.0	25	36	US-09-954-427-58350
c 8	16	80.0	25	67	US-60-233-166-58350
c 9	15	75.0	25	36	US-09-954-427-58351
c 10	15	75.0	25	67	US-60-233-166-58351
c 11	15	75.0	25	79	US-60-353-987-635066
c 12	14	70.0	25	36	US-09-954-427-58352
c 13	14	70.0	25	67	US-60-233-166-58352
c 14	14	70.0	41	36	US-09-953-198-241
c 15	13	65.0	13	21	US-09-540-119B-19
c 16	13	65.0	13	21	US-09-540-119B-20
c 17	13	65.0	25	36	US-09-954-427-379210
c 18	13	65.0	25	36	US-09-954-427-408651
c 19	13	65.0	25	36	US-09-954-427-408670
c 20	13	65.0	25	67	US-60-233-166-379210
c 21	13	65.0	25	67	US-60-233-166-408651

C 22 13 65.0 25 67 US-60-233-166-408670
C 23 13 65.0 25 79 US-60-353-387-14566
C 24 13 65.0 25 79 US-60-353-387-14566
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C 27 13 65.0 25 79 US-60-353-387-14566
C 28 13 65.0 25 79 US-60-353-387-14566
C 29 13 65.0 25 79 US-60-353-387-14566
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C 31 13 65.0 25 79 US-60-353-387-14566
C 32 13 65.0 25 79 US-60-353-387-14566
C 33 13 65.0 25 79 US-60-353-387-14566
C 34 13 65.0 25 79 US-60-353-387-14566
C 35 13 65.0 25 79 US-60-353-387-14566
C 36 13 65.0 25 79 US-60-353-387-14566
C 37 13 65.0 25 79 US-60-353-387-14566
C 38 13 65.0 25 79 US-60-353-387-14566
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C 40 13 65.0 25 79 US-60-353-387-14566
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C 42 13 65.0 25 79 US-60-353-387-14566
C 43 13 65.0 25 79 US-60-353-387-14566
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C 45 13 65.0 25 79 US-60-353-387-14566

ALIGNMENTS

RESULT 1
PCT-US97-23619-13
; Sequence 13, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

Sequence 408670, A
Sequence 14566, A
Sequence 226117, A
Sequence 949348, A
Sequence 885, A
Sequence 17, A
Sequence 8256, A
Sequence 1170, A
Sequence 1171, A
Sequence 1172, A
Sequence 1173, A
Sequence 1174, A
Sequence 1175, A
Sequence 9743, A
Sequence 9746, A
Sequence 5, A
Sequence 5, A
Sequence 67371, A
Sequence 67372, A
Sequence 67371, A
Sequence 67372, A
Sequence 62, A
Sequence 58419, A
Sequence 317896, A

; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..20
; OTHER INFORMATION: /note= "oligo 20/21"
PCT-US97-23619-13
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTTTGGTCTCTAGA 20
Db 1 CATTTTTGGTCTCTAGA 20
RESULT 2
US-08-770-564A-13
; Sequence 13, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-13
Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTTTTGGTCTCTAGA 20
Db 1 CATTTTTGGTCTCTAGA 20
RESULT 3
US-08-521-634-10/c

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; Sequence 10, Application US/08521634
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,634
; FILING DATE: 31-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 7-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 7-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Tracy J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 15389-000850
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (oligonucleotide)
US-08-521-634-10

Query Match 100.0%; Score 20; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTGCTCTAGA 20
Db 28 CATTGTTGTTGCTCTAGA 9

RESULT 4
US-09-540-119B-16
; Sequence 16, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-16

Query Match 95.0%; Score 19; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTGCTCTAG 19
Db 2 CATTGTTGTTGCTCTAG 20

RESULT 5
US-09-587-662A-5
; Sequence 5, Application US/09587662A
; GENERAL INFORMATION:
; APPLICANT: Au, Jessie L.-S.
; APPLICANT: Wientjes, M. Guillaume
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING DRUG ACTIVITY
; TITLE OF INVENTION: THROUGH TELOMERE DAMAGE
; FILE REFERENCE: JAG-004
; CURRENT APPLICATION NUMBER: US/09/587,662A
; CURRENT FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/137,549
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer/probe
US-09-587-662A-5

Query Match 85.0%; Score 17; DB 22; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTGCTCT 17
Db 8 CATTGTTGTTGCTCT 24

RESULT 6
US-08-973-589-18
; Sequence 18, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; TITLE OF INVENTION: TELOMERASE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-08-973-589-18
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Query Match 80.0%; Score 16; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CATTGTTGTTGCTC 16
Db 7 CATTGTTGTTGCTC 22

RESULT 7

US-09-954-427-58350/c
; Sequence 58350, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-09-954-427-58350

Query Match 80.0%; Score 16; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTTGTGTTGCTCTAG 19
Db 25 TTTTGTGTTGCTCTAG 10

RESULT 8

US-60-233-166-58350/c
; Sequence 58350, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58350
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-60-233-166-58350

Query Match 80.0%; Score 16; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTTTGTGTTGCTCTAG 19
Db 25 TTTTGTGTTGCTCTAG 10

RESULT 9

US-09-954-427-58351/c
; Sequence 58351, Application US/09954427

; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-09-954-427-58351

Query Match 75.0%; Score 15; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTTTGTGTTGCTCTAG 19
Db 25 TTTTGTGTTGCTCTAG 11

RESULT 10

US-60-233-166-58351/c
; Sequence 58351, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58351
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-60-233-166-58351

Query Match 75.0%; Score 15; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTTTGTGTTGCTCTAG 19
Db 25 TTTTGTGTTGCTCTAG 11

RESULT 11

US-60-353-987-635066
; Sequence 635066, Application US/60353987
; GENERAL INFORMATION:
; APPLICANT: Mittmann, Michael
; TITLE OF INVENTION: Methods of Genetic Analysis of Probes: HG-UI133
; FILE REFERENCE: 3121
; CURRENT APPLICATION NUMBER: US/60/353,987
; CURRENT FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 997516
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 635066
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-353-987-635066

Query Match 75.0%; Score 15; DB 79; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 TTTTGTGTTGCTCTA 18
|||||
Db 4 TTTTGTGTTGCTCTA 18

RESULT 12
US-09-954-427-58352/c
; Sequence 58352, Application US/09954427
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/09/954,427
; CURRENT FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-09-954-427-58352

Query Match 70.0%; Score 14; DB 36; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TTTGTTTGTCTAG 19
|||||
Db 25 TTTGTTTGTCTAG 12

RESULT 13
US-60-233-166-58352/c
; Sequence 58352, Application US/60233166
; GENERAL INFORMATION:
; APPLICANT: Mittmann
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis of the Rat
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 3112
; CURRENT APPLICATION NUMBER: US/60/233,166
; CURRENT FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 420907
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58352
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank AA819129
US-60-233-166-58352

Query Match 70.0%; Score 14; DB 67; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 TTTGTTTGTCTAG 19
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Db 25 TTTGTTTGTCTAG 12

RESULT 14
US-09-953-198-241
; Sequence 241, Application US/09953198

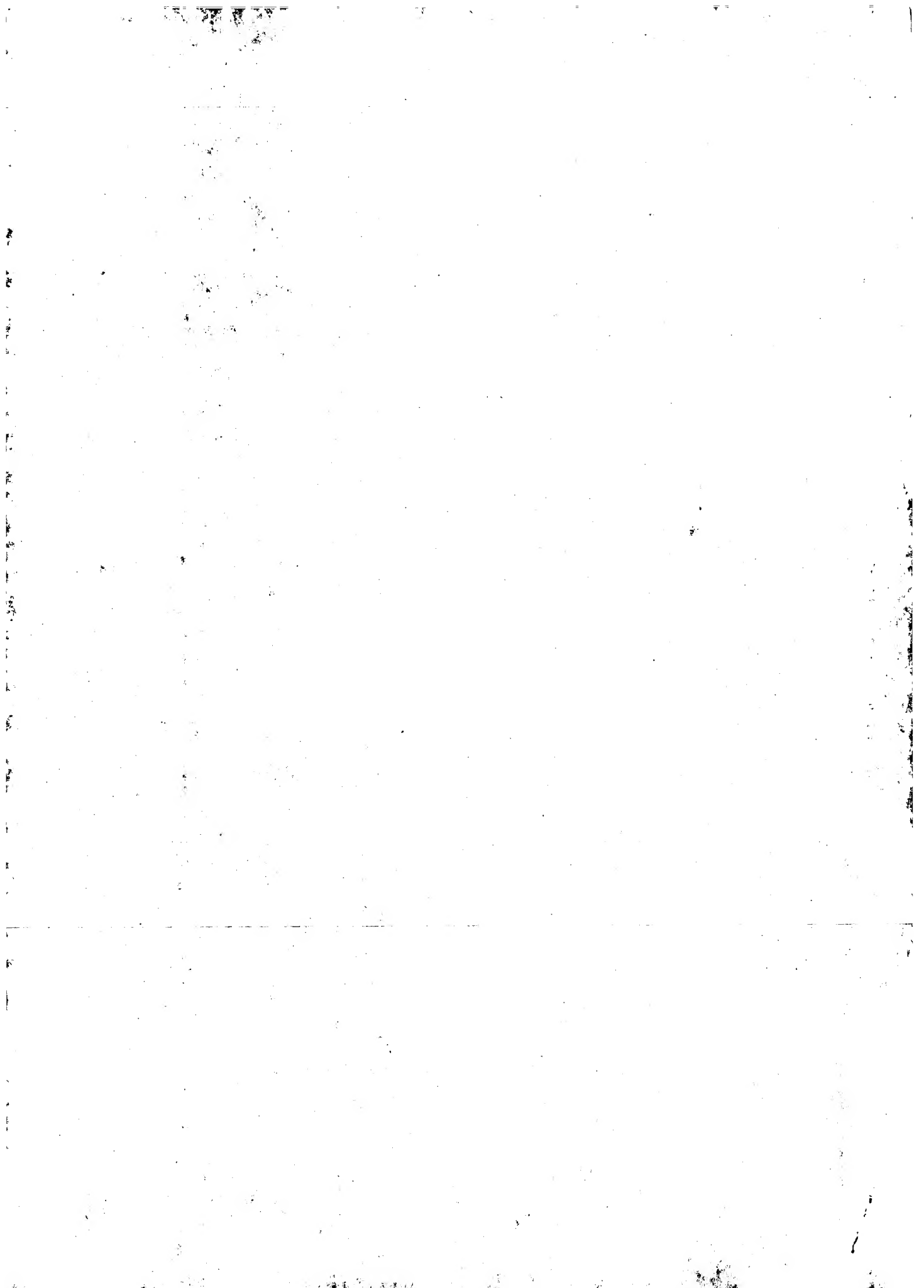
; GENERAL INFORMATION:
; APPLICANT: COMPUGEN LTD
; TITLE OF INVENTION: DATA BASE OF SNP
; FILE REFERENCE: 1351253
; CURRENT APPLICATION NUMBER: US/09/953,198
; CURRENT FILING DATE: 2001-08-12
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-953-198-241

Query Match 70.0%; Score 14; DB 36; Length 41;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ATTTTGTGTTGCT 15
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Db 2 ATTTTGTGTTGCT 15

RESULT 15
US-09-540-119B-19
; Sequence 19, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-19

Query Match 65.0%; Score 13; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 TTTTGTGTTGCT 15
|||||
Db 1 TTTTGTGTTGCT 13

Search completed: June 23, 2003, 16:08:24
Job time : 1678.53 secs



GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model.

Run on: June 23, 2003, 06:41:29 ; Search time 160.717 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20

Sequence: 1 CATTGTTTGTGCTCTAGA 20

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Post-processing: Listing first 45 summaries

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Published Applications NA.*
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	12	60.0	35	10	US-09-765-272-248
5	12	60.0	38	9	US-10-085-906-285
6	12	60.0	40	10	US-09-245-802-103
7	12	60.0	40	10	US-09-245-802-110
8	12	60.0	40	10	US-09-765-272-253
9	12	60.0	42	9	US-09-769-787-375
10	11	55.0	20	9	US-09-403-609-15
11	11	55.0	20	9	US-09-918-026A-53
12	11	55.0	21	9	US-10-109-728A-15
13	11	55.0	21	9	US-09-997-868-13
14	11	55.0	21	10	US-09-263-959-969
15	11	55.0	24	9	US-09-940-185-2806
16	11	55.0	25	9	US-10-098-263B-72610
17	11	55.0	25	9	US-10-098-263B-92356
18	11	55.0	25	9	US-10-098-263B-118744
19	11	55.0	26	10	US-09-426-548-133

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c	21	11	55.0	27	9	US-09-232-785-359	Sequence 359, Appl
c	22	11	55.0	28	10	US-09-975-408-41	Sequence 41, Appl
c	23	11	55.0	28	12	US-10-075-579-41	Sequence 41, Appl
c	24	11	55.0	29	10	US-09-887-576-424	Sequence 424, Appl
c	25	11	55.0	31	9	US-09-815-533-2	Sequence 2, Appl
c	26	11	55.0	33	10	US-09-765-272-370	Sequence 370, Appl
c	27	11	55.0	39	10	US-09-057-351-12	Sequence 12, Appl
c	28	11	55.0	41	9	US-10-085-906-99	Sequence 99, Appl
c	29	11	55.0	47	9	US-09-853-526-196	Sequence 196, Appl
c	30	11	55.0	47	10	US-09-901-484A-196	Sequence 196, Appl
c	31	10	50.0	17	8	US-08-983-605-224	Sequence 224, Appl
c	32	10	50.0	17	9	US-10-041-856-21	Sequence 21, Appl
c	33	10	50.0	17	9	US-09-825-805-557	Sequence 557, Appl
c	34	10	50.0	17	9	US-10-163-552-984	Sequence 984, Appl
c	35	10	50.0	18	9	US-10-198-069-43	Sequence 43, Appl
c	36	10	50.0	20	9	US-09-971-843-22	Sequence 22, Appl
c	37	10	50.0	20	9	US-10-271-887-74	Sequence 74, Appl
c	38	10	50.0	22	9	US-10-133-205-6	Sequence 6, Appl
c	39	10	50.0	22	9	US-10-112-653-55	Sequence 55, Appl
c	40	10	50.0	22	9	US-10-017-995-61	Sequence 61, Appl
c	41	10	50.0	22	9	US-09-776-479-61	Sequence 61, Appl
c	42	10	50.0	23	9	US-10-112-653-767	Sequence 767, Appl
c	43	10	50.0	23	9	US-10-017-995-794	Sequence 794, Appl
c	44	10	50.0	23	9	US-09-776-479-794	Sequence 794, Appl
c	45	10	50.0	23	9	US-09-998-027-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-10-044-692-312

; Sequence 312, Application US/10044692

; Publication No. US20030096344A1

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; Lingner, Joachim

; Nakamura, Toru

; Chapman, Karen B.

; Morin, Gregg B.

; Harley, Calvin

; Andrews, William H.

; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

; NUMBER OF SEQUENCES: 335

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/044,692

; FILING DATE: 11-Jan-2002

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: 08/912,951

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

```

; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312
Query Match 60.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 2
US-10-044-539-312
; Sequence 312, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; INVENTOR: Lingner, Joachim
; INVENTOR: Nakamura, Toru
; INVENTOR: Chapman, Karen B.
; INVENTOR: Morin, Gregory B.
; INVENTOR: Harley, Calvin
; INVENTOR: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
; THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,539
; FILING DATE: 11-Jan-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/912,951
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 312:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312
Query Match 60.0%; Score 12; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 3
US-09-057-351-23
; Sequence 23, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-23

Query Match          60.0%; Score 12; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+03; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 9 GTTGTCTCTAGA 20
Db 1 GTTGTCTCTAGA 12

RESULT 4
US-09-765-272-248
; Sequence 248, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
; APPLICANT: Choi et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 248:

US-09-765-272-248
Query Match          60.0%; Score 12; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 4 TTTTGTGTTGCT 15
Db 12 TTTTGTGTTGCT 23

RESULT 5
US-10-085-906-285
; Sequence 285, Application US/10085906
; Publication No. US20030054371A1
; GENERAL INFORMATION:
; APPLICANT: Ying, Vincent
; APPLICANT: Wu, Paul
; APPLICANT: Gray, Gary S.

; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE
; FILE REFERENCE: GNN-5343CP2
; CURRENT APPLICATION NUMBER: US/10/085,906
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 60/126,215
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: US 09/534,061
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT/US00/07938
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 285
; LENGTH: 38
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-906-285

Query Match          60.0%; Score 12; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ATTTTGTGTTG 13
Db 1 ATTTTGTGTTG 12

RESULT 6
US-09-245-802-103
; Sequence 103, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 103:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
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; TOPOLOGY: circular
;
; US-09-245-802-103
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
; Matches 12; Conservative 0; Mismatches 0;
;
QY 3 TTTTTCGTTGTC 14
DB 23 TTTTTCGTTGTC 34

RESULT 7
US-09-245-802-110/c
; Sequence 110, Application US/09245802
; Patent No. US20010049125A1
; GENERAL INFORMATION:
; APPLICANT: STEMMER PH.D., WILLEM P.C.
; APPLICANT: LIPSHUTZ, ROBERT J.
; TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3634
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/245,802
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,502
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/05480
; FILING DATE: 18-APR-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY, ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 16528J-015410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: circular
; TOPOLOGY: circular
;
; US-09-245-802-110
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
; Matches 12; Conservative 0; Mismatches 0;
;
QY 3 TTTTTCGTTGTC 14
DB 38 TTTTTCGTTGTC 27

RESULT 8
US-09-765-272-253/c
; Sequence 253, Application US/09765272
; Patent No. US20020061545A1

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```

; GENERAL INFORMATION:
; APPLICANT: Choi, et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/765,272
; FILING DATE: 22-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 253:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-09-765-272-253
;
; Query Match 60.0%; Score 12; DB 10; Length 40;
; Best Local Similarity 100.0%; Pred. No. 2.4e+03; Indels 0; Gaps 0;
; Matches 12; Conservative 0; Mismatches 0;
;
QY 1 CATTTTGTGTTT 12
DB 33 CATTTTGTGTTT 22

RESULT 9
US-09-769-787-375/c
; Sequence 375, Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hanebro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: CB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 375
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
;
; US-09-769-787-375

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Query Match      60.0%; Score 12; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTT 12
   |||||
Db 40 CATTGTTGTTT 29

RESULT 10
US-09-403-609-15/c
; Sequence 15, Application US/09403609
; Publication No. US20030087229A1
; GENERAL INFORMATION:
; APPLICANT: HAKENBECK, Regine
; TITLE OF INVENTION: DNA PROBES, METHOD AND KIT FOR IDENTIFYING
; TITLE OF INVENTION: ANTIBIOTIC-RESISTANT STRAINS OF BACTERIA
; FILE REFERENCE: 012627-011
; CURRENT APPLICATION NUMBER: US/09/403,609
; CURRENT FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/DE98/01134
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: DE 197 17 346.2
; PRIOR FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-403-609-15

Query Match      55.0%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTT 11
   |||||
Db 20 CATTGTTGTTT 10

RESULT 11
US-09-918-026A-53/c
; Sequence 53, Application US/09918026A
; Publication No. US20030096772A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; APPLICANT: Kristina M. Lemonidis
; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL ACYLTRANSFERASE-2 EX
; FILE REFERENCE: ISPH-0588
; CURRENT APPLICATION NUMBER: US/09/918,026A
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 65
; SEQ ID NO 53
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-026A-53

Query Match      55.0%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGTTGCTCTA 18
   |||||
Db 14 TGTTGCTCTA 4

RESULT 12
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US-10-109-725A-15
; Sequence 15, Application US/10109725A
; Patent No. US20020177154A1
; GENERAL INFORMATION:
; APPLICANT: Gonzalgo, Mark L.
; APPLICANT: Jones, Peter A.
; APPLICANT: Liang, Gangning
; TITLE OF INVENTION: CANCER DIAGNOSTIC METHOD BASED UPON DNA METHYLATION DIFFERENCES
; FILE REFERENCE: 47675-21
; CURRENT APPLICATION NUMBER: US/10/109,725A
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/887,941
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p16 promoter region-specific Ms-SNUPE primer
US-10-109-725A-15

Query Match      55.0%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTG 13
   |||||
Db 2 TTTTGTGTTG 12

RESULT 13
US-09-997-868-13/c
; Sequence 13, Application US/09997868
; Publication No. US20030031854A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.,
; Groskreutz, Debyra J.
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,868
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/887265
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/803631
; FILING DATE: 06-DEC-1992
; APPLICATION NUMBER: PCT/US92/10621
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0748P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
```

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match          55.0%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 TTTGCTCTAGA 20
Db      14 TTTGCTCTAGA 4

RESULT 14
US-09-263-959-969/c
; Sequence 969: Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/263,959
; FILING DATE: 05-MAR-1999
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 920010.426C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4500
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 969:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-263-959-969

Query Match          55.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TTTTGTGTTG 13
Db      18 TTTTGTGTTG 8

RESULT 15
US-09-940-185-2806/c
; Sequence 2806: Application US/05940185
; Publication No. US20030096239A1
; GENERAL INFORMATION:
; APPLICANT: Gunderson, Kevin
```

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;
; APPLICANT: Chee, Mark
; TITLE OF INVENTION: Probes and Decoder Oligonucleotides
; FILE REFERENCE: A-69605-1
; CURRENT APPLICATION NUMBER: US/09/940,185
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/227,948
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/228,854
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 4768
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2806
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Computer Generated Probe Sequence.
US-09-940-185-2806

Query Match          55.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 TTTGTTTGCTC 16
Db      13 TTTGTTTGCTC 3

Search completed: June 23, 2003, 20:01:34
Job time : 161.717 secs
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 31.3147 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-13

Perfect score: 20
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/prodata/2/ina/5B-COMB.seq.*
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4: /cgn2_6/prodata/2/ina/6B-COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCTUS-COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-08-770-565-13	Sequence 13, Appl
2	18	90.0	28	US-08-318-867A-19	Sequence 19, Appl
3	18	90.0	28	US-08-952-089A-5	Sequence 5, Appl
4	12	60.0	26	US-08-330-123A-23	Sequence 23, Appl
5	12	60.0	26	US-08-482-115B-23	Sequence 23, Appl
6	12	60.0	26	US-08-660-678A-23	Sequence 23, Appl
7	12	60.0	26	US-08-710-249-26	Sequence 26, Appl
8	12	60.0	26	US-08-485-778-19	Sequence 19, Appl
9	12	60.0	26	US-08-472-802C-24	Sequence 24, Appl
10	12	60.0	26	US-08-520-550A-19	Sequence 19, Appl
11	12	60.0	26	US-08-998-443-23	Sequence 23, Appl
12	12	60.0	26	US-08-974-549A-598	Sequence 598, Appl
13	12	60.0	26	US-09-060-523-23	Sequence 23, Appl
14	12	60.0	26	US-09-220-157A-26	Sequence 26, Appl
15	12	60.0	26	US-09-286-959B-4	Sequence 4, Appl
16	12	60.0	26	US-09-580-517-23	Sequence 23, Appl
17	12	60.0	27	US-08-770-565-26	Sequence 26, Appl
18	12	60.0	30	US-08-833-377-5	Sequence 5, Appl
19	12	60.0	35	US-08-961-083-248	Sequence 248, Appl
20	12	60.0	40	US-08-425-684-103	Sequence 103, Appl
21	12	60.0	40	US-08-425-684-110	Sequence 110, Appl
22	12	60.0	40	US-08-675-502-103	Sequence 103, Appl
23	12	60.0	40	US-08-675-502-110	Sequence 110, Appl
24	12	60.0	40	US-08-961-083-253	Sequence 253, Appl
25	12	60.0	41	US-08-332-420-57	Sequence 57, Appl
26	12	60.0	42	US-08-639-256-6	Sequence 6, Appl
27	12	60.0	43	US-08-639-256-7	Sequence 7, Appl

28	11	55.0	21	4	US-09-094-207A-15	Sequence 15, Appl
29	11	55.0	21	4	US-09-311-912-51	Sequence 51, Appl
c 30	11	55.0	21	4	US-08-026-143B-13	Sequence 13, Appl
c 31	11	55.0	21	5	PCT-US92-10621-13	Sequence 13, Appl
c 32	11	55.0	21	5	PCT-US94-02213-13	Sequence 13, Appl
c 33	11	55.0	24	2	US-08-529-190B-44	Sequence 44, Appl
34	11	55.0	24	2	US-08-859-998-119	Sequence 119, Appl
35	11	55.0	24	4	US-09-225-928-119	Sequence 119, Appl
c 36	11	55.0	25	3	US-09-010-641-15	Sequence 15, Appl
c 37	11	55.0	25	4	US-09-356-281-15	Sequence 15, Appl
38	11	55.0	27	2	US-08-766-439-17	Sequence 17, Appl
c 39	11	55.0	28	4	US-09-710-200-41	Sequence 41, Appl
40	11	55.0	30	2	US-08-766-439-89	Sequence 89, Appl
41	11	55.0	30	2	US-08-766-439-91	Sequence 91, Appl
42	11	55.0	33	3	US-08-961-083-370	Sequence 370, Appl
43	11	55.0	37	2	US-08-702-572-11	Sequence 11, Appl
c 44	11	55.0	39	1	US-08-330-123A-12	Sequence 12, Appl
c 45	11	55.0	39	1	US-08-482-115B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-13
; Sequence 13, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770.565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-13

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20

Db 1 CATTGTTGTTGCTCTAGA 20
|||||

RESULT 2
US-08-318-867A-19/c
; Sequence 19, Application US/08318867A
; Patent No. 5714323
; GENERAL INFORMATION:
; APPLICANT: ATUSHI OHSHIMA
; APPLICANT: SUMIKO INOUE
; APPLICANT: MASAYORI INOUE
; TITLE OF INVENTION: OVER EXPRESSION OF SINGLE-STRANDED
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES, P.C.
; STREET: 230 S. 15th St.
; CITY: PHILADELPHIA, PA
; COUNTRY: U.S.A.
; ZIP: 19102

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,867A
; FILING DATE: MAY 4, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: GERARD J. WEISER
; REFERENCE/DOCKET NUMBER: 377.6120P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 875-8383
; TELEFAX: (215) 875-8394
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-318-867A-19

Query Match 90.0%; Score 18; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTGCTCTAGA 20
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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 3
US-08-952-089A-5/c
; Sequence 5, Application US/08952089A
; Patent No. 6165749
; GENERAL INFORMATION:
; APPLICANT: SAGAWA, HIROAKI
; APPLICANT: UENO, HARUMI
; APPLICANT: OSHIMA, ATSUSHI
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: PLASMID
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,089A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WEINER, MARC S.
; REGISTRATION NUMBER: 32,181
; REFERENCE/DOCKET NUMBER: 1422-0319P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-952-089A-5

Query Match 90.0%; Score 18; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTTTGTGTTGCTCTAGA 20
|||
Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 4
US-08-330-123A-23
; Sequence 23, Application US/08330123A
; Patent No. 5583016
; GENERAL INFORMATION:
; APPLICANT: VILLEPONTREAU, Bryant
; APPLICANT: FENG, Junli
; APPLICANT: FUNK, Walter
; APPLICANT: ANDREWS, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,123A
; FILING DATE: 27-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15389-000810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 60.0%; Score 12; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20
Db 1 GTTTGCTCTAGA 12

RESULT 5

US-08-482-115B-23
; Sequence 23, Application US/08482115B
; Patent No. 5776679
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELEPHONE: (415) 576-0200

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 60.0%; Score 12; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20
Db 1 GTTTGCTCTAGA 12

RESULT 6

US-08-660-678A-23
; Sequence 23, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996

CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.

REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 60.0%; Score 12; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTTGCTCTAGA 20
Db 1 GTTTGCTCTAGA 12

RESULT 7

US-08-710-249-26
; Sequence 26, Application US/08710249
; Patent No. 5858777
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLSCULE TYPE: DNA
US-08-710-249-26

Query Match 60.0%; Score 12; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 9 GTTGTCTCTAGA 20
|||||
Db 1 GTTGTCTCTAGA 12

RESULT 8
US-08-485-778-19
Sequence 19, Application US/08485778
Patent No. 5876979
GENERAL INFORMATION:
APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel Athena
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria Antonia Blasco
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,778

FILING DATE: 07-JE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-05A4
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-485-778-19

Query Match 60.0%; Score 12; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

QY 9 GTTGTCTCTAGA 20
|||||
Db 1 GTTGTCTCTAGA 12

RESULT 9
US-08-472-802C-24
Sequence 24, Application US/08472802C
Patent No. 5958680
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sich, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-24

Query Match 60.0%; Score 12; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 10

US-08-520-550A-19
Sequence 19, Application US/08520550A
Patent No. 6013468

GENERAL INFORMATION:

APPLICANT: Andrews, William H.
APPLICANT: Avilion, Ariel A.
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Greider, Carol
APPLICANT: Marhuenda, Maria A. B.
APPLICANT: Villeponteau, Bryant
TITLE OF INVENTION: RNA Component of Telomerase
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: US
ZIP: 02173

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,550A
FILING DATE: 29-AUG-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: CSHL94-05A3B

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-520-550A-19

Query Match 60.0%; Score 12; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 11

US-08-998-443-23
Sequence 23, Application US/08998443
Patent No. 6054575

GENERAL INFORMATION:

APPLICANT: Villeponteau, Bryant
APPLICANT: Funk, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,443
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678
FILING DATE: 05-JUN-1996

APPLICATION NUMBER: US 08/330,123

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/272,102

FILING DATE: 07-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Storella, John R.

REGISTRATION NUMBER: 32,944

REFERENCE/DOCKET NUMBER: 015389-000811US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-998-443-23

Query Match 60.0%; Score 12; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
DB 1 GTTGTCTCTAGA 12

RESULT 12

US-08-974-549A-598
Sequence 598, Application US/08974549A
Patent No. 6166178

```

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 598:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
NAME/KEY: -
LOCATION: 1..26

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OTHER INFORMATION: /note= "R3c primer"
US-08-974-549A-598
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Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GTTTGCTCTAGA 20
DB 1 GTTTGCTCTAGA 12
RESULT 13
US-09-060-523-23
Sequence 23, Application US/09060523
Patent No. 6258535
GENERAL INFORMATION:
APPLICANT: Villeganteau, Bryant
APPLICANT: Ferguson, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,523
FILING DATE: 14-APR-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/660,678
FILING DATE: 05-JUN-1996
APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000813US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-060-523-23
Query Match 60.0%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GTTTGCTCTAGA 20
DB 1 GTTTGCTCTAGA 12

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RESULT 14
US-09-220-157A-26
; Sequence 26, Application US/09220157A
; Patent No. 6300110
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; APPLICANT: Adams, Robert R.
; TITLE OF INVENTION: Methods and Reagents for Regulating
; TITLE OF INVENTION: Telomere Length and Telomerase Activity
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,157A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/710,249
; FILING DATE: 13-SEP-1996
; APPLICATION NUMBER: US 08/583,808
; FILING DATE: 05-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/003,492
; FILING DATE: 08-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001220US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-220-157A-26

Query Match 60.0%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
|||||
Db 1 GTTGTCTCTAGA 12

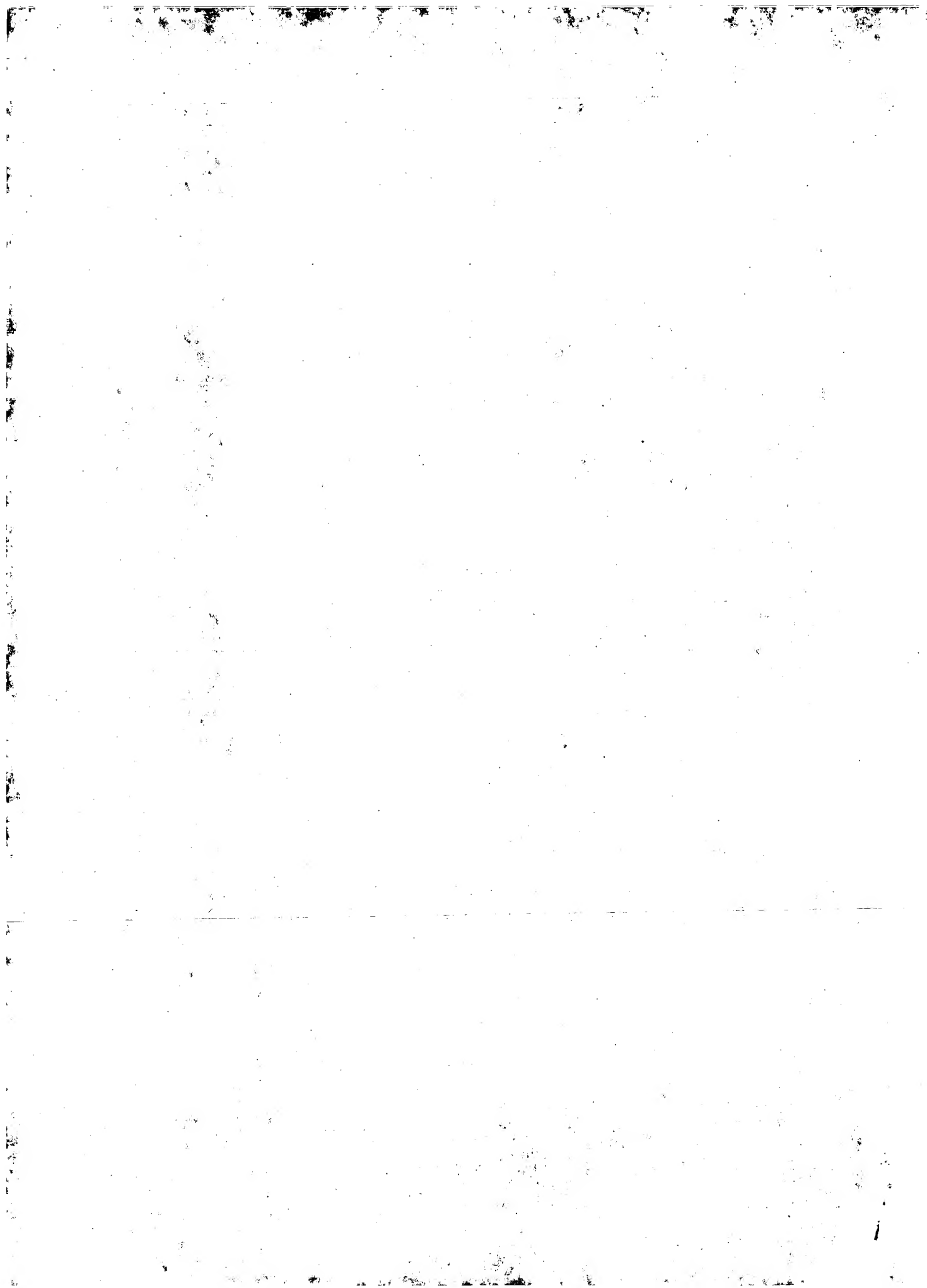
RESULT 15
US-09-286-959B-4
; Sequence 4, Application US/09286959B
; Patent No. 6300131
; GENERAL INFORMATION:
; APPLICANT: Johns Hopkins University
; APPLICANT: Greider, Carol W.
; APPLICANT: Le, Siyuan
; TITLE OF INVENTION: TELOMERASE-ASSOCIATED PROTEINS
; FILE REFERENCE: 07265/157001
; CURRENT APPLICATION NUMBER: US/09/286,959B
; CURRENT FILING DATE: 1999-04-06

; PRIOR APPLICATION NUMBER: 60/080,783
; PRIOR FILING DATE: 1998-04-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-286-959B-4

Query Match 60.0%; Score 12; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GTTGTCTCTAGA 20
|||||
Db 1 GTTGTCTCTAGA 12

Search completed: June 23, 2003, 10:17:09
Job time : 32.3147 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 132.908 Seconds
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Title: US-08-770-564A-13

Perfect score: 20
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Scoring table:
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Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0

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- 19: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
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- 22: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 24: /SID22/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	19 AAV41180	RNA component of h
2	19	95.0	20	23 AAS15934	Human telomerase p
3	18	90.0	25	22 AAC93100	Human telomerase p
4	18	90.0	28	18 AAT93259	Primer used in pre
5	16	80.0	22	18 AAT58812	Human telomerase p
6	13	65.0	13	23 AAS15937	Human telomerase p
7	13	65.0	13	23 AAS15938	Human telomerase p
8	13	65.0	24	22 AAH39806	SNP specific lower
9	12	60.0	12	23 ABH86386	Oligonucleotide pr

10	12	60.0	13	23 AAS15935	Human telomerase p
11	12	60.0	13	23 ABC09084	Oligonucleotide SE
c 12	12	60.0	13	23 ABC09085	Oligonucleotide SE
13	12	60.0	13	23 ABH44170	Oligonucleotide SE
c 14	12	60.0	13	23 ABH44171	Oligonucleotide SE
15	12	60.0	13	23 ABH59432	Oligonucleotide SE
c 16	12	60.0	13	23 ABH59433	Oligonucleotide SE
c 17	12	60.0	13	23 AAT32141	DNA sequencing "pr
c 18	12	60.0	17	17 AAT32141	FC fragment of IGG
19	12	60.0	21	22 AAH62524	SCFV1 DNA sequen
20	12	60.0	24	20 AAZ39443	Human SCFV1 primer
21	12	60.0	24	20 AAZ39443	Human SCFV1 primer
22	12	60.0	25	22 AAF23878	RNA component of h
23	12	60.0	26	17 AAT10304	RNA component of h
24	12	60.0	26	17 AAT10299	Primer for product
25	12	60.0	26	17 AAT11044	Human telomerase p
26	12	60.0	26	18 AAT58811	Human hTR gene RT-
27	12	60.0	26	19 AAV19489	Telomerase PCR pri
28	12	60.0	26	19 AAV17033	Human telomerase R
29	12	60.0	26	20 AAX90788	Human telomerase R
30	12	60.0	26	20 AAX77402	PCR primer for Hum
31	12	60.0	26	20 AAX01542	Human telomerase R
32	12	60.0	26	21 AAH88250	Human telomerase (
33	12	60.0	26	24 ABK48024	Human telomerase (
34	12	60.0	26	24 AAD24246	RNA component of h
35	12	60.0	27	19 AAV41193	Human telomerase R
36	12	60.0	27	24 ABA95497	Antisense oligonuc
37	12	60.0	30	19 AAV63648	Human telomerase R
38	12	60.0	30	20 AAZ23630	Human clone 28-1 t
39	12	60.0	30	22 AAS09475	Antisense oligonuc
40	12	60.0	33	24 AAL42603	Human serine/threo
41	12	60.0	35	19 AAV27458	Streptococcus pneu
42	12	60.0	35	24 ABQ84926	Streptococcus pneu
43	12	60.0	40	17 AAT59500	Plasmid p182Sfil c
c 44	12	60.0	40	17 AAT59507	Plasmid p182Sfil c
c 45	12	60.0	40	19 AAV27463	Streptococcus pneu
			40	20 AAX88932	Circular plasmid e

ALIGNMENTS

RESULT 1
AAV41180
ID AAV41180 standard; DNA; 20 BP.
XX AC AAV41180;
XX DT 08-OCT-1998 (first entry)
XX RNA component of human telomerase (hTR) antisense oligo 20/21.
DE RNA component; human telomerase; antisense oligonucleotide; infection;
KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW immune system down-regulation; anti-inflammatory therapy; ss.
XX Synthetic.
OS Homo sapiens.
XX WO9828442-A1.
PN 02-JUL-1998.
PD 19-DEC-1997; 97WO-US23619.
PF 20-DEC-1996; 96US-0770565.
PR 20-DEC-1996; 96US-0770564.
XX (GERO-) GERON CORP.
XX Kealey JT, Kim NW, Pruhan R, Weinrich SL, Wu F;
XX WPI; 1998-377670/32.
DR

XX New polynucleotide(s) anti-sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 11; Page 65; 80pp; English.
 XX
 CC Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridize to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridize to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting assembly
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 3 G; 11 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAGA 20
 Db 1 CATTGTTGTTGCTCTAGA 20

RESULT 2

AAS15934
 ID AAS15934 standard; DNA; 20 BP.
 AC AAS15934;
 XX
 DT 27-FEB-2002 (first entry)
 DE Human telomerase polynucleotide inhibitor #15.
 XX
 KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
 KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
 KW fertility; inflammatory condition; tumour; cancer; veterinary;
 KW immunosuppression; telomerase inhibitor; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "N3'-P5' phosphoramidate linkages"
 XX
 PN WO200174136-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US10476.
 XX
 PR 31-MAR-2000; 2000US-0540119.
 XX
 PA (GERO-) GERON CORP.

XX
 PI Gryaznov SM, Pruzan R, Weinrich SL;
 XX WPI; 2001-656955/75.
 XX
 PT New polynucleotide useful for inhibiting telomerase activity in cells,
 PT or for treating telomerase-mediated condition or disease, such as
 PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
 XX
 PS Claim 9; Page 36; 48pp; English.
 XX
 CC The invention relates to polynucleotide inhibitors (I) and methods for
 CC inhibiting telomerase activity (I) are useful in inhibiting telomerase
 CC activity and proliferation of a telomerase positive cell, and in
 CC manufacturing a medicament for inhibiting telomerase activity in a cell
 CC and in treating telomerase-mediated condition or disease, such as
 CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
 CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
 CC useful in treating a tumour or in manufacturing a medicament for the
 CC treatment of tumour. The polynucleotide inhibitors may also be used in
 CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
 CC activity in cells in vivo is useful in prophylactic and therapeutic
 CC methods of treating cancer and other disorders involving inappropriate
 CC expression of telomerase, and in treating veterinary proliferative
 CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
 CC for immunosuppression and for selectively down-regulating specific
 CC branches of the immune system. The present sequence represents
 CC human telomerase polynucleotide inhibitor #15, as described in the
 CC method of the invention.
 XX

SQ Sequence 20 BP; 3 A; 3 C; 3 G; 11 T; 0 other;

Query Match 95.0%; Score 19; DB 23; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGTTGTTGCTCTAG 19
 Db 2 CATTGTTGTTGCTCTAG 20

RESULT 3

AAC93100
 ID AAC93100 standard; DNA; 25 BP.
 AC AAC93100;
 XX
 DT 23-MAR-2001 (first entry)
 DE Human telomerase PCR primer #1.
 XX
 KW Telomerase; cancer; telomere damage; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200074667-A2.
 XX
 PD 14-DEC-2000.
 XX
 XX 05-JUN-2000; 2000WO-US15544.
 XX
 PR 04-JUN-1999; 99US-0137549.
 XX
 PA (AUJL/) AU J L.
 PA (WIEN/) WIENTJES G.
 XX
 PI Au JL, Wientjes G;
 XX
 XX WPI; 2001-071022/08.
 XX
 PT Inhibiting or reducing growth of cell for treating cancer, comprising
 PT administering telomere damage-inducing agent and telomerase inhibitory
 PT agent to the cell -

```

XX Example 7; Page 62; 97pp; English.
XX
CC The present invention provides a method for inhibiting or reducing the
CC growth of a cell which involves administering to the cell a telomere
CC damage inducing agent and a telomerase inhibitory agent. This can be
CC used in the treatment of aberrant cell growth, including cancers.
XX
SQ Sequence 25 BP; 4 A; 5 C; 4 G; 12 T; 0 other;
    Query Match          90.0%; Score 18; DB 22; Length 25;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 CATTTCCTGCTCTA 18
    DB 8 CATTTCCTGCTCTA 25

RESULT 4
AAT93259/c
ID AAT93259 standard; DNA; 28 BP.
XX
AC AAT93259;
XX
DT 27-MAR-1998 (first entry)
XX
DE Primer used in preparation of expression plasmid.
XX
KW Plasmid vector; gene expression; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9734006-A1.
XX
PD 18-SEP-1997.
XX
PF 10-MAR-1997; 97WO-JP00748.
XX
PR 18-JUL-1996; 96JP-0208897.
XX
PR 13-MAR-1996; 96JP-0085801.
XX
PA (TAKI ) TAKARA SHUZO CO LTD.
XX
PI Kato I, Oshima A, Sagawa H, Ueno H;
XX
WPI; 1997-470885/43.
XX
PT Plasmid for expression of heterologous genes in a host - contains a
PT promoter sequence recognised by a non-host RNA polymerase
XX
PS Disclosure; Page 53; 102pp; Japanese.
XX
CC The present sequence was used in the preparation of a plasmid
CC vector for the expression of foreign genes in a host, e.g. E. coli,
CC contains a promoter sequence, which is recognised by a non-host RNA
CC polymerase and a replication origin which increases the number of
CC copies when induced by an extracellular augmentation factor. The
CC use of the plasmid vector allows the efficient expression of
CC proteins which may be fatal or harmful to a host, e.g. the
CC restriction enzyme AccII. The vector allows expression of the
CC restriction enzyme gene even in the absence of a modification
CC enzyme gene.
XX
SQ Sequence 28 BP; 15 A; 7 C; 4 G; 2 T; 0 other;
    Query Match          90.0%; Score 18; DB 18; Length 28;
    Best Local Similarity 100.0%; Pred. No. 5.1;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 3 TTTTCCTGCTCTAGA 20
    DB 21 TTTTCCTGCTCTAGA 4

```

RESULT 5

```

AAT58812
ID AAT58812 standard; DNA; 22 BP.
XX
AC AAT58812;
XX
DT 20-NOV-1997 (first entry)
XX
DE Human telomerase PCR 3'-primer hal88.
XX
KW Cancer; eukaryotic parasite, hTR; vertebrate telomerase; yeast;
KW protozoa; tumour; antibody; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9640868-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09517.
XX
PR 07-JUN-1995; 95US-0478352.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Autexier C, Greider C;
XX
WPI; 1997-099928/09.
XX
PT DNA encoding essential RNA components of human telomerase - also
PT truncated or recombinant telomerase, useful for diagnosis and
PT treatment of cancer and infection by eukaryotic parasites
XX
PS Example 5; Page 32; 48pp; English.
XX
CC The present sequence represents PCR 3'-primer hal88 used for
CC amplifying the human telomerase (hTR). The RNA and DNA can be used in
CC hybridisation assays to detect or quantify telomerase activity in cells,
CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
CC (yeast and protozoa) or tumours. It is also useful as primers for
CC amplification assays. The truncated or recombinant vertebrate telomerase
CC is used therapeutically to increase telomerase activity (also as
CC as antisense molecules, are used to reduce such activity. Typical
CC applications are initiation/restoration of activity to cause senescence
CC or to prevent immortalisation of cells in tumours or parasites. The DNA
CC is also used to produce recombinant telomerase, which can then be used
CC conventionally to raise antibodies for diagnostic detection of
CC telomerase. Detecting telomerase allows early diagnosis of tumour or
CC infection, before clinical signs manifest. Telomerase inhibitors
CC directed against e.g. Trypanosoma should cause fewer side effects than
CC drugs currently used to treat such infections. The DNA encodes those
CC parts of hTR RNA essential for activity but are significantly shorter
CC than the endogenous RNA component.
XX
SQ Sequence 22 BP; 3 A; 4 C; 4 G; 11 T; 0 other;
    Query Match          80.0%; Score 16; DB 18; Length 22;
    Best Local Similarity 100.0%; Pred. No. 48;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 CATTTCCTGCTCTC 16
    DB 7 CATTTCCTGCTCTC 22

RESULT 6
AAS15937
ID AAS15937 standard; DNA; 13 BP.
XX
AC AAS15937;

```

```

XX AC AAS15938;
XX DT 27-FEB-2002 (first entry)
XX DE Human telomerase polynucleotide inhibitor #18.
XX KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
XX KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
XX KW fertility; inflammatory condition; tumour; cancer; veterinary;
XX KW immunosuppression; telomerase inhibitor; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..13
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "N3'-P5' phosphoramidate linkages"
XX PN WO200174136-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10476.
XX PR 31-MAR-2000; 2000US-0540119.
XX PA (GERO-) GERON CORP.
XX PI Gryaznov SM, Pruzan R, Weinrich SL;
XX PI WPI; 2001-656955/75.
XX DR
XX XX New polynucleotide useful for inhibiting telomerase activity in cells,
XX FT or for treating telomerase-mediated condition or disease, such as
XX FT cancer, tumours, Hodgkin's disease, or inflammatory conditions -
XX PS Example 3; Page 32; 48pp; English.
XX CC The invention relates to polynucleotide inhibitors (I) and methods for
XX CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase
XX CC activity and proliferation of a telomerase positive cell, and in
XX CC manufacturing a medicament for inhibiting telomerase activity in a cell
XX CC and in treating telomerase-mediated condition or disease, such as
XX CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
XX CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
XX CC useful in treating a tumour or in manufacturing a medicament for the
XX CC treatment of tumour. The polynucleotide inhibitors may also be used in
XX CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
XX CC activity in cells in vivo is useful in prophylactic and therapeutic
XX CC methods of treating cancer and other disorders involving inappropriate
XX CC expression of telomerase, and in treating veterinary proliferative
XX CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
XX CC for immunosuppression and for selectively down-regulating specific
XX CC branches of the immune system. The present sequence represents
XX CC human telomerase polynucleotide inhibitor #18, as described in the
XX CC method of the invention.
XX SQ Sequence 13 BP; 0 A; 1 C; 2 G; 10 T; 0 other;
XX Query Match 65.0%; Score 13; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred No. 1.4e+03;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 3 TTTTGTGTTGCT 15
DB 1 TTTTGTGTTGCT 13
RESULT 7
AAS15938
ID AAS15938 standard; DNA; 13 BP.
XX

```

```

AC AAS15938;
DT 27-FEB-2002 (first entry)
DE Human telomerase polynucleotide inhibitor #19.
KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
KW fertility; inflammatory condition; tumour; cancer; veterinary;
KW immunosuppression; telomerase inhibitor; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..13
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "N3'-P5' phosphoramidate linkages"
XX PN WO200174136-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10476.
XX PR 31-MAR-2000; 2000US-0540119.
XX PA (GERO-) GERON CORP.
XX PI Gryaznov SM, Pruzan R, Weinrich SL;
XX PI WPI; 2001-656955/75.
XX DR
XX XX New polynucleotide useful for inhibiting telomerase activity in cells,
XX FT or for treating telomerase-mediated condition or disease, such as
XX FT cancer, tumours, Hodgkin's disease, or inflammatory conditions -
XX PS Example 3; Page 32; 48pp; English.
XX CC The invention relates to polynucleotide inhibitors (I) and methods for
XX CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase
XX CC activity and proliferation of a telomerase positive cell, and in
XX CC manufacturing a medicament for inhibiting telomerase activity in a cell
XX CC and in treating telomerase-mediated condition or disease, such as
XX CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
XX CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
XX CC useful in treating a tumour or in manufacturing a medicament for the
XX CC treatment of tumour. The polynucleotide inhibitors may also be used in
XX CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
XX CC activity in cells in vivo is useful in prophylactic and therapeutic
XX CC methods of treating cancer and other disorders involving inappropriate
XX CC expression of telomerase, and in treating veterinary proliferative
XX CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
XX CC for immunosuppression and for selectively down-regulating specific
XX CC branches of the immune system. The present sequence represents
XX CC human telomerase polynucleotide inhibitor #19, as described in the
XX CC method of the invention.
XX SQ Sequence 13 BP; 1 A; 2 C; 2 G; 8 T; 0 other;
XX Query Match 65.0%; Score 13; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred No. 1.4e+03;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 TTTGTTTGCTCTA 18
DB 1 TTTGTTTGCTCTA 13
RESULT 8
AAS15938
ID AAS15938 standard; DNA; 24 BP.
XX

```

XX AAH39806;
 XX
 XX 14-AUG-2001 (first entry)
 XX
 XX SNP specific lower PCR primer SEQ ID 2602.
 XX
 XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
 KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;
 KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
 KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
 KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
 KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200129262-A2.
 XX
 XX 26-APR-2001.
 XX
 XX 13-OCT-2000; 2000WO-US28436.
 XX
 XX 15-OCT-1999; 99US-0160096.
 XX
 XX (ORCH-) ORCHID BIOSOURCES INC.
 XX
 XX Picoult-Newburg L, Pohl M;
 XX
 XX WPI; 2001-290930/30.
 XX
 XX New genotyping oligonucleotide, useful for detecting the presence,
 PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample -
 XX
 XX Claim 1; Page 63; 83pp; English.
 XX
 XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension. (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a PCR primer specific
 CC for a human SNP containing DNA sequence.
 XX
 XX Sequence 24 BP; 5 A; 5 C; 3 G; 11 T; 0 other;
 SQ
 Query Match 65.0%; Score 13; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTGC 14
 |||||
 Db 5 ATTTTGTGTTGC 17
 |||||
 RESULT 9
 ABH86386

ID ABH86386 standard; DNA; 12 BP.
 XX
 XX AC ABH86386;
 XX
 XX DT 22-FEB-2002 (first entry)
 XX
 XX DE Oligonucleotide primer SEQ ID NO 286379 for detecting SNP TSC0012703.
 XX
 XX KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200177384-A2.
 XX
 XX PD 18-OCT-2001.
 XX
 XX PF 06-APR-2001; 2001WO-IB00713.
 XX
 XX PR 07-APR-2000; 2000DE-1019173.
 XX
 XX PA (EPIC-) EPIGENOMICS AG.
 XX
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX
 XX DR WPI; 2001-657177/75.
 XX
 XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX
 XX PS Claim 1; SEQ ID 286379; 29pp + Sequence Listing; German.
 XX
 XX CC This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIFO at
 CC ftp.wifo.int/pub/published_pct_sequences.
 XX
 XX SQ Sequence 12 BP; 1 A; 0 C; 2 G; 9 T; 0 other;
 Query Match 60.0%; Score 12; DB 23; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTG 13
 |||||
 Db 1 ATTTTGTGTTG 12
 |||||
 RESULT 10
 AAS15935
 ID AAS15935 standard; DNA; 13 BP.
 XX
 XX AC AAS15935;
 XX
 XX DT 27-FEB-2002 (first entry)
 XX
 XX DE Human telomerase polynucleotide inhibitor #16.
 XX
 XX KW Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;
 KW breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;
 KW fertility; inflammatory condition; tumour; cancer; veterinary;
 KW immunosuppression; telomerase inhibitor; ss.
 XX

```
OS Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..13
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "N3'-P5' phosphoramidate linkages"
XX
XX WO200174136-A2.
XX
XX PD 11-OCT-2001.
XX
XX PP 30-MAR-2001; 2001WO-US10476.
XX
XX PR 31-MAR-2000; 2000US-0540119.
XX
XX PA (GERO-) GERON CORP.
XX
XX PI Gryaznov SM, Puzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX PP New polynucleotide useful for inhibiting telomerase activity in cells,
XX or for treating telomerase-mediated condition or disease, such as
XX cancer, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX PS Claim 8; Page 36; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
XX inhibiting telomerase activity. (I) are useful in inhibiting telomerase
XX activity and proliferation of a telomerase positive cell, and in
XX manufacturing a medicament for inhibiting telomerase activity in a cell
XX and in treating telomerase-mediated condition or disease, such as
XX adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
XX Hodgkin's disease, fertility and inflammatory conditions. (I) are also
XX useful in treating a tumour or in manufacturing a medicament for the
XX treatment of tumour. The polynucleotide inhibitors may also be used in
XX diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
XX activity in cells in vivo is useful in prophylactic and therapeutic
XX methods of treating cancer and other disorders involving inappropriate
XX expression of telomerase, and in treating veterinary proliferative
XX diseases. Inhibition of telomerase in haematopoietic stem cells is useful
XX for immunosuppression and for selectively down-regulating specific
XX branches of the immune system. The present sequence represents
XX human telomerase polynucleotide inhibitor #16, as described in the
XX method of the invention.
XX
XX Sequence 13 BP; 2 A; 1 C; 1 G; 9 T; 0 other;
XX
XX Query Match 60.0%; Score 12; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CATTITTTGTTT 12
XX Db 2 CATTITTTGTTT 13
XX
XX RESULT 11
XX ABC09084
XX ID ABC09084 standard; DNA; 13 BP.
XX
XX AC ABC09084;
XX
XX XX 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 9075 for detecting SNP TSC0002428.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
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OS Homo sapiens.
XX WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PP 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
XX WPI; 2001-657177/75.
XX
XX PT Set of oligonucleotides, useful for diagnosis and cell typing, is
XX designed to detect single nucleotide polymorphisms and cytosine
XX methylation status -
XX
XX PS Claim 1; SEQ ID 9075; 29pp + Sequence Listing; German.
XX
XX This invention describes novel oligonucleotide primers or peptide nucleic
XX acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
XX and cytosine methylation status in chemically pretreated genomic DNA. The
XX oligonucleotides are used for diagnosis and/or prognosis of cancer and a
XX range of diseases including immune system, gastrointestinal, respiratory,
XX central nervous system, cardiovascular and metabolic disorders. The
XX oligomers are also used for detecting cell type differentiation.
XX ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
XX ABT00010-ABT02073 represent the oligomers described in the invention.
XX NOTE: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format from WIPO-at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 13 BP; 1 A; 0 C; 3 G; 9 T; 0 other;
XX
XX Query Match 60.0%; Score 12; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+03;
XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 ATTTTITGTTTG 13
XX Db 1 ATTTTITGTTTG 12
XX
XX RESULT 12
XX ABC09085/c
XX ID ABC09085 standard; DNA; 13 BP.
XX
XX AC ABC09085;
XX
XX XX 20-FEB-2002 (first entry)
XX
XX DE Oligonucleotide SEQ ID NO 9076 for detecting SNP TSC0002428.
XX
XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
XX peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
XX central nervous system; gastrointestinal; respiratory; immune; metabolic.
XX
XX OS Homo sapiens.
XX
XX PN WO200177384-A2.
XX
XX PD 18-OCT-2001.
XX
XX PP 06-APR-2001; 2001WO-IB00713.
XX
XX PR 07-APR-2000; 2000DE-1019173.
XX
XX PA (EPIG-) EPIGENOMICS AG.
XX
XX PI Olek A, Piepenbrock C, Berlin K;
```

XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 9076; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 other;
 SQ Query Match 60.0%; Score 12; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTG 13
 Db 13 ATTTTGTGTTG 2
 RESULT 13
 ABH44170
 ID ABH44170 standard; DNA; 13 BP.
 XX AC ABH44170;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 244147 for detecting SNP TSC0059579.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 244147; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 9 A; 3 C; 0 G; 1 T; 0 other;
 SQ Query Match 60.0%; Score 12; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTG 13
 Db 13 ATTTTGTGTTG 2
 RESULT 13
 ABH44170
 ID ABH44170 standard; DNA; 13 BP.
 XX AC ABH44170;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 244147 for detecting SNP TSC0059579.
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 244147; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a

CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 2 A; 0 C; 2 G; 9 T; 0 other;
 SQ Query Match 60.0%; Score 12; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTG 13
 Db 2 ATTTTGTGTTG 13
 RESULT 14
 ABH44171/c
 ID ABH44171 standard; DNA; 13 BP.
 XX AC ABH44171;
 XX 22-FEB-2002 (first entry)
 XX Oligonucleotide SEQ ID NO 244148 for detecting SNP TSC0059579;
 XX SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX OS Homo sapiens.
 XX WO200177384-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-IB00713.
 XX 07-APR-2000; 2000DE-1019173.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2001-657177/75.
 XX Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status -
 XX Claim 1; SEQ ID 244148; 29pp + Sequence Listing; German.
 XX This invention describes novel oligonucleotide primers or peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 13 BP; 9 A; 2 C; 0 G; 2 T; 0 other;
 SQ Query Match 60.0%; Score 12; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 ATTTTGTGTTG 13
 DB 12 ATTTTGTGTTG 1

RESULT 15
 ABH59432
 ID ABH59432 standard; DNA; 13 BP.
 XX
 AC ABH59432;
 XX
 DT 22-FEB-2002 (first entry)
 XX
 DE Oligonucleotide SEQ ID NO 259409 for detecting SNP TSC0063000.
 XX
 KW SNP; single nucleotide polymorphism; human; diagnosis; PNA; cancer; CNS;
 KW peptide nucleic acid; cytosine methylation; cardiovascular; primer; ss;
 KW central nervous system; gastrointestinal; respiratory; immune; metabolic.
 XX
 OS Homo sapiens.
 XX
 PN WO200177384-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WO-IB00713.
 XX
 PR 07-APR-2000; 2000DE-1019173.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2001-657177/75.
 XX
 PT Set of oligonucleotides, useful for diagnosis and cell typing, is
 PT designed to detect single nucleotide polymorphisms and cytosine
 PT methylation status
 XX
 PS Claim 1; SEQ ID 259409; 29pp + Sequence Listing; German.
 XX
 CC This invention describes novel oligonucleotide primers of peptide nucleic
 CC acid (PNA) oligomers for detecting single nucleotide polymorphisms (SNP)
 CC and cytosine methylation status in chemically pretreated genomic DNA. The
 CC oligonucleotides are used for diagnosis and/or prognosis of cancer and a
 CC range of diseases including immune system, gastrointestinal, respiratory,
 CC central nervous system, cardiovascular and metabolic disorders. The
 CC oligomers are also used for detecting cell type differentiation.
 CC ABC00010-ABC99989, ABF00010-ABF99989, ABH00010-ABH99989 and
 CC ABI00010-ABI82073 represent the oligomers described in the invention.
 CC NOTE: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 13 BP; 0 A; 1 C; 3 G; 9 T; 0 other;

Query Match 60.0%; Score 12; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred No. 4.4e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TTTTGTGTTGC 14
 DB 1 TTTTGTGTTGC 12

Search completed: June 23, 2003, 05:43:41
 Job time : 134.216 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 232.59 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-13
Perfect score: 20
Sequence: 1 CATTGTTGTTGCTCTAGA 20

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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- 2: gb_htg.*
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- 4: gb_om.*
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- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
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- 15: em_ba.*
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- 30: em_htg_hum.*
- 31: em_htg_inv.*
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- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_man.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	6	AR063837	AR063837 Sequence
C	2	18	90.0	28	AR122661	AR122661 Sequence
C	3	18	90.0	28	BD000545	BD000545 Restricti
C	4	18	90.0	28	I83455	I83455 Sequence.19
5	17	85.0	24	6	AX058270	AX058270 Sequence
6	13	65.0	22	6	AX462591	AX462591 Sequence
7	13	65.0	24	6	AX117479	AX117479 Sequence
8	12	60.0	24	6	A24429	A24429 oligonucleo
9	12	60.0	25	6	AX057458	AX057458 Sequence
10	12	60.0	26	6	A94988	A94988 Sequence 2
11	12	60.0	26	6	AR016055	AR016055 Sequence
12	12	60.0	26	6	AR028786	AR028786 Sequence
13	12	60.0	26	6	AR059216	AR059216 Sequence
14	12	60.0	26	6	AR075527	AR075527 Sequence
15	12	60.0	26	6	AR161925	AR161925 Sequence
16	12	60.0	26	6	AX022187	AX022187 Sequence
17	12	60.0	26	6	AX033377	AX033377 Sequence
18	12	60.0	26	6	AX468455	AX468455 Sequence
19	12	60.0	26	6	BD011297	BD011297 Human tel
20	12	60.0	26	6	E36508	E36508 Method for
21	12	60.0	26	6	E37046	E37046 Human telom
22	12	60.0	26	6	I31770	I31770 Sequence 23
23	12	60.0	27	6	AR063850	AR063850 Sequence
24	12	60.0	27	6	AX317989	AX317989 Sequence
25	12	60.0	30	6	A84595	A84595 Sequence 5
26	12	60.0	30	6	AR079892	AR079892 Sequence
27	12	60.0	35	6	AR120372	AR120372 Sequence
C	28	12	60.0	38	A02008	A02008 Bacterial s
C	29	12	60.0	38	A06778	A06778 Nucleotide
C	30	12	60.0	39	11	AL824208 Arabidops
C	31	12	60.0	40	6	AR053679 Sequence
C	32	12	60.0	40	6	AR053686 Sequence
C	33	12	60.0	40	6	AR120377 Sequence
C	34	12	60.0	41	6	AR003335 Sequence
C	35	12	60.0	42	6	AR001574 Sequence
C	36	12	60.0	43	6	AR001575 Sequence
C	37	12	60.0	45	6	A02009 Artificial
C	38	12	60.0	45	6	A06779 Nucleotide
C	39	12	60.0	50	6	AX161232 Sequence
40	12	60.0	50	6	E23942	E23942 Oligonucleo
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C	42	11	55.0	20	6	A83837 Sequence 15
C	43	11	55.0	20	6	AX487392 Sequence
44	11	55.0	21	6	AR159606	AR159606 Sequence
C	45	11	55.0	21	6	AR193717 Sequence

ALIGNMENTS

RESULT 1
AR063837
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AR063837
Sequence 13 from patent US 5846723.
AR063837
AR063837.1 GI:5993145

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.
Methods for detecting the RNA component of telomerase
Patent: US 5846723-A 13 08-DEC-1998;
Location/Qualifiers

linear PAT 29-SEP-1999

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RESULT 2
LOCUS AR122661/c 28 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 5 from patent US 6165749.
ACCESSION AR122661
VERSION AR122661.1 GI:14106978
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Sagawa,H., Ueno,H., Oshima,A. and Kato,I.
TITLE Plasmid
JOURNAL Patent: US 6165749-A 5 26-DEC-2000;
FEATURES
Location/Qualifiers
source 1. .28
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BASE COUNT 15 a 7 c 4 g 2 t
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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTTTGTGTTGCTCTAGA 20
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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 3
LOCUS BD000545/c 28 bp DNA linear PAT 31-JAN-2002
DEFINITION Restriction enzyme and gene thereof.
ACCESSION BD000545
VERSION BD000545.1 GI:18623658
KEYWORDS JP 2000325094-A/4.
SOURCE unidentified.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Sagawa,H., Ueno,H., Oshima,A. and Kato,I.
TITLE Restriction enzyme and gene thereof
JOURNAL Patent: JP 2000325094-A 4 28-NOV-2000;
COMMENT TAKARA SHUZO CO LTD
OS Unidentified
PN JP 2000325094-A/4
PD 28-NOV-2000
PF 20-APR-2000 JP 2000120124
PI HIROAKI SAGAWA, HARUMI UENO, ATSUSHI OHSIMA, IKUNOSHIN KATO PC
C12N15/09, C12N9/16//((C12N9/16, C12R1:19), C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 4
LOCUS I83455/c 28 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 19 from patent US 5714323.
ACCESSION I83455
VERSION I83455.1 GI:3406985
KEYWORDS
SOURCE Unknown.
ORGANISM
REFERENCE
1 (bases 1 to 28)
AUTHORS Oshima,A., Inouye,S. and Inouye,M.
TITLE Over expression of single-stranded molecules
JOURNAL Patent: US 5714323-A 19 03-FEB-1998;
FEATURES
Location/Qualifiers
source 1. .28
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BASE COUNT 15 a 7 c 4 g 2 t
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Db 21 TTTTGTGTTGCTCTAGA 4

RESULT 5
LOCUS AX058270 24 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 5 from Patent WO0074667.
ACCESSION AX058270
VERSION AX058270.1 GI:12310769
KEYWORDS
SOURCE synthetic construct.
ORGANISM
REFERENCE
1 (bases 1 to 24)
AUTHORS Au,J.B. and Wientjes,G.
TITLE Compositions active in telomere damage comprising a taxane and
JOURNAL Patent: WO 0074667-A 5 14-DEC-2000;
FEATURES Au, Jessie L.S. (US) ; Wientjes, Guillaume (US)
Location/Qualifiers
source 1. .24
/organism="synthetic construct"
/db_xref="taxon:32630"
/notes="primer/probe"

BASE COUNT 3 a 5 c 4 g 12 t
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Db 21 TTTTGTGTTGCTCTAGA 4
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RESULT 6
AX462591
LOCUS
DEFINITION
Sequence 335 from Patent EP1217079.
ACCESSION
AX462591
VERSION
AX462591.1 GI:21885804
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii.
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Aegilops.
1
Bernard, M., Sourdis, P. and Guyomarch, H.
Microsatellite markers from Triticum tauschii
Patent: EP 1217079-A 335 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 7
AX117479
LOCUS
DEFINITION
Sequence 2602 from Patent WO0129262.
ACCESSION
AX117479
VERSION
AX117479.1 GI:14034430
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Picoult-Newburg, L. and Pohl, M.
TITLE
Genotyping reagents, kits and methods of use thereof
JOURNAL
Patent: WO 0129262-A 2602 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"
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ORIGIN
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DB 5 ATTTTGTGTC 17
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RESULT 8
A24429
LOCUS
DEFINITION
oligonucleotide TPI.
ACCESSION
A24429
VERSION
A24429.1 GI:2293585
AX462591
LOCUS
DEFINITION
Sequence 335 from Patent EP1217079.
ACCESSION
AX462591
VERSION
AX462591.1 GI:21885804
KEYWORDS
SOURCE
ORGANISM
Aegilops tauschii.
Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Aegilops.
1
Bernard, M., Sourdis, P. and Guyomarch, H.
Microsatellite markers from Triticum tauschii
Patent: EP 1217079-A 335 26-JUN-2002;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 6 TTTGTTGCTCTA 18
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RESULT 7
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LOCUS
DEFINITION
Sequence 2602 from Patent WO0129262.
ACCESSION
AX117479
VERSION
AX117479.1 GI:14034430
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Picoult-Newburg, L. and Pohl, M.
TITLE
Genotyping reagents, kits and methods of use thereof
JOURNAL
Patent: WO 0129262-A 2602 26-APR-2001;
Orchid Biosciences, Inc. (US)
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/note="Primer"
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Best Local Similarity 100.0%; Pred. No. 3.6e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 ATTTTGTGTC 14
|||||
DB 5 ATTTTGTGTC 17
|||||
RESULT 8
A24429
LOCUS
DEFINITION
oligonucleotide TPI.
ACCESSION
A24429
VERSION
A24429.1 GI:2293585

KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 24)
REFERENCE
AUTHORS
Picoult-Newburg, L. and Pohl, M.
TITLE
Genotyping reagents, kits and methods of use thereof
JOURNAL
Patent: WO 0129262-A 2602 26-APR-2001;
Orchid Biosciences, Inc. (US)
FEATURES
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DB 3 ATTTTGTGTC 14
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AX057458
LOCUS
DEFINITION
Sequence 62 from Patent WO0077257.
ACCESSION
AX057458
VERSION
AX057458.1 GI:12310196
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
REFERENCE
AUTHORS
Baidya, N., Chen, Y.D., Holding, J. and Yu, Y.T.
TITLE
Gene specific arrays and the use thereof
JOURNAL
Patent: WO 0077257-A 62 21-DEC-2000;
Clingenix, Inc. (US)
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
DB 14 ATTTTGTGTC 25
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RESULT 10
A94988
LOCUS
DEFINITION
Sequence 2 from Patent EP0926245.
ACCESSION
A94988
VERSION
A94988.1 GI:6779168
KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified.
unclassified.
1 (bases 1 to 26)
REFERENCE
AUTHORS
Emrich, T.D.
TITLE
Method for detection of carcinoma of the urinary bladder within a
JOURNAL
Patent: EP 0926245-A 2 30-JUN-1999;
ROCHE DIAGNOSTICS GMBH (DE)
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Db 1 GTTTGCTCTAGA 12

RESULT 11
LOCUS AR016055 26 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 23 from patent US 5776679.
ACCESSION AR016055
VERSION AR016055.1 GI:3972332
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 23 07-JUL-1998;
FEATURES Location/Qualifiers
source 1..26
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ORIGIN

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Db 1 GTTTGCTCTAGA 12

RESULT 12
LOCUS AR028786 26 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 26 from patent US 5858777.
ACCESSION AR028786
VERSION AR028786.1 GI:5940759
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
TITLE Methode and reagents for regulating telomere length and telomerase activity
JOURNAL Patent: US 5858777-A 26 12-JAN-1999;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 3 c 9 g 7 t
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTTTGCTCTAGA 12

RESULT 13
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DEFINITION Sequence 23 from patent US 5837857.
ACCESSION AR059216
VERSION AR059216.1 GI:5984793
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 23 17-NOV-1998;
FEATURES Location/Qualifiers
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Query Match 60.0%; Score 12; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+05;
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Qy 9 GTTGGCTCTAGA 20
Db 1 GTTTGCTCTAGA 12

RESULT 14
LOCUS AR075527 26 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 24 from patent US 5956680.
ACCESSION AR075527
VERSION AR075527.1 GI:10002275
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5956680-A 24 28-SEP-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GTTGGCTCTAGA 20
Db 1 GTTTGCTCTAGA 12

RESULT 15
LOCUS AR161925 26 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 23 from patent US 6258535.
ACCESSION AR161925
VERSION AR161925.1 GI:16228953
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 6258535-A 23 10-JUL-2001;
FEATURES Location/Qualifiers
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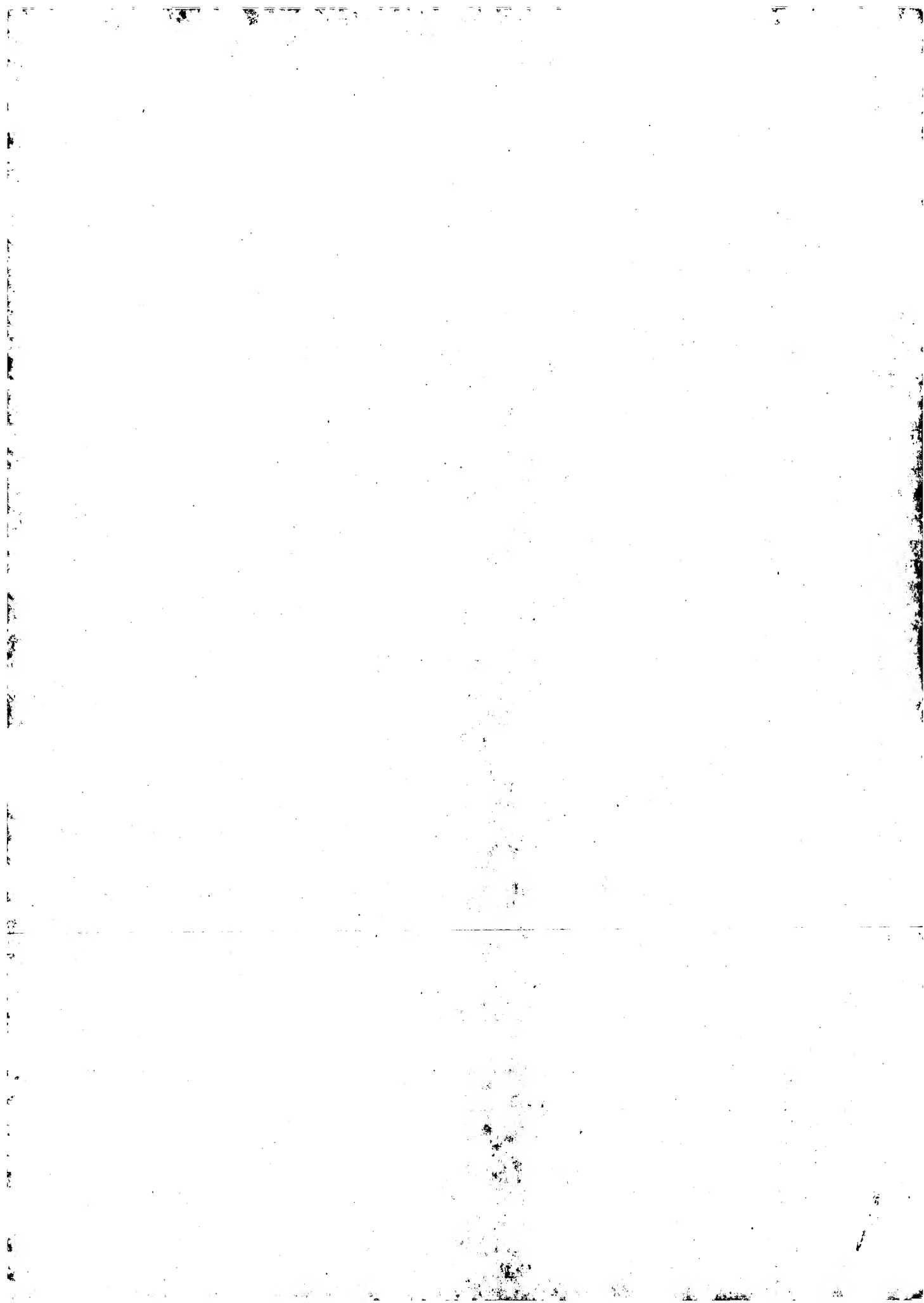
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Qy 9 GTTGGCTCTAGA 20
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 Db 1 GTTGGCTCTAGA 12

Search completed: June 23, 2003, 06:34:25
 Job time : 234.051 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 406.104 Seconds
(without alignments)
292.710 Million cell updates/sec

Title: US-08-770-564A-14
Perfect score: 17
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	100.0	19	1	PCT-US03-04088-16
C 2	17	100.0	19	1	Sequence 16, Appl
C 3	17	100.0	22	1	Sequence 280, Appl
C 4	17	100.0	30	10	PCT-US02-33146-10
C 5	17	100.0	30	10	Sequence 10, Appl
C 6	15	88.2	25	9	US-10-330-872-4
C 7	14.4	84.7	25	9	Sequence 4, Appli
C 8	14	82.4	25	12	Sequence 27, Appl
C 9	14	82.4	25	12	Sequence 681796,
C 10	13.8	81.2	25	12	Sequence 52, Appl
C 11	13.4	78.8	25	5	US-09-536-058D-52
C 12	13.4	78.8	25	12	Sequence 148950,
C 13	13.4	78.8	25	9	Sequence 6883, Ap
C 14	13.4	78.8	25	12	Sequence 7843, Ap
C 15	13.4	78.8	25	12	Sequence 12244, A
C 16	13.4	78.8	25	12	Sequence 16616, A
C 17	13.4	78.8	25	12	Sequence 148950,
C 18	13.4	78.8	25	12	Sequence 6883, Ap
C 19	13.4	78.8	25	12	Sequence 7843, Ap
C 20	13	76.5	15	10	US-10-287-787-15506, A

C 21	13	76.5	16	9	US-10-310-188-5556	Sequence 5556, Ap
C 22	13	76.5	17	9	US-10-303-778-7849	Sequence 7849, Ap
C 23	13	76.5	17	9	US-10-310-188-14135	Sequence 14135, A
C 24	13	76.5	17	9	US-10-310-188-57644	Sequence 57644, A
C 25	13	76.5	17	10	US-10-299-054A-1993	Sequence 1993, Ap
C 26	13	76.5	17	10	US-10-299-054A-1994	Sequence 1994, Ap
C 27	13	76.5	18	9	US-10-310-188-39627	Sequence 39627, A
C 28	13	76.5	18	10	US-10-287-787-23414	Sequence 23414, A
C 29	13	76.5	18	10	US-10-287-787-23415	Sequence 23415, A
C 30	13	76.5	24	10	US-10-287-787-12803	Sequence 12803, A
C 31	13	76.5	25	12	US-60-427-808-467694	Sequence 467694, A
C 32	13	76.5	25	12	US-60-427-808-391360	Sequence 391360, A
C 33	13	76.5	25	12	US-60-427-808-421414	Sequence 421414, A
C 34	13	76.5	25	12	US-60-427-808-455025	Sequence 455025, A
C 35	13	76.5	39	10	US-10-287-787-12804	Sequence 12804, A
C 36	12.8	75.3	23	9	US-10-310-188-62469	Sequence 62469, A
C 37	12.8	75.3	25	9	US-10-355-577-40464	Sequence 40464, A
C 38	12.8	75.3	25	9	US-10-355-577-70065	Sequence 70065, A
C 39	12.8	75.3	25	12	US-60-427-808-23365	Sequence 23365, A
C 40	12.8	75.3	25	12	US-60-427-808-182757	Sequence 182757, A
C 41	12.8	75.3	25	12	US-60-427-808-249883	Sequence 249883, A
C 42	12.8	75.3	25	12	US-60-427-808-273706	Sequence 273706, A
C 43	12.8	75.3	25	12	US-60-427-808-382705	Sequence 382705, A
C 44	12.8	75.3	25	12	US-60-427-808-496697	Sequence 496697, A
C 45	12.8	75.3	25	12	US-60-427-808-518595	Sequence 518595, A

ALIGNMENTS

RESULT 1

PCT-US03-04088-16/c
; Sequence 16, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-16

Query Match 100.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
 Db 18 CGGGCCAGCAGCTGACA 2

RESULT 2
 PCT-US03-04088-280
 ; Sequence 280, Application PC/TUS0304088
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: McSwiggen, James
 ; APPLICANT: Beigelman, Leonid
 ; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
 ; FILE REFERENCE: 02-708-A (400/080)
 ; CURRENT APPLICATION NUMBER: PCT/US03/04088
 ; CURRENT FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: US 60/396,600
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/358,580
 ; PRIOR FILING DATE: 2002-02-20
 ; PRIOR APPLICATION NUMBER: US 60/363,124
 ; PRIOR FILING DATE: 2002-03-11
 ; PRIOR APPLICATION NUMBER: US 60/386,782
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/406,784
 ; PRIOR FILING DATE: 2002-08-29
 ; PRIOR APPLICATION NUMBER: US 60/408,378
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/409,293
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: US 60/440,129
 ; PRIOR FILING DATE: 2003-01-15
 ; NUMBER OF SEQ ID NOS: 626
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 280
 ; TYPE: RNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense
 ; OTHER INFORMATION: region
 PCT-US03-04088-280

Query Match 100.0%; Score 17; DB 1; Length 19;
 Best Local Similarity 94.1%; Pred. No. 1.7e+02;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
 Db 2 CGGGCCAGCAGCTGACA 18

RESULT 3
 PCT-US02-33146-10
 ; Sequence 10, Application PC/TUS0233146
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Rochester Medical Center
 ; APPLICANT: Rowley, Peter
 ; TITLE OF INVENTION: Telomerase Interference
 ; FILE REFERENCE: FP-71506-2/RFT/SRN
 ; CURRENT APPLICATION NUMBER: PCT/US02/33146
 ; CURRENT FILING DATE: 2002-12-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 22
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 PCT-US02-33146-10

Query Match 100.0%; Score 17; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTGACA 17
 Db 5 CGGGCCAGCAGCTGACA 21

RESULT 4
 US-10-330-872-4
 ; Sequence 4, Application US/10330872
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Weinrich, Scott
 ; APPLICANT: Atkinson III, Edward
 ; APPLICANT: Lichtsteiner, Serge
 ; APPLICANT: Vasserot, Alain
 ; APPLICANT: Pruzan, Ronald
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
 ; TITLE OF INVENTION: Inhibitors
 ; FILE REFERENCE: 011/006C
 ; CURRENT APPLICATION NUMBER: US/10/330,872
 ; CURRENT FILING DATE: 2002-12-24
 ; PRIOR APPLICATION NUMBER: 08/510,736
 ; PRIOR FILING DATE: 1995-08-04
 ; PRIOR APPLICATION NUMBER: 08/833,377
 ; PRIOR FILING DATE: 1997-04-04
 ; PRIOR APPLICATION NUMBER: 09/420,056
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: 09/717,828
 ; PRIOR FILING DATE: 2000-11-20
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 30
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-872-4

Query Match 100.0%; Score 17; DB 10; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
 Db 4 CGGGCCAGCAGCTGACA 20

RESULT 5
 US-10-330-872A-4
 ; Sequence 4, Application US/10330872A
 ; GENERAL INFORMATION:
 ; APPLICANT: Geron Corporation
 ; APPLICANT: Weinrich, Scott
 ; APPLICANT: Atkinson III, Edward
 ; APPLICANT: Lichtsteiner, Serge
 ; APPLICANT: Vasserot, Alain
 ; APPLICANT: Pruzan, Ronald
 ; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
 ; TITLE OF INVENTION: Inhibitors
 ; FILE REFERENCE: 011/006C
 ; CURRENT APPLICATION NUMBER: US/10/330,872A
 ; CURRENT FILING DATE: 2002-12-24
 ; PRIOR APPLICATION NUMBER: 08/510,736
 ; PRIOR FILING DATE: 1995-08-04
 ; PRIOR APPLICATION NUMBER: 08/833,377
 ; PRIOR FILING DATE: 1997-04-04
 ; PRIOR APPLICATION NUMBER: 09/420,056
 ; PRIOR FILING DATE: 1999-10-18
 ; PRIOR APPLICATION NUMBER: 09/717,828
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4


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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-4

Query Match      100.0%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTGACA 17
    |||||
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-10-359-935-27
; Sequence 27, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; Fung, Junli
; Funk, Walter
; Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-359-935-27

Query Match      88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGGCAGCAGCTGACA 17
    |||||
Db 9 GGGCAGCAGCTGACA 23
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RESULT 7
US-60-427-808-681796/c
; Sequence 681796, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 681796
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-681796

Query Match      84.7%; Score 14.4; DB 12; Length 25;
Best Local Similarity 93.8%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCCAGCAGCTGACA 17
    |||||
Db 24 GGGCCAGCAGCTGACA 9

RESULT 8
US-09-536-058D-52/c
; Sequence 52, Application US/09536058D
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAI, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058D
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058D-52

Query Match      82.4%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTG 14
    |||||
Db 23 CGGGCCAGCAGCTG 10

RESULT 9
US-60-427-808-148950
; Sequence 148950, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
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US-60-427-808-148950

Query Match 82.4%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 10 CGGGCCAGCAGCTG 23

RESULT 10

US-09-749-2808-6883/c
; Sequence 6883, Application US/097492808
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: Nucleic Acids Containing Single
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/09/749,2808
; CURRENT FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/173,419
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 10038
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 6883
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)...(26)
; OTHER INFORMATION: Nucleotide deleted between bases 25 and 26
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43987514
US-09-749-2808-6883

Query Match 81.2%; Score 13.8; DB 5; Length 50;
Best Local Similarity 88.2%; Pred. No. 6.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
DB 36 CGGGCCAGCAGCGCCA 20

RESULT 11

US-10-303-778-7843/c
; Sequence 7843, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7843
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-7843

Query Match 78.8%; Score 13.4; DB 9; Length 22;
Best Local Similarity 93.3%; Pred. No. 9.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTGAC 16
DB 21 GGGACAGCAGCTGAC 7

RESULT 12

US-60-427-808-12244/c
; Sequence 12244, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 12244
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-12244

Query Match 78.8%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 9.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGACA 17
DB 20 GGGCCAGCAGCTGACA 6

RESULT 13

US-60-427-808-16616
; Sequence 16616, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 16616
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-16616

Query Match 78.8%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 9.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTGAC 16
DB 4 GGGCCAGCAGCTCAC 18

RESULT 14

US-60-427-808-153744
; Sequence 153744, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 153744
; LENGTH: 25
; TYPE: DNA

; ORGANISM: Mus musculus
US-60-427-808-153744

Query Match 78.8%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 9.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 8 GGCCAGCAGCTGACA 22

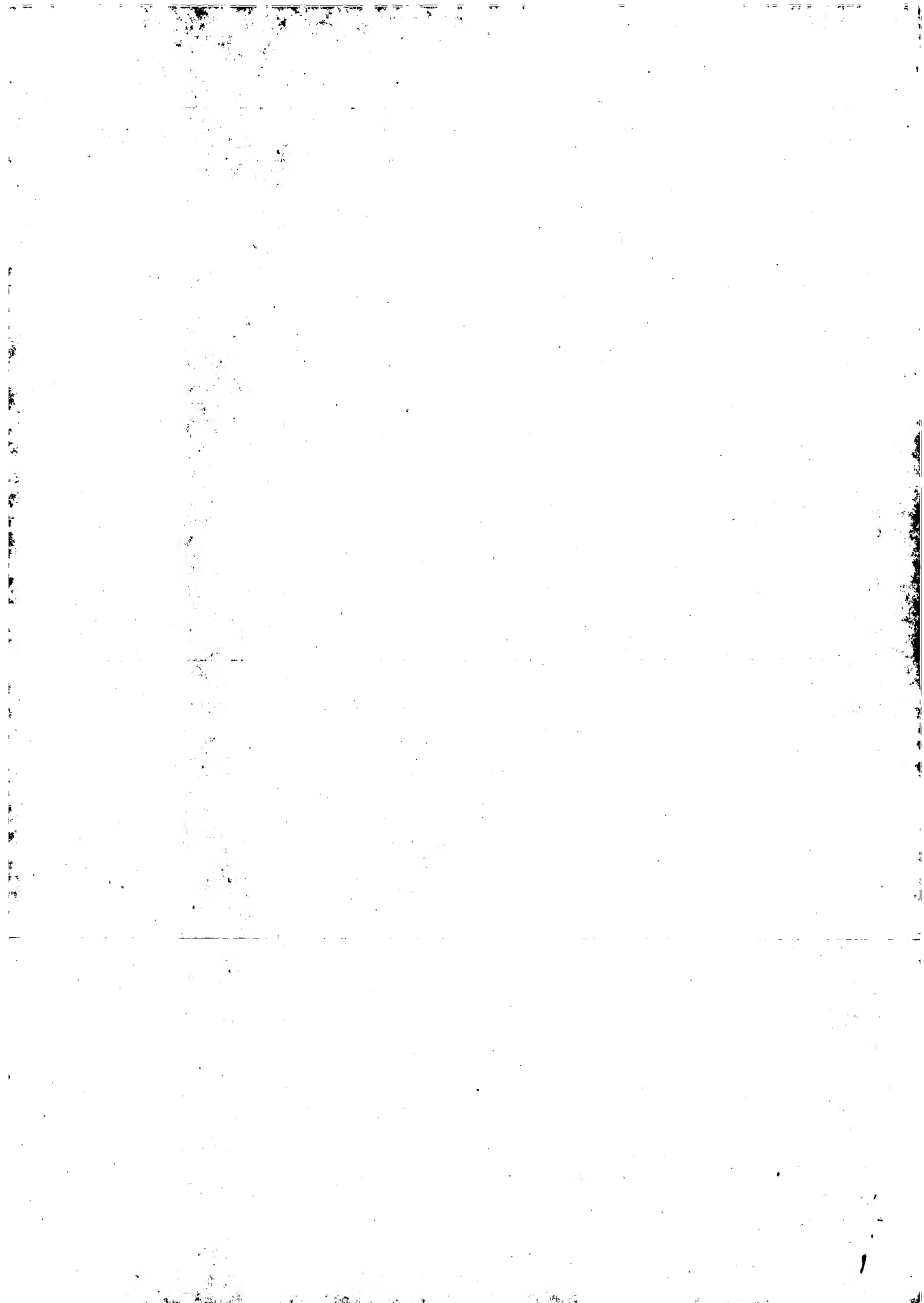
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US-60-427-808-834500/c
; Sequence 834500, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 834500
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-834500

Query Match 78.8%; Score 13.4; DB 12; Length 25;
Best Local Similarity 93.3%; Pred. No. 9.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCCAGCAGCTGAC 16
|||||
DB 22 GGCCAGCAGCTGAC 8

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 1442.49 Seconds
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Title: US-08-770-564A-14

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Gapop 10.0, Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	17	100.0	25	US-09-601-267-20
4	17	100.0	30	US-08-510-736-4
5	17	100.0	30	US-09-717-828A-4
6	17	100.0	30	US-09-717-828B-4
7	17	100.0	30	US-09-717-829A-4
8	15	88.2	25	US-08-472-802A-27
9	15	88.2	25	US-08-472-802B-27
10	15	88.2	25	US-08-482-115A-26
11	15	88.2	25	US-08-521-634-44
12	15	88.2	25	US-09-057-351-27
13	14.4	84.7	25	US-09-396-196F-47051
14	14.4	84.7	25	US-09-396-196G-47051
15	14	82.4	24	US-09-536-058C-52
16	14	82.4	24	US-09-536-058C-52
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C 26 13.4 78.8 42 15 US-09-103-636-2542
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C 28 13 76.5 24 9 US-08-521-634-11
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C 31 13 76.5 47 1 PCT-US02-25943-58545
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ALIGNMENTS

RESULT 1
PCT-US97-23619-14
; Sequence 14, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

Sequence 33812, A
Sequence 107046, A
Sequence 18, Appl
Sequence 18, Appl
Sequence 2542, Ap
Sequence 2894, Ap
Sequence 11, Appl
Sequence 54639, A
Sequence 64639, A
Sequence 58545, A
Sequence 3647, Ap
Sequence 3647, Ap
Sequence 294, Appl
Sequence 14, Appl
Sequence 66914, A
Sequence 40137, A
Sequence 40139, A
Sequence 40141, A
Sequence 40152, A
Sequence 40153, A
Sequence 40155, A
Sequence 40156, A
Sequence 40157, A

LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..17
OTHER INFORMATION: /note="polynucleotide Rp2"
PCT-US97-23619-14

Query Match 100.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
DB 1 CGGGCCAGCAGCTGACA 17

RESULT 2

US-08-770-564A-14
; Sequence 14, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Realey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002200US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-564A-14
Query Match 100.0%; Score 17; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTGACA 17
DB 1 CGGGCCAGCAGCTGACA 17
RESULT 3
US-09-601-267-20

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; Sequence 20, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol Keith
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601,267
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-601-267-20

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Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      7 CGGGCCAGCAGCTGACA 23

RESULT 4
US-08-510-736-4
; Sequence 4, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-510-736-4
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Query Match      100.0%; Score 17; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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        |||||
DB      4 CGGGCCAGCAGCTGACA 20

RESULT 5
US-09-717-828A-4
; Sequence 4, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomeraseOilbase
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
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DB      4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-09-717-828B-4
; Sequence 4, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomeraseOilbase
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 4
; LENGTH: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828B-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

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US-09-717-829A-4
; Sequence 4, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Prizant, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: Purifiedtelomerasolibase
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 4
; TYPE: DNA
; LENGTH: 30
; ORGANISM: Artificial Sequence
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-4
Query Match 100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 8
US-08-472-802A-27
; Sequence 27, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

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; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-27
Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23

RESULT 9
US-08-472-802B-27
; Sequence 27, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123

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FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802B-27

Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
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DB 9 GGCCAGCAGCTGACA 23

RESULT 10

US-08-482-115A-26
Sequence 26, Application US/08482115A
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-26

Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

RESULT 11

US-08-521-634-44
Sequence 44, Application US/08521634
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,634
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,115
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
ANTI-SENSE: YES
US-08-521-634-44

Query Match 88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

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RESULT 12
US-09-057-351-27
; Sequence 27, Application US/09057351
; GENERAL INFORMATION:
; APPLICANT: Valleponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; STREET: Townsend and Townsend and Crew LLP
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Scarella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match 88.2%; Score 15; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23

RESULT 13
US-09-396-196F-47051/c
; Sequence 47051, Application US/09396196F
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196F
; CURRENT FILING DATE: 2001-09-15
; Query Match 82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCCAGCAGCTGACA 17
Db 24 GGCCAGCAGCTGACA 9

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; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196F-47051

Query Match 84.7%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCCAGCAGCTGACA 17
Db 24 GGCCAGCAGCTGACA 9

RESULT 14
US-09-396-196G-47051/c
; Sequence 47051, Application US/09396196G
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47051
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-47051

Query Match 84.7%; Score 14.4; DB 17; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCCAGCAGCTGACA 17
Db 24 GGCCAGCAGCTGACA 9

RESULT 15
US-09-536-058-52/c
; Sequence 52, Application US/09536058
; GENERAL INFORMATION:
; APPLICANT: Beger, Carmela
; APPLICANT: Barber, Jack
; APPLICANT: Wong-Staal, Flossie
; TITLE OF INVENTION: BRCA-1 Regulators and Methods of Use
; FILE REFERENCE: P-IU 3842
; CURRENT APPLICATION NUMBER: US/09/536,058
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-536-058-52

Query Match 82.4%; Score 14; DB 20; Length 24;

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Best Local Similarity 100.0%; Pred. No. 1.8e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTG 14
Db 23 CGGGCCAGCAGCTG 10

Search completed: June 25, 2003, 06:20:30
Job time : 1444.11 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 51.6773 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564A-14
Perfect score: 17
Sequence: 1 CGGCGCAGCAGTGACA 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	88.2	25	10	US-09-057-351-27
2	13.4	78.8	26	10	US-09-815-171A-18
3	12.4	72.9	24	9	US-10-027-961A-1
4	12.4	72.9	24	9	US-10-175-268-1
5	12.4	72.9	24	10	US-09-803-552-1
6	12.4	72.9	24	10	US-09-803-347-1
7	12.4	72.9	24	10	US-09-931-700-13
8	12.4	72.9	24	10	US-09-803-549-1
9	12.4	72.9	24	10	US-09-803-402-1
10	12.4	72.9	24	10	US-09-968-445-1
11	12.4	72.9	50	9	US-09-943-722-9
12	12.2	71.8	25	9	US-10-098-2638-37688
13	12.2	71.8	25	9	US-10-098-2638-38944
14	12	70.6	23	9	US-10-320-230-30
15	12	70.6	23	10	US-09-817-387-18
16	12	70.6	25	9	US-10-215-112-2064
17	12	70.6	31	9	US-09-912-263-184
18	12	70.6	38	9	US-09-930-423-2661
19	12	70.6	38	9	US-09-930-423-2713

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20 12 70.6 48 9 US-09-848-754A-7985 Sequence 7985, Ap
21 12 70.6 48 9 US-09-848-754A-8229 Sequence 8229, Ap
22 12 70.6 50 9 US-09-943-722-5 Sequence 5, Appli
23 11.8 69.4 19 9 US-10-044-692-168 Sequence 168, App
24 11.8 69.4 19 9 US-10-044-539-168 Sequence 168, App
25 11.8 69.4 20 9 US-09-915-814-148 Sequence 148, App
26 11.8 69.4 21 9 US-10-044-692-275 Sequence 275, App
27 11.8 69.4 21 9 US-10-044-539-275 Sequence 275, App
28 11.8 69.4 24 9 US-09-940-185-704 Sequence 704, App
29 11.8 69.4 25 9 US-09-940-185-4670 Sequence 4670, Ap
30 11.8 69.4 30 9 US-09-957-483-39 Sequence 39, Appl
31 11.8 69.4 34 9 US-09-957-483-13 Sequence 13, Appl
32 11.8 69.4 38 9 US-09-930-423-3161 Sequence 3161, Ap
33 11.8 69.4 50 9 US-09-920-394-6 Sequence 6, Appli
34 11.4 67.1 19 10 US-09-942-374-4 Sequence 4, Appli
35 11.4 67.1 25 9 US-10-215-112-1826 Sequence 1826, Ap
36 11.4 67.1 25 9 US-10-215-112-12785 Sequence 12785, A
37 11.4 67.1 31 9 US-09-961-077-417 Sequence 417, App
38 11.4 67.1 31 9 US-09-912-263-75 Sequence 75, Appl
39 11.4 67.1 31 9 US-09-999-220B-82 Sequence 82, Appl
40 11.4 67.1 31 9 US-09-999-220B-89 Sequence 89, Appl
41 11.4 67.1 31 9 US-09-999-220B-101 Sequence 101, App
42 11.4 67.1 39 9 US-10-087-993-17 Sequence 17, Appl
43 11.4 67.1 39 10 US-09-905-999-9 Sequence 9, Appli
44 11.4 67.1 45 9 US-09-925-922-8 Sequence 8, Appli
45 11.4 67.1 48 10 US-09-822-698A-62 Sequence 62, Appli
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ALIGNMENTS

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RESULT 1
US-09-057-351-27
; Sequence 27, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
```

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; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  GCCCAGCAGCTGACA 17
Db      9  GCCCAGCAGCTGACA 23

RESULT 2
US-09-815-171A-18/c
; Sequence 18, Application US/09815171A
; Patent No. US20020064780A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Zichi, Dominic
; APPLICANT: Jenison, Robert D
; APPLICANT: Schneider, Daniel J
; TITLE OF INVENTION: Method and Apparatus for the Automated Generation of
; FILE REFERENCE: SML.03
; CURRENT APPLICATION NUMBER: US/09/815,171A
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/616,284
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/356,233
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/232,946
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 08/792,075
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: 09/143,190
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 08/469,609
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/536,428
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in ver. 2.0
; SEQ ID NO 18
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-815-171A-18

Query Match      78.8%; Score 13.4; DB 10; Length 26;
Best Local Similarity 93.3%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  GCCCAGCAGCTGACA 17
Db      25  GCCCAGCAGCTCACA 11

RESULT 3
US-10-027-961A-1/c
; Sequence 1, Application US/10027961A
; Publication No. US20030032789A1
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; GENERAL INFORMATION:
; APPLICANT: O'NEILL, GARY P.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; FILE REFERENCE: 19029PCADA
; CURRENT APPLICATION NUMBER: US/10/027,961A
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/599,781
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 08/930,589
; PRIOR FILING DATE: 1996-02-22
; PRIOR APPLICATION NUMBER: PCT/CA94/00501
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 08/084,033
; PRIOR FILING DATE: 1993-09-27
; PRIOR APPLICATION NUMBER: 08/064,271
; PRIOR FILING DATE: 1993-05-06
; PRIOR APPLICATION NUMBER: 07/994,760
; PRIOR FILING DATE: 1992-12-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Human
US-10-027-961A-1

Query Match      72.9%; Score 12.4; DB 9; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  CGGGCCAGCAGCTG 14
Db      18  CGGGCCAGGAGCTG 5

RESULT 4
US-10-175-268-1/c
; Sequence 1, Application US/10175268
; Publication No. US20030032827A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/175,268
; FILING DATE: 19-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-175-268-1

Query Match 72.9%; Score 12.4; DB 9; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCGAGGCTG 14
Db 18 CGGGCCGAGGCTG 5

RESULT 5
US-09-803-552-1/c
; Sequence 1, Application US/09803552
; Patent No. US20010031882A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,552
; FILING DATE: 09-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/803,552
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-552-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCGAGGCTG 14
Db 18 CGGGCCGAGGCTG 5

RESULT 6

US-09-803-347-1/c
; Sequence 1, Application US/09803347
; Patent No. US20020010351A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,347
; FILING DATE: 12-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/803,347
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-347-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCGAGGCTG 14
Db 18 CGGGCCGAGGCTG 5

RESULT 7

US-09-931-700-13
; Sequence 13, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4

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; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid,
; OTHER INFORMATION: AM-R antisense probe (nucleotides 788-811)
US-09-931-700-13

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGACA 17
DB 10 GCCAGCAGATGACA 23

RESULT 8
US-09-803-549-1/c
; Sequence 1, Application US/09803549
; Patent No. US2002082435A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,549
; FILING DATE: 09-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/803,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-549-1

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; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-549-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 18 CGGGCCAGGAGCTG 5

RESULT 9
US-09-803-402-1/c
; Sequence 1, Application US/09803402
; Patent No. US20020091279A1
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan
; TITLE OF INVENTION: Lipoxin Compounds
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/803,402
; FILING DATE: 09-Mar-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/712,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/077,300
; FILING DATE: 15-JUNE-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: BWI-112CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-803-402-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
DB 18 CGGGCCAGGAGCTG 5

RESULT 10
US-09-968-445-1/c
; Sequence 1, Application US/09968445
; Patent No. US20020111505A1

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GENERAL INFORMATION:
APPLICANT: Charles N. Serhan
TITLE OF INVENTION: Lipoxin Compounds
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,445
FILING DATE: 01-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260,030
FILING DATE: 15-JUNE-1994
APPLICATION NUMBER: 08/077,300
FILING DATE: 15-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: BWI-112CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-968-445-1

Query Match 72.9%; Score 12.4; DB 10; Length 24;
Best Local Similarity 92.9%; Pred. No. 5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
Db 18 CGGGCCAGCAGCTG 5

RESULT 11
US-09-943-722-9
Sequence 9, Application US/09943722
Publication No. US20020192660A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/943,722
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,049
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-09-943-722-9

Query Match 72.9%; Score 12.4; DB 9; Length 50;
Best Local Similarity 92.9%; Pred. No. 4.8e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCGAGCAGCTGACA 17
Db 33 GCGAGCAGCTGACA 46

RESULT 12
US-10-098-263B-37688/c
Sequence 37688, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 37688
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-37688

Query Match 71.8%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 21 CGGTCCAGCAGCTGACA 5

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RESULT 13
US-10-098-263B-38944/c
; Sequence 38944, Application US/10098263B
; Publication No. US2003010410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 38944
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-38944
Query Match 71.8%; Score 12.2; DB 9; Length 25;
Best Local Similarity 82.4%; Pred. No. 6.3e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CGGCCGACGCTGACA 17
Db 23 CGGCCGACGCTGACA 7

RESULT 14
US-10-320-230-30
; Sequence 30, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoerster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(23)
US-10-320-230-30
Query Match 70.6%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGA 15
Db 9 GCCAGCAGCTGA 20

RESULT 15
US-09-817-387-18
; Sequence 18, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotides, linkages between positions 1
; OTHER INFORMATION: to 12 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 12 to 20 are phosphodiester
; OTHER INFORMATION: positions 13 to 23 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: linkages between positions 20 to 23 are
; OTHER INFORMATION: phosphorothioates
US-09-817-387-18
Query Match 70.6%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCCAGCAGCTG 14
Db 1 GCCAGCAGCTG 12

Search completed: June 25, 2003, 22:25:10
Job time : 52.6773 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 25.8048 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-14
Perfect score: 17 CCGGCCAGCAGCTGACA 17
Sequence: 1

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-770-565-14
2	17	100.0	30	2	US-08-833-377-5
3	15	88.2	25	1	US-08-482-115B-26
4	15	88.2	25	2	US-08-472-802C-27
5	12.4	72.9	24	1	US-08-064-271-1
6	12.4	72.9	24	3	US-08-712-610-1
7	12.4	72.9	24	3	US-08-930-589A-1
8	12.4	72.9	24	4	US-09-309-423-1
9	12.4	72.9	24	4	US-09-011-922A-13
10	12.4	72.9	24	4	US-09-599-781-1
11	12.4	72.9	27	3	US-08-832-399-3
12	12.4	72.9	27	4	US-09-372-498-3
13	12.4	72.9	30	3	US-08-513-974B-136
14	12.4	72.9	48	1	US-07-720-222-41
15	12.4	72.9	48	1	US-08-066-961-2
16	12.4	72.9	50	2	US-08-850-049-9
17	12.4	72.9	50	2	US-08-050-478-9
18	12.4	72.9	50	4	US-07-858-747B-9
19	12.4	72.9	50	4	US-09-414-117-9
20	12.4	72.9	50	4	US-09-678-437-9
21	12.2	71.8	29	1	US-08-082-843-1
22	12	70.6	18	4	US-08-584-040-8292
23	12	70.6	18	4	US-08-584-040-8293
24	12	70.6	50	2	US-08-850-049-5
25	12	70.6	50	2	US-08-050-478-5
26	12	70.6	50	4	US-07-858-747B-5
27	12	70.6	50	4	US-09-414-117-5

28	12	70.6	50	4	US-09-678-437-5	Sequence 5, Appli
29	11.8	69.4	19	4	US-08-974-549A-401	Sequence 401, App
30	11.8	69.4	20	4	US-08-687-421-329	Sequence 329, App
31	11.8	69.4	21	4	US-08-974-549A-508	Sequence 508, App
32	11.8	69.4	30	1	US-07-602-608-19	Sequence 19, Appl
33	11.8	69.4	30	1	US-08-261-578-19	Sequence 19, Appl
34	11.8	69.4	30	4	US-08-974-549A-723	Sequence 723, Appl
35	11.8	69.4	34	4	US-09-560-367A-13	Sequence 13, Appl
36	11.8	69.4	36	2	US-08-925-708-4	Sequence 4, Appli
37	11.8	69.4	36	2	US-08-925-708-5	Sequence 5, Appli
38	11.8	69.4	40	1	US-08-087-772A-10	Sequence 10, Appl
39	11.8	69.4	49	1	US-08-530-492-89	Sequence 89, Appl
40	11.8	69.4	49	4	US-08-906-517-89	Sequence 89, Appl
41	11.4	67.1	24	1	US-08-072-063-3	Sequence 3, Appli
42	11.4	67.1	24	1	US-08-064-693-3	Sequence 3, Appli
43	11.4	67.1	24	4	US-08-885-366-3	Sequence 3, Appli
44	11.4	67.1	24	5	PCT-US93-04754-3	Sequence 3, Appli
45	11.4	67.1	27	3	US-08-513-974B-87	Sequence 87, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-14
; Sequence 14, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-00230005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-14

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGGCCAGCAGCTGACA 17

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Db      1 CGGCCAGCAGCTGACA 17

RESULT 2
US-08-833-377-5
; Sequence 5, Application US/08833377
; Patent No. 5968506
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; APPLICANT: Kealey, James T.
; TITLE OF INVENTION: Purified Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/833,377
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US 08/510,736
; FILING DATE: 04-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-001110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..30
; OTHER INFORMATION: /note= "Oligo 13"
; US-08-833-377-5

Query Match      100.0%; Score 17; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CGGCCAGCAGCTGACA 17
        |||
Db      4 CGGCCAGCAGCTGACA 20

RESULT 3
US-08-482-115B-26
; Sequence 26, Application US/08482115B

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; Patent No. 5776579
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Assays for the RNA Component of Human
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,115B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000830US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0300
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-482-115B-26

Query Match      88.2%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GGCCAGCAGCTGACA 17
        |||
Db      9 GGCCAGCAGCTGACA 23

RESULT 4
US-08-472-802C-27
; Sequence 27, Application US/08472802C
; Patent No. 5958680
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-27

Query Match 88.2%; Score 15; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

RESULT 5
US-08-064-271-1/c
Sequence 1, Application US/08064271
Patent No. 5543297
GENERAL INFORMATION:
APPLICANT: Kennedy, Brian P.
APPLICANT: Cromlish, Wanda A.
APPLICANT: Mancini, Joseph A.
APPLICANT: O'Neil, Gary
APPLICANT: Vickers, Philip J.
APPLICANT: Wong, Elizabeth
TITLE OF INVENTION: HUMAN CYCLOOXYGENASE-2 CDNA AND
ASSAY FOR EVALUATING CYCLOOXYGENASE ACTIVITY
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.4kb
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/064,271
FILING DATE: 19930506
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Panzer, Curtis C.
REGISTRATION NUMBER: 33,752

REFERENCE/DOCKET NUMBER: 189061A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3199
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-064-271-1

Query Match 72.9%; Score 12.4; DB 1; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
|||||
DB 18 CGGGCCAGCAGCTG 5

RESULT 6
US-08-712-610-1/c
Sequence 1, Application US/08712610
Patent No. 6048897
GENERAL INFORMATION:
APPLICANT: Charles N. Serhan
TITLE OF INVENTION: Lipoxin Compounds
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,610
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/260,030
FILING DATE: 15-JUNE-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,300
FILING DATE: 15-JUNE-1993
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: BWI-112CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
ANTI-SENSE: NO
US-08-712-610-1

Query Match 72.9%; Score 12.4; DB 3; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14

Db 18 CGGGCCAGGAGCTG 5

RESULT 7

US-08-930-589A-1/c
; Sequence 1, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK PROSST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FASTSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,589A

FILING DATE: 28-JUN-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coppola, Joseph A.

REGISTRATION NUMBER: 38,413

REFERENCE/DOCKET NUMBER: 19029PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: 732-594-6734

TELEFAX: 732-594-4720

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-930-589A-1

Query Match 72.9%; Score 12.4; DB 3; Length 24;

Best Local Similarity 92.9%; Pred. No. 1.9e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGGAGCTG 14

Db 18 CGGGCCAGGAGCTG 5

RESULT 8

US-09-309-423-1/c
; Sequence 1, Application US/09309423
; Patent No. 6316648
; GENERAL INFORMATION:
; APPLICANT: Charles N. Serhan

; TITLE OF INVENTION: Lipoxin Compounds

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: Massachusetts

COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/309,423
FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/260,030

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,300

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: BWI-112CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

ANTI-SENSE: NO

US-09-309-423-1

Query Match 72.9%; Score 12.4; DB 4; Length 24;

Best Local Similarity 92.9%; Pred. No. 1.9e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGGCCAGGAGCTG 14

Db 18 CGGGCCAGGAGCTG 5

RESULT 9

US-09-011-922A-13

; Sequence 13, Application US/09011922A

; Patent No. 6320022

; GENERAL INFORMATION:

; APPLICANT: Cuttitta, Frank; Martinez,

; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward

; APPLICANT: J. Hook; William; Walsh, Thomas; Grey,

; APPLICANT: Kaken, Macri Charles

; TITLE OF INVENTION: Functional Role of

; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related

; TITLE OF INVENTION: Product (PAMP) in Human Pathology and

; TITLE OF INVENTION: Physiology

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: MS WORD 97

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,922A

FILING DATE: 17-Feb-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/60/002,514

;; FILING DATE: 18-Aug-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/60/002,936
;; FILING DATE: 30-Aug-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/60/013,172
;; FILING DATE: 12-Mar-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/13286
;; FILING DATE: 16-Aug-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Leslie A. Serunian
;; REGISTRATION NUMBER: 35,353
;; REFERENCE/DOCKET NUMBER: 2026-4202US3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 758-4800
;; TELEFAX: (212) 751-6849
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 nucleotides
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: oligonucleotide
;; HYPOTHETICAL: No
;; ANTI-SENSE: Yes
;; FEATURE:
;; NAME/KEY: AM-R(788-811)
;; OTHER INFORMATION: AM-R antisense probe
;; US-09-011-922A-13

Query Match 72.9%; Score 12.4; DB 4; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGACA 17
Db 10 GCCAGCAGATGACA 23

RESULT 10
US-09-599-781-1/C
; Sequence 1, Application US/09599781
; Patent No. 6362327
; GENERAL INFORMATION:
; APPLICANT: MERCK PROST CANADA & CO.
; O'NEILL, GARY P.
; MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; CYCLOOXYGENASE-2
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/599,781
; FILING DATE: 21-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/084,033
; FILING DATE: 27-Sep-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A
; REGISTRATION NUMBER: 38,413

;; REFERENCE/DOCKET NUMBER: 19029PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 732-594-6734
;; TELEFAX: 732-594-4720
;; TELEX: <unknown>
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 24 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-599-781-1

Query Match 72.9%; Score 12.4; DB 4; Length 24;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGCTG 14
Db 18 CGGGCCAGGAGCTG 5

RESULT 11
US-08-832-399-3
; Sequence 3, Application US/08832399
; Patent No. 6008050
; GENERAL INFORMATION:
; APPLICANT: Bergema, Derk
; APPLICANT: Shabon, Usman
; TITLE OF INVENTION: NOVEL HUMAN NEUROTENSIN RECEPTOR TYPE 2
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY:
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,399
; FILING DATE: 02-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-832-399-3

Query Match 72.9%; Score 12.4; DB 3; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4 GCCAGCAGCTGACA 17
Db 6 GCCAGCAGATGACA 19

RESULT 12
US-09-372-498-3
; Sequence 3, Application US/09372498
; Patent No. 6166182
; GENERAL INFORMATION:
; APPLICANT: Derek J. Bergama
; APPLICANT: Usman Shabon
; TITLE OF INVENTION: NOVEL HUMAN NEUTROSENSIN RECEPTOR TYPE 2
; FILE REFERENCE: GH-50020-1
; CURRENT APPLICATION NUMBER: US/09/372,498
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: 08/832,399
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-372-498-3

Query Match 72.9%; Score 12.4; DB 4; Length 27;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGACA 17
Db 6 GCCAGCAGATGACA 19

RESULT 13
US-08-513-974B-136/c
; Sequence 136, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Maesaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: E36
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA: JP 7-007177
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA: JP 6-326611
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA: JP 6-270017
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA: JP 6-236357
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA: JP 6-236356
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA: JP 6-189274
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA: JP 6-189273
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA: JP 6-189272
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-974B-136

Query Match 72.9%; Score 12.4; DB 3; Length 30;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGACA 17
Db 16 GCCAGCAGATGACA 3

RESULT 14
US-07-720-222-41
; Sequence 41, Application US/07720222
; Patent No. 5190873
; GENERAL INFORMATION:
; APPLICANT: Lernhardt, Waldemar
; APPLICANT: Bourdon, Mario
; APPLICANT: Youderian, Phil
; TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bingham & Fitting
; STREET: 11230 Sorrento Valley Road, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/720,222
;; FILING DATE: 19910621
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bingham, Douglas A.
;; REGISTRATION NUMBER: 32,457
;; REFERENCE/DOCKET NUMBER: CIB0012P
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-587-3533
;; INFORMATION FOR SEQ ID NO: 41:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 48 base pairs
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-07-720-222-41

Query Match 72.9%; Score 12.4; DB 1; Length 48;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTGA 15
| | | | | | | | | | | | | | |
DB 6 GAGCCAGCAGCTGA 19

RESULT 15
US-08-066-961-2/c
; Sequence 2, Application US/08066961
; Patent No. 5432271
; GENERAL INFORMATION:
; APPLICANT: Barns, Susan M.
; APPLICANT: Halbert, Donald N.
; APPLICANT: Lane, David J.
; TITLE OF INVENTION: Nucleic Acid Probes for the Detection of
; TITLE OF INVENTION: Neisseria Gonorrhoeae
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 55 Shuman Blvd., Suite 600
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/066,961
; FILING DATE: 19930525
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775,210
; FILING DATE: 10-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/356,155
; FILING DATE: 24-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesser, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 5825-02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 48 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; US-08-066-961-2
Query Match 72.9%; Score 12.4; DB 1; Length 48;
Best Local Similarity 92.9%; Pred. No. 1.9e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTG 14
| | | | | | | | | | | | | | |
DB 25 CGTGCAGCAGCTG 12
Search completed: June 25, 2003, 00:24:42
Job time : 25.8048 secs



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 876.482 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17 CGGGCCAGCAGTGACA 17
Sequence:

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	76.5	46	14	H51364
C 2	13	76.5	49	9	AI159805
C 3	12	70.6	38	17	AZ815373
C 4	12	70.6	40	9	AI570731
5	12	70.6	49	9	AA914273
C 6	12	70.6	50	9	AU103700

C 7	64.7	30	13	BI463777
C 8	64.7	37	9	AI181597
C 9	64.7	41	12	BG718339
10	64.7	41	13	BI465330
C 11	64.7	46	9	AA871967
C 12	64.7	46	9	AA542511
C 13	64.7	49	9	AA213878
C 14	64.7	50	9	AU107010
C 15	64.7	50	9	AU107011
C 16	64.7	50	9	AU107012
C 17	64.7	50	9	AU107015
C 18	64.7	50	9	AU107015
C 19	58.8	22	17	AZ797063
C 20	58.8	29	17	AZ636336
C 21	58.8	33	17	AZ344584
C 22	58.8	34	17	AZ581060
C 23	58.8	35	17	AZ645669
C 24	58.8	35	17	TA291H03Q
C 25	58.8	38	17	AZ317175
C 26	58.8	39	9	AU007553
C 27	58.8	39	9	AU010017
C 28	58.8	40	14	H29926
C 29	58.8	40	17	AZ576156
C 30	58.8	42	17	AZ760286
C 31	58.8	45	14	T69111
C 32	58.8	46	9	AA932841
C 33	58.8	46	9	AI284114
C 34	58.8	46	13	BI523407
C 35	58.8	46	13	BI523407
C 36	58.8	46	14	H23758
C 37	58.8	46	17	AZ776000
C 38	58.8	49	9	AA237940
C 39	58.8	49	17	AQ073133
C 40	58.8	50	9	AU102703
C 41	58.8	50	9	AU103464
C 42	58.8	50	9	AU107013
C 43	58.8	50	9	AU107184
C 44	58.8	50	9	AU107185
C 45	58.8	50	9	AU107189

ALIGNMENTS

RESULT 1
H51364
LOCUS
DEFINITION
H51364 46 bp mRNA linear EST 18-SEP-1995
IMAGE:179484 5', similar to SP:ACON_PIG P16276 ACONITATE HYDRATASE
PRECURSOR ;, mRNA sequence.
ACCESSION H51364
VERSION H51364.1 GI:991205
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marr, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Insert Size: 701
High quality sequence starts: 1
High quality sequence stops: 1

Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 701 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
Location/Qualifiers
1. .46
/organism="Homo sapiens"
/db_xref="GDB:3841680"
/db_xref="taxon:9606"
/clone="IMAGE:179484"
/clone_lib="Soares adult brain N2b5HB55Y"
/sex="Male"
/dev_stage="55-year old"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: brain; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M. Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla." 8 a 12 c 12 g 13 t 1 others

BASE COUNT 8 a 12 c 12 g 13 t 1 others
ORIGIN

Query Match 76.5%; Score 13; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. NO. 4.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCCCAGCAGCTGA 15
|||||
Db 1 GCCCAGCAGCTGA 13

RESULT 2
A1159805/c
LOCUS
DEFINITION
qc73c05.x1 Soares placenta 8to9weeks 2NBHP8to9W Homo sapiens cDNA
clone IMAGE:1715240 3', similar to TR-Q15726 Q15726 MALIGNANT
MELANOMA METASTASIS-SUPPRESSOR. ;, mRNA sequence.

ACCESSION A1159805.1 GI:3693164
VERSION EST.
KEYWORDS human.
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 545 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 1.
Location/Qualifiers
1. .49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1715240"
/clone_lib="Soares placenta 8to9weeks 2NBHP8to9W"
/dev_stage="two placenta; One from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: placenta; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo." 5 a 16 c 22 g 6 t

BASE COUNT 5 a 16 c 22 g 6 t
ORIGIN

Query Match 76.5%; Score 13; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. NO. 4.5e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCAGCAGCT 13
|||||
Db 45 CGGCGCAGCAGCT 33

RESULT 3
A2815373/c
LOCUS
DEFINITION
A2815373 Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0083M06 R, DNA sequence.

ACCESSION A2815373
VERSION A2815373.1 GI:12985281
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 38)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddun@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0683 row: M column: 06
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers
1. .38
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0083M06"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

FEATURES source
source

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 7 a 13 c 12 g 6 t

Query Match 70.6%; Score 12; DB 17; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 1 CGGGCCAGCAGC 12
|||||
DB 24 CGGGCCAGCAGC 13

RESULT 4
AI570731/c
LOCUS
DEFINITION
tr66c01.x1 NCI CGAP Pan1 Homo sapiens cDNA clone IMAGE:2223264 3', similar to TR:Q14678 O14678 PEROXISOMAL MEMBRANE PROTEIN 69. ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AI570731
AI570731.1 GI:4534105
human.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 40)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 2315 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=NO.

FEATURES
source
1..40
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2223264"
/clone_lib="NCI CGAP Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.72 kb. Life Technologies catalog #:

BASE COUNT 6 a 15 c 10 g 9 t

Query Match 70.6%; Score 12; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.4e+04; Indels 0; Gaps 0;
Matches 12; Conservative 0; Mismatches 0;

QY 3 GGGCCAGCAGCTG 14
|||||
DB 13 GGGCCAGCAGCTG 2

RESULT 5
AA914273
LOCUS
DEFINITION
AA914273
AA914273.1 GI:3053665
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 49)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Giesel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Scheilenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:684612

Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..49
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dt) primer [5', TGTTACCAATCTGAAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTTTTTTTT T3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 10 a 15 c 16 g 8 t

FEATURES
source
1..49
Location/Qualifiers
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="IMAGE:1314316"
/clone_lib="Soares_mammary_gland_NDMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

Query Match 70.6%; Score 12; DB 9; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCCAGCAGCTG 14
 |||||
 Db 8 GCGCCAGCAGCTG 19

RESULT 6
 AUI03700/c 50 bp mRNA linear EST 30-AUG-2001
 LOCUS AUI03700 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
 DEFINITION CAS01030, mRNA sequence.

ACCESSION AUI03700
 VERSION AUI03700.1 GI:13553221
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
 , H., Ota, T., Isogai, T., Tanaka, T., Mochishita, S., Okubo, K., Sakaki
 , Y., Nakamura, Y., Suyama, A. and Sugano, S.
 TITLE Diverse transcriptional initiation revealed by fine, large-scale
 mapping of mRNA start sites
 JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
 MEDLINE 21270072
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp
 Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
 , S. Construction and characterization of a full length-enriched and
 a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
 source
 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CAS01030"
 /note="Differential display comparison of untreated and
 dimethylfumarate treated U937 cells"
 8 a 14 c 15 g 13 t

BASE COUNT 8 a 14 c 15 g 13 t

ORIGIN
 1 CGGCGCCAGCAGC 12
 |||||
 21 CGGCGCCAGCAGC 10

Query Match 70.6%; Score 12; DB 9; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGCCAGCAGC 12
 |||||
 Db 21 CGGCGCCAGCAGC 10

RESULT 7
 BI463777/c 30 bp mRNA linear EST 21-AUG-2001
 LOCUS BI463777 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5269437 5',
 DEFINITION mRNA sequence.

ACCESSION BI463777
 VERSION BI463777.1 GI:15254433
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 30)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rsb@nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Invitrogen Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM1679 row: m column: 22
 High quality sequence stop: 30.
 Location/Qualifiers
 1..30
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5269437"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /notes="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.2 kb and
 normalized to R0.5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI), National
 Institutes of Health). Note: this is a NIH_MGC Library."
 1 a 11 c 12 g 6 t

BASE COUNT 1 a 11 c 12 g 6 t

ORIGIN
 Query Match 64.7%; Score 11; DB 13; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.5e+04; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCCAGCAGC 12
 |||||
 Db 27 GCGCCAGCAGC 17

RESULT 8
 AUI1597/c 37 bp mRNA linear EST 08-OCT-1998
 LOCUS AUI1597 uc3d11.r1 Soares_mammary_gland NBMG Mus musculus cDNA clone
 DEFINITION IMAGE:1430325 5' similar to SW:CIH_HUMAN Q99828 SNK INTERACTING
 PROTEIN 2-28 ;, mRNA sequence.

ACCESSION AUI1597
 VERSION AUI1597.1 GI:3732235
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 37)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theisinger, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:914393
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

```
1. .37
  /organism="Mus musculus"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="IMAGE:1430325"
  /clone_lib="Soares_mammary_gland_NbMMG"
  /sex="male"
  /tissue_type="mammary gland"
  /dev_stage="4 weeks"
  /lab_host="DH10B"
```

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTACCAATCTGAGTGGAGCGCGCGAATGTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

BASE COUNT

ORIGIN

7 a 10 c 13 g 7 t

Query Match

Best Local Similarity 64.7%; Score 11; DB 9; Length 37;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCAGCAGCT 13

|||||

Db 28 GGGCAGCAGCT 18

RESULT 9

BG718339

LOCUS

602696344F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4828451 5',
EST.

ACCESSION

BG718339

VERSION

BG718339.1 GI:13997526

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10746 row: g column: 12

High quality sequence stop: 41.

Location/Qualifiers

1. .41

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4828451"

/clone_lib="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: Sali-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
size-selected for average insert size 2.2 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT

ORIGIN

7 a 12 c 19 g 3 t

Query Match

Best Local Similarity 64.7%; Score 11; DB 12; Length 41;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGC 12

|||||

Db 14 GGGCCAGCAGC 24

RESULT 10

BI465330

LOCUS

603206653F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5272405 5',
EST.

DEFINITION

mRNA sequence.

ACCESSION

BI465330

VERSION

BI465330.1 GI:15255986

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 41)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11687 row: i column: 14

High quality sequence stop: 41.

Location/Qualifiers

1. .41

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5272405"

/clone_lib="NIH_MGC_97"

/lab_host="DH10B"

/note="Organ: testis; Vector: pBluescriptR (modified

pBluescript KS+); Site_1: BamHI; Site_2: Sali-XhoI (gtcgag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',

size-selected for average insert size 2.2 kb and

normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the

Cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIH/NHGRI, National

Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."

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Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."

Institutes of Health). Note: this is a NIH_MGC Library."

RESULT 11
AA871967/c
LOCUS

DEFINITION

AA871967 46 bp mRNA linear EST 16-MAR-1998
vq43h03.r1 Barstead bowel MRLB9 Mus musculus cDNA clone
IMAGE:1097045 5' similar to TR:Q28298 Q28298 RIBOSOME RECEPTOR. 1,
mRNA sequence.

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA871967.1 GI:2967412

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 46)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

The WashU-HHMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouse@wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:603277

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28m3 rev2 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..46

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:1097045"

/clone.lib="Barstead bowel MRLB9"

/tissue_type="bowel"

/dev_stage="8 weeks"

/lab_host="DH10B"

/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site 1: EcoRI; Site 2: NotI; 1st strand cDNA
was primed with a NotI oligo(dT) primer [5'
TGTCAGATCTGAGTGGAGCGCGCCCTTTTATTTTATTTTATTTT
3'].

Double-stranded cDNA was ligated to Eco RI adaptors
[AATCGATCCG], digested with NotI and cloned into the
NotI and Eco RI sites of the modified pT73 vector.

Source irradiated bowel harvested 72 hours after
irradiation (1400 Gys). Library constructed by Bob
Barstead.

9 a 13 c 17 g 7 t

BASE COUNT

ORIGIN

Query Match 64.7%; Score 11; DB 9; Length 46;

Best Local Similarity 100.0%; Pred. No. 4.7e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGC 12

DB 36 GGGCCAGCAGC 26

RESULT 12

AA542511

LOCUS

DEFINITION

fa07d05.r1 Zebrafish ICRFzfls Danio rerio cDNA clone 41C23 5'

ACCESSION
VERSION

KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA542511 GI:2289446

zebrafish.

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Cypriniformes
; Cyprinidae; Danio.

1 (bases 1 to 46)

Clark, M., Lehrach, H., Appel, B., Eisen, J., Johnson, S., Marra, M.,
Eddy, S., Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G.,
Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Martin, J., Moore, B.,
Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
T., Waterston, R. and Wilson, R.

WashU Zebrafish EST Project

Unpublished (1997)

Contact: Steve Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Steve Johnson lab internal ID - P2-226 NOTE - For this library, the
CLONE id field represents a position identifier on the original
cDNA library preparation plate. cDNA Library Preparation: Matthew
Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by:
Washington University Genome Sequencing Center. Clone distribution:
Genome Systems, St. Louis, and Max Planck Institut fuer Molekulare
Genetik, Berlin Tel +49 30 84 13 1235

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: T7 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..46

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="41C23"

/clone.lib="Zebrafish ICRFzfls"

/sex="mixed"

/tissue_type="pooled 26-somite embryos"

/lab_host="XLI-blue MRP"

/note="vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st
strand cDNA was primed with a NotI - oligo(dT)15 primer
[5'pGACTAGTCTAGATCGAGCGCGCCCTTTTATTTT3'], on
mRNA from pooled 26 somite zebrafish embryos;

double-stranded cDNA was ligated to Sal I adaptors
digested with NotI and cloned into the NotI and Sal I
sites of the pSPORT1 vector (BRL). Library was constructed
by Matthew Clark (Lehrach lab; ICRF London and Max
Planck Institut fuer Molekulare Genetik, Berlin) and was
not biochemically normalised. 70,000 clones from this
library were arrayed on high density filters and
subsequently screened by oligonucleotide hybridization
fingerprinting to identify unique or minimally redundant
clones for more intensive analysis."

13 a 8 c 12 g 13 t

BASE COUNT

ORIGIN

Query Match 64.7%; Score 11; DB 9; Length 46;

Best Local Similarity 100.0%; Pred. No. 4.7e+04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGCAGCTGA 15

DB 7 CCAGCAGCTGA 17

RESULT 13

AA213878

LOCUS

DEFINITION

zr91b05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683025 5'

similar to TR:GI002369 GI002369 COATOMER PROTEIN. ;, mRNA sequence.


```

similar to TR:G577061 G577061 LPAP. ; mRNA sequence.
ACCESSION AA213878
VERSION AA213878.1 GI:1812507
SOURCE EST.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 49)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert length: 991 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..49
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:683025"
/clone_lib="NCI CGAP GCBI"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTCTTTTCTTTT-3',
]. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 5 a 16 c 17 g 10 t 1 others
ORIGIN
Query Match 64.7%; Score 11; DB 9; Length 49;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCCCGACGACG 12
|||||
Db 41 GGCCCGACGACG 31

RESULT 14
AUI07010/c
LOCUS AUI07010 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC05190, mRNA sequence.
ACCESSION AUI07010
VERSION AUI07010.1 GI:13556531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J., Hata
H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Sakaki
Y., Nakamura.Y., Suyama.A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HRC05201"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 10 a 16 c 20 g 4 t
ORIGIN
Query Match 64.7%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCGACGACT 13
|||||
Db 41 GGCCGACGACT 31

RESULT 15
AUI07011/c
LOCUS AUI07011 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC05201, mRNA sequence.
ACCESSION AUI07011
VERSION AUI07011.1 GI:13556532
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki.Y., Taira.H., Tsunoda.T., Mizushima-Sugano.J., Sese,J., Hata
H., Ota.T., Isogai.T., Tanaka.T., Morishita.S., Okubo.K., Sakaki
Y., Nakamura.Y., Suyama.A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
TITLE mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki.Y., Yoshitomo-Nakagawa.K., Maruyama.K., Suyama.A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HRC05201"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
BASE COUNT 10 a 16 c 19 g 5 t
ORIGIN
Query Match 64.7%; Score 11; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 3 GCCCAGCAGCT 13
Db 41 GCCCAGCAGCT 31

Search completed: June 23, 2003, 10:10:37
Job time : 878.636 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 ; Search time 746.239 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564A-14
Perfect score: 17
Sequence: 1 CGGGCCAGCAGCTGACA 17

Scoring table: OLIGO NUC
Gapop_60.0 , Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Pending Patents_NA_New.*

1: /cgn2_6/ptodata/1/pna/US06_NEW COMB.seq.*
2: /cgn2_6/ptodata/1/pna/US06_NEW COMB.seq.*
3: /cgn2_6/ptodata/1/pna/US07_NEW COMB.seq.*
4: /cgn2_6/ptodata/1/pna/US08_NEW COMB.seq.*
5: /cgn2_6/ptodata/1/pna/US09_NEW COMB.seq.*
6: /cgn2_6/ptodata/1/pna/US09_NEW COMB.seq.*
7: /cgn2_6/ptodata/1/pna/US09_NEW COMB.seq.*
8: /cgn2_6/ptodata/1/pna/US10_NEW COMB.seq.*
9: /cgn2_6/ptodata/1/pna/US10_NEW COMB.seq.*
10: /cgn2_6/ptodata/1/pna/US10_NEW COMB.seq.*
11: /cgn2_6/ptodata/1/pna/US10_NEW COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US60_NEW COMB.seq.*
13: /cgn2_6/ptodata/1/pna/US60_NEW COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17	100.0	19	1	PCT-US03-04088-16
2	17	100.0	19	1	PCT-US03-04088-280
3	17	100.0	22	1	PCT-US02-33146-10
4	17	100.0	30	10	US-10-330-872-4
5	17	100.0	30	10	US-10-330-872A-4
6	15	88.2	25	9	US-10-359-935-27
C 7	14	82.4	24	6	US-09-536-0580-52
8	14	82.4	25	12	US-60-427-808-148950
C 9	13	76.5	15	10	US-10-287-787-16506
C 10	13	76.5	15	10	US-10-287-787-18526
C 11	13	76.5	16	9	US-10-310-188-5556
12	13	76.5	17	9	US-10-303-778-7849
13	13	76.5	17	9	US-10-310-188-14135
14	13	76.5	17	9	US-10-310-188-57644
C 15	13	76.5	17	10	US-10-299-054A-1993
C 16	13	76.5	17	10	US-10-299-054A-1994
17	13	76.5	18	9	US-10-310-188-39627
C 18	13	76.5	18	10	US-10-287-787-23414
C 19	13	76.5	18	10	US-10-287-787-23415
C 20	13	76.5	24	10	US-10-287-787-12803

21	13	76.5	25	12	US-60-427-808-467694	Sequence 467694,
22	13	76.5	25	12	US-60-427-836-391360	Sequence 391360,
23	13	76.5	25	12	US-60-427-836-421414	Sequence 421414,
24	13	76.5	25	12	US-60-427-836-455025	Sequence 455025,
C 25	13	76.5	39	10	US-10-287-787-12804	Sequence 12804, A
26	12	70.6	15	10	US-10-367-892-15273	Sequence 15273, A
C 27	12	70.6	18	10	US-10-287-949A-3950	Sequence 3950, Ap
C 28	12	70.6	18	10	US-10-287-949A-3951	Sequence 3951, Ap
C 29	12	70.6	19	1	PCT-US03-04250-62	Sequence 62, Appl
C 30	12	70.6	19	1	PCT-US03-04250-320	Sequence 320, Appl
C 31	12	70.6	20	9	US-10-303-778-16537	Sequence 16537, A
C 32	12	70.6	21	1	PCT-US03-04250-556	Sequence 556, App
C 33	12	70.6	21	1	PCT-US03-04250-557	Sequence 557, App
C 34	12	70.6	21	1	PCT-US03-04250-558	Sequence 558, App
C 35	12	70.6	21	1	PCT-US03-04250-559	Sequence 559, App
C 36	12	70.6	21	1	PCT-US03-04250-560	Sequence 560, App
C 37	12	70.6	21	1	PCT-US03-04250-561	Sequence 561, App
C 38	12	70.6	21	1	PCT-US03-04250-562	Sequence 562, App
C 39	12	70.6	21	1	PCT-US03-04250-563	Sequence 563, App
C 40	12	70.6	21	1	PCT-US03-04250-564	Sequence 564, App
41	12	70.6	21	1	PCT-US03-04250-565	Sequence 565, App
42	12	70.6	21	1	PCT-US03-04250-566	Sequence 566, App
43	12	70.6	23	6	US-09-398-858-30	Sequence 30, Appl
44	12	70.6	23	9	US-10-320-230-30	Sequence 30, Appl
45	12	70.6	23	9	US-10-348-110-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

PCT-US03-04088-16/c
; Sequence 16, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 16
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
; OTHER INFORMATION: region
PCT-US03-04088-16

Query Match 100.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
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DB 18 CGGGCCAGCAGCTGACA 2

RESULT 2
PCT-US03-04088-280
; Sequence 280, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: McSwiggan, James
; APPLICANT: Belgelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 280
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siRNA antisense
; OTHER INFORMATION: region
PCT-US03-04088-280

Query Match 100.0%; Score 17; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 28;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
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DB 2 CGGGCCAGCAGCTGACA 18

RESULT 3
PCT-US02-33146-10
; Sequence 10, Application PC/TUS0233146
; GENERAL INFORMATION:
; APPLICANT: University of Rochester Medical Center
; APPLICANT: Rowley, Peter
; TITLE OF INVENTION: Telomerase Interference
; FILE REFERENCE: FP-71506-2/RFT/SRN
; CURRENT APPLICATION NUMBER: PCT/US02/33146
; CURRENT FILING DATE: 2002-12-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-33146-10

Query Match 100.0%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 28;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCCAGCAGCTGACA 17
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DB 5 CGGGCCAGCAGCTGACA 21

RESULT 4
US-10-330-872-4
; Sequence 4, Application US/10330872
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872-4

Query Match 100.0%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
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DB 4 CGGGCCAGCAGCTGACA 20

RESULT 5
US-10-330-872A-4
; Sequence 4, Application US/10330872A
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Weinrich, Scott
; APPLICANT: Atkinson III, Edward
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: Using Purified Telomerase to Identify Telomerase Activators and
; FILE REFERENCE: 011/006C
; CURRENT APPLICATION NUMBER: US/10/330,872A
; CURRENT FILING DATE: 2002-12-24
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/717,828
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 30
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-872A-4

Query Match      100.0%; Score 17; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
      |||||
Db      4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-10-359-935-27
; Sequence 27, Application US/10359935
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
;           Feng, Junli
;           Funk, Walter
;           Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,935
; FILING DATE: 07-Feb-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:

US-10-359-935-27

Query Match      88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GGCCAGCAGCTGACA 17
      |||||
Db      9 GGCCAGCAGCTGACA 23

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RESULT 7
US-09-536-058D-52/c
; Sequence 52, Application US/09536058D
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAAL, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058D
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058D-52

Query Match      82.4%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
      |||||
Db      23 CGGGCCAGCAGCTG 10

RESULT 8
US-60-427-808-148950
; Sequence 148950, Application US/60427808
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528
; CURRENT APPLICATION NUMBER: US/60/427,808
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 148950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-60-427-808-148950

Query Match      82.4%; Score 14; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
      |||||
Db      10 CGGGCCAGCAGCTG 23

RESULT 9
US-10-287-787-16506/c
; Sequence 16506, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Caulobacter crescentus complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/287,787
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 27958
; SOFTWARE: Proprietary
; SEQ ID NO 16506
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Caulobacter crescentus complete genome.

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; FEATURE:
; LOCATION: (2498897) ... (2498911)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectionObjectNumber = 18293
US-10-287-787-16506

Query Match 76.5%; Score 13; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTG 14
DB 14 GGGCCAGCAGCTG 2

RESULT 10
US-10-287-787-18526/c
; Sequence 18526, Application US/10287787
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7849
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-7849

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
DB 1 GGGCCAGCAGCTGA 13

RESULT 13
US-10-310-188-14135
; Sequence 14135, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14135
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-14135

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
DB 1 GGGCCAGCAGCTGA 13

RESULT 14
US-10-310-188-57644
; Sequence 57644, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57644
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-57644

Query Match 76.5%; Score 13; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCCAGCAGCTGA 15
DB 1 GGGCCAGCAGCTGA 13

RESULT 15
US-10-310-188-57644
; Sequence 57644, Application US/10310188
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL REGULATORY GENES
; FILE REFERENCE: 47487
; CURRENT APPLICATION NUMBER: US/10/310,188
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 86841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57644
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-310-188-5556

Query Match 76.5%; Score 13; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTG 14
DB 16 GGGCCAGCAGCTG 4

RESULT 12
US-10-303-778-7849
; Sequence 7849, Application US/10303778
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QY 1 CGGGCCAGCAGCT 13
 Db 1 CGGGCCAGCAGCT 13

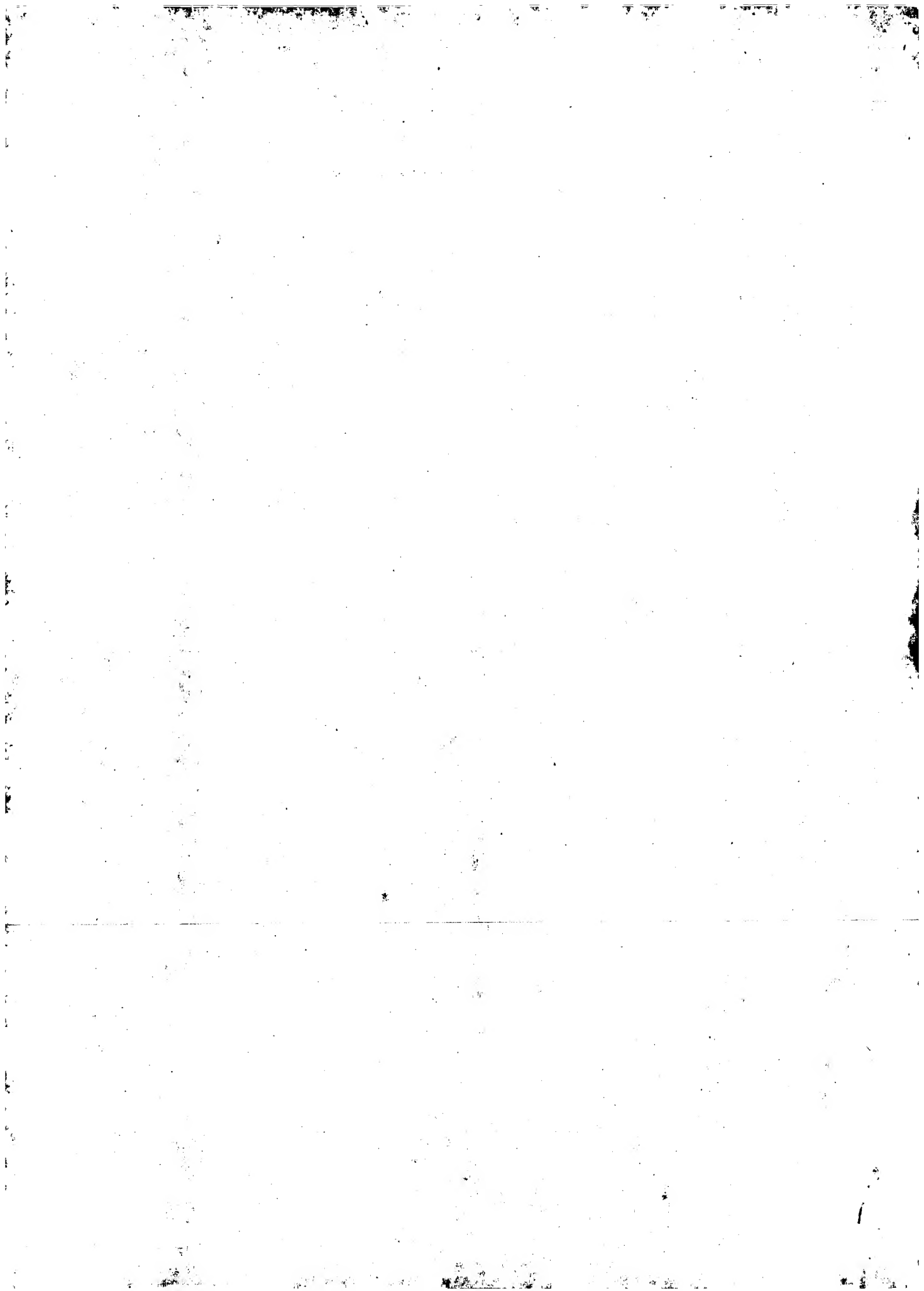
RESULT 15

US-10-299-054A-1993/c
 ; Sequence 1993, Application US/10299054A
 ; GENERAL INFORMATION:
 ; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
 ; TITLE OF INVENTION: Mycobacterium tuberculosis complete genome.
 ; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
 ; CURRENT APPLICATION NUMBER: US/10/299,054A
 ; CURRENT FILING DATE: 2003-03-03
 ; NUMBER OF SEQ ID NOS: 11910
 ; SOFTWARE: Proprietary
 ; SEQ ID NO 1993
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis complete genome.
 ; FEATURE:
 ; LOCATION: (766683)...(766700)
 ; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 2403
 US-10-299-054A-1993

Query Match 76.5%; Score 13; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGGCCAGCAGCTG 14
 Db 13 GGGCCAGCAGCTG 1

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 Job time : 746.239 secs



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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 1425.83 Seconds
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Title: US-08-770-564A-14
Perfect score: 17
Sequence: 1 CGGGCCAGCAGCTGACA 17

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

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- 71: /cgn2_6/ptodata/2/pna/US6027 COMB.seq:*
- 72: /cgn2_6/ptodata/2/pna/US6028 COMB.seq:*
- 73: /cgn2_6/ptodata/2/pna/US6029 COMB.seq:*
- 74: /cgn2_6/ptodata/2/pna/US6030 COMB.seq:*
- 75: /cgn2_6/ptodata/2/pna/US6031 COMB.seq:*
- 76: /cgn2_6/ptodata/2/pna/US6032 COMB.seq:*
- 77: /cgn2_6/ptodata/2/pna/US6033 COMB.seq:*
- 78: /cgn2_6/ptodata/2/pna/US6034 COMB.seq:*
- 79: /cgn2_6/ptodata/2/pna/US6035 COMB.seq:*
- 80: /cgn2_6/ptodata/2/pna/US6036 COMB.seq:*
- 81: /cgn2_6/ptodata/2/pna/US6037 COMB.seq:*
- 82: /cgn2_6/ptodata/2/pna/US6038 COMB.seq:*
- 83: /cgn2_6/ptodata/2/pna/US6039 COMB.seq:*
- 84: /cgn2_6/ptodata/2/pna/US6040 COMB.seq:*
- 85: /cgn2_6/ptodata/2/pna/US6041 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	1	PCT-US97-23619-14
2	17	100.0	17	11	US-08-770-564A-14
3	17	100.0	25	23	US-09-601-267-20
4	17	100.0	30	9	US-08-510-736-4
5	17	100.0	30	28	US-09-717-828A-4
6	17	100.0	30	28	US-09-717-828B-4
7	17	100.0	30	28	US-09-717-829A-4
8	15	88.2	25	8	US-08-472-802A-27
9	15	88.2	25	8	US-08-472-802B-27
10	15	88.2	25	8	US-08-482-115A-26
11	15	88.2	25	9	US-08-521-634-44
12	15	88.2	25	14	US-09-057-351-27
13	14	82.4	24	20	US-09-536-058-52
14	14	82.4	24	20	US-09-536-058C-52
15	14	82.4	42	13	US-08-973-589-12
16	13	76.5	14	15	US-09-164-961-2894
17	13	76.5	24	9	US-08-521-634-11
18	13	76.5	25	17	US-09-396-196F-64639
19	13	76.5	25	17	US-09-396-196F-107046
20	13	76.5	25	17	US-09-396-196G-64639
21	13	76.5	25	17	US-09-396-196G-107046


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; Sequence 20, Application US/09601267
; GENERAL INFORMATION:
; APPLICANT: William Nicol KEITH
; TITLE OF INVENTION: Promoter Regions of the Mouse and Human Telomerase RNA Component
; FILE REFERENCE: 9013.18
; CURRENT APPLICATION NUMBER: US/09/601,267
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: PCT/GB99/00308
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: GB 9801902.9
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-601-267-20

Query Match      100.0%; Score 17; DB 23; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
        |||
DB      7 CGGGCCAGCAGCTGACA 23

RESULT 4
US-08-510-736-4
; Sequence 4, Application US/08510736
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Methods for Purifying Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/510,736
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 015389-001100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-510-736-4
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Query Match      100.0%; Score 17; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
        |||
DB      4 CGGGCCAGCAGCTGACA 20

RESULT 5
US-09-717-828A-4
; Sequence 4, Application US/09717828A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: Purified Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 (edited)
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-828A-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTGACA 17
        |||
DB      4 CGGGCCAGCAGCTGACA 20

RESULT 6
US-09-717-828B-4
; Sequence 4, Application US/09717828B
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L.
; APPLICANT: Atkinson III, Edward M.
; APPLICANT: Lichtsteiner, Serge P.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Pruzan, Ronald A.
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase01base
; CURRENT APPLICATION NUMBER: US/09/717,828B
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO 4
; LENGTH: 30
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829B-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 7
US-09-717-829A-4
; Sequence 4, Application US/09717829A
; GENERAL INFORMATION:
; APPLICANT: Weinrich, Scott L
; APPLICANT: Atkinson III, Edward M
; APPLICANT: Lichtsteiner, Serge P
; APPLICANT: Vasserot, Alain P
; APPLICANT: Pruzan, Ronald A
; TITLE OF INVENTION: A Method for Purifying Telomerase
; FILE REFERENCE: PurifiedTelomerase011base
; CURRENT APPLICATION NUMBER: US/09/717,829A
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 09/420,056
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 08/833,377
; PRIOR FILING DATE: 1997-04-04
; PRIOR APPLICATION NUMBER: 08/510,736
; PRIOR FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1 edited
; SEQ ID NO: 1
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: Biotin 5'-terminal
; OTHER INFORMATION: Description of Artificial Sequence: Affinity Agent
US-09-717-829A-4

Query Match      100.0%; Score 17; DB 28; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTGACA 17
Db 4 CGGGCCAGCAGCTGACA 20

RESULT 8
US-08-472-802A-27
; Sequence 27, Application US/08472802A
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Fung, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 52,944
; REFERENCE/DOCKET NUMBER: 15389-000820
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-472-802A-27

Query Match      88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
Db 9 GGCCAGCAGCTGACA 23

RESULT 9
US-08-472-802B-27
; Sequence 27, Application US/08472802B
; GENERAL INFORMATION:
; APPLICANT: Vilpenteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,802B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
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FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802B-27

Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

RESULT 10
US-08-482-115A-26
Sequence 26, Application US/08482115A
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/482,115A
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000830
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115A-26

Query Match 88.2%; Score 15; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

RESULT 11
US-08-521-634-44
Sequence 44, Application US/08521634
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
FILING DATE: 08/482,115
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: US 08/472,802
FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
FILING DATE: 08/330,123
APPLICATION NUMBER: US 08/272,102
FILING DATE: 7-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Tracy J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 15389-000850
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (primer)
ANTI-SENSE: YES
US-08-521-634-44

Query Match 88.2%; Score 15; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCCAGCAGCTGACA 17
|||||
DB 9 GGCCAGCAGCTGACA 23

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-536-058-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

RESULT 14
US-09-536-058C-52/c
; Sequence 52, Application US/09536058C
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAL, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058C
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058C-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

RESULT 15
US-08-973-589-12/c
; Sequence 12, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-536-058-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

RESULT 14
US-09-536-058C-52/c
; Sequence 52, Application US/09536058C
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAL, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058C
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058C-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

RESULT 15
US-08-973-589-12/c
; Sequence 12, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-536-058-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

RESULT 14
US-09-536-058C-52/c
; Sequence 52, Application US/09536058C
; GENERAL INFORMATION:
; APPLICANT: BEGER, CARMELA
; APPLICANT: BARBER, JACK
; APPLICANT: WONG-STAAL, FLOSSIE
; TITLE OF INVENTION: BRCA-1 REGULATORS AND METHODS OF USE
; FILE REFERENCE: 039316/0601
; CURRENT APPLICATION NUMBER: US/09/536,058C
; CURRENT FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 236
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-536-058C-52

Query Match      82.4%; Score 14; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CGGGCCAGCAGCTG 14
Db      23 CGGGCCAGCAGCTG 10

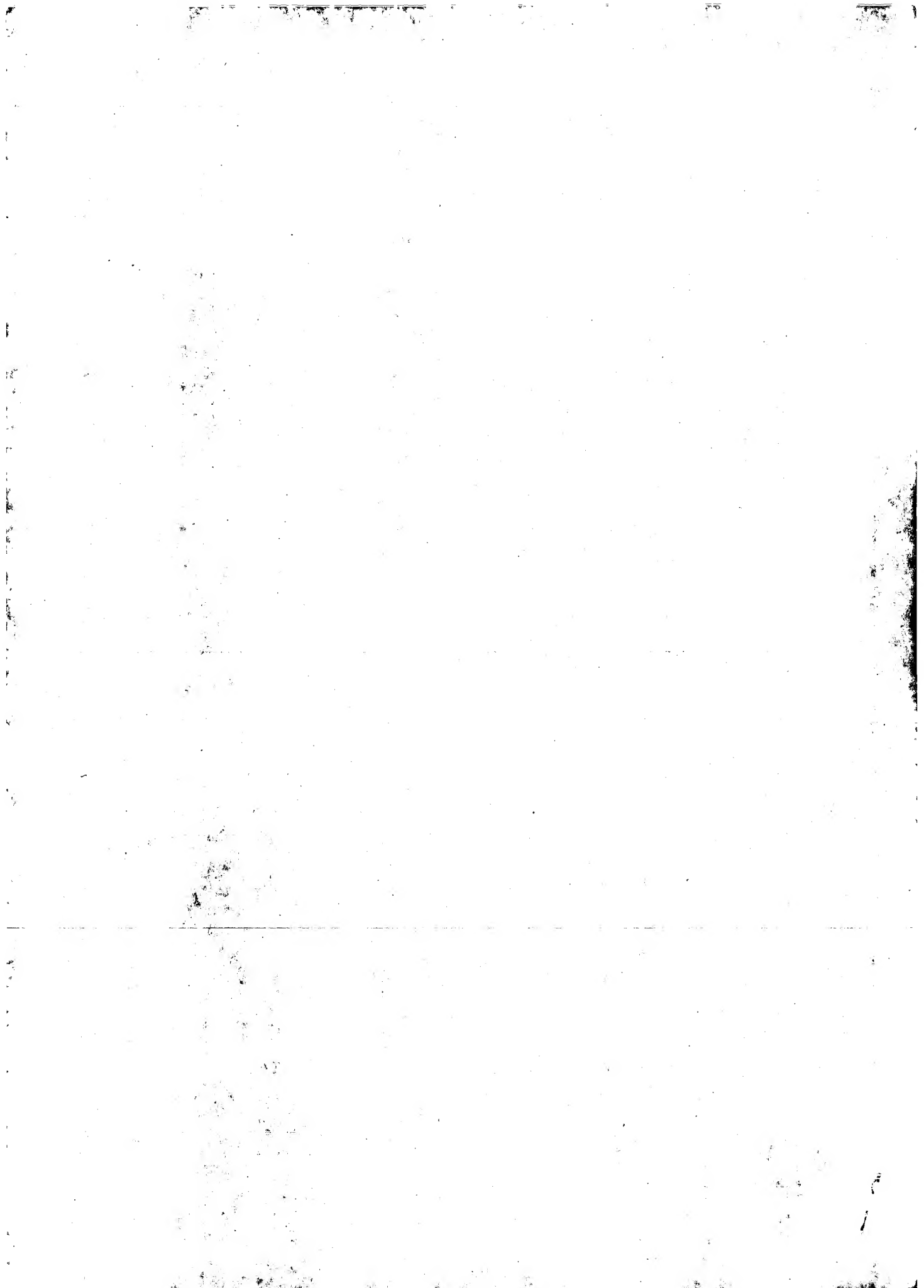
RESULT 15
US-08-973-589-12/c
; Sequence 12, Application US/08973589
; GENERAL INFORMATION:
; APPLICANT: Greider, Carol
; APPLICANT: Autexier, Chantal
; APPLICANT: Pruzan, Ronald
; TITLE OF INVENTION: ESSENTIAL OLIGONUCLEOTIDES OF VERTEBRATE
; FILE REFERENCE: CSHL95-02A
; CURRENT APPLICATION NUMBER: US/08/973,589
; CURRENT FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: PCT/US96/09517
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/478,352
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
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US-08-973-589-12

Query Match 82.4%; Score 14; DB 13; Length 42;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCCAGCAGCTG 14
 |||||
 Db 39 CGGGCCAGCAGCTG 26

Search completed: June 23, 2003, 16:08:25
 Job time : 1426.91 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 136.61 Seconds
(without alignments)
182.610 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17
Sequence: 1 CCGGCCAGCAGCTGACA 17

Scoring table:
OLIGO_NUC
Gapop_60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	88.2	25	10	US-09-057-351-27
2	12	70.6	23	3	US-10-320-230-30
3	12	70.6	23	10	US-09-817-387-18
4	12	70.6	25	9	US-10-215-112-2064
5	12	70.6	38	9	US-09-930-423-2661
6	12	70.6	38	9	US-09-330-423-2713
7	12	70.6	48	9	US-09-848-754A-7985
8	12	70.6	48	9	US-09-848-754A-8229
9	12	70.6	50	9	US-09-943-722-5
10	12	70.6	50	9	US-09-943-722-9
11	11	64.7	19	10	US-09-879-792-9
12	11	64.7	19	10	US-09-942-374-4
13	11	64.7	20	9	US-10-181-846-121
14	11	64.7	21	9	US-09-949-427-318
15	11	64.7	25	9	US-10-098-263B-32486
16	11	64.7	26	10	US-09-815-171A-18
17	11	64.7	28	9	US-09-872-712-9
18	11	64.7	30	9	US-09-972-656-120
19	11	64.7	31	9	US-09-961-077-417

20	11	64.7	36	9	US-10-244-715-21
21	11	64.7	36	10	US-09-504-231A-1733
22	11	64.7	36	10	US-09-504-231A-1783
23	11	64.7	36	10	US-09-274-553D-1733
24	11	64.7	36	10	US-09-274-553D-1783
25	11	64.7	38	9	US-09-730-289B-2007
26	11	64.7	38	9	US-09-730-289B-2355
27	11	64.7	38	9	US-09-730-289B-2444
28	11	64.7	38	9	US-09-730-289B-2667
29	11	64.7	38	9	US-09-780-533A-4597
30	11	64.7	38	9	US-09-877-478-2554
31	11	64.7	39	9	US-09-423-800-17
32	11	64.7	39	9	US-09-423-800-18
33	11	64.7	39	9	US-10-182-018-17
34	11	64.7	39	9	US-10-182-018-18
35	11	64.7	48	9	US-09-848-754A-8533
36	11	64.7	48	9	US-09-848-754A-8533
37	10	58.8	14	10	US-09-504-231A-1442
38	10	58.8	14	10	US-09-274-553D-1442
39	10	58.8	15	9	US-10-104-611-26
40	10	58.8	15	9	US-10-112-547-26
41	10	58.8	15	9	US-10-112-547-26
42	10	58.8	17	9	US-09-818-875-3966
43	10	58.8	17	9	US-09-818-875-3967
44	10	58.8	17	9	US-09-877-478-1409
45	10	58.8	17	9	US-09-877-478-1410

ALIGNMENTS

RESULT 1
US-09-057-351-27
Sequence 27, Application US/09057351
Patent No. US2001003439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Funk, Junli
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-057-351-27

Query Match      88.2%; Score 15; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACGACGCTGACA 17
DB 9 GGCACGACGCTGACA 23

RESULT 2
US-10-320-230-30
; Sequence 30, Application US/10320230
; Publication No. US20030110529A1
; GENERAL INFORMATION:
; APPLICANT: Lowe, Keith S.
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Gregory, Carolyn A.
; APPLICANT: McElver, John A.
; APPLICANT: Hoarster, George J.
; TITLE OF INVENTION: Cyclin D Polynucleotides, Polypeptides
; TITLE OF INVENTION: and Methods of Use
; FILE REFERENCE: 0926D
; CURRENT APPLICATION NUMBER: US/10/320,230
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/101,551
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 03/398,858
; PRIOR FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(23)
US-10-320-230-30

Query Match      70.6%; Score 12; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCACGACGCTGA 15
DB 9 GCCACGACGCTGA 20

RESULT 3
US-09-817-387-18
; Sequence 18, Application US/09817387
; Patent No. US20010039263A1
; GENERAL INFORMATION:
; APPLICANT: Max-Planck-Centrum fur Molekulare Medizin
; TITLE OF INVENTION: Chimeric Oligonucleotides and the Use Thereof
; FILE REFERENCE: 101195-24
; CURRENT APPLICATION NUMBER: US/09/817,387
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: DE 197 20 151.2
; PRIOR FILING DATE: 1997-05-02
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 18
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule:
; OTHER INFORMATION: oligonucleotide
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotides, linkages between positions 1
; OTHER INFORMATION: to 12 are phosphorothioates, linkages between
; OTHER INFORMATION: positions 12 to 20 are phosphodiester
; OTHER INFORMATION: positions 13 to 23 carry 2'-OCH3 modified ribosyl
; OTHER INFORMATION: residues
; OTHER INFORMATION: linkages between positions 20 to 23 are
; OTHER INFORMATION: phosphorothioates
US-09-817-387-18

Query Match      70.6%; Score 12; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACGACGCTG 14
DB 1 GGCACGACGCTG 12

RESULT 4
US-10-215-112-2064
; Sequence 2064, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; TITLE OF INVENTION: Test3
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2064
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-2064

Query Match      70.6%; Score 12; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCACGACGCT 13
DB 4 GGCACGACGCT 15

RESULT 5
US-09-930-423-2661
; Sequence 2661, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Bratt, Larry
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2661
; LENGTH: 38
; TYPE: RNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-930-423-2661

Query Match 70.6%; Score 12; DB 9; Length 38;
Best Local Similarity 91.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGA 15
||| ||||| :||
Db 1 GCCAGCAGCTGA 12

RESULT 6

US-09-930-423-2713
; Sequence 2713, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBH00-918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2713
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-930-423-2713

Query Match 70.6%; Score 12; DB 9; Length 38;
Best Local Similarity 91.7%; Pred. No. 9.1e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCAGCAGCTGA 15
||| ||||| :||
Db 1 GCCAGCAGCTGA 12

RESULT 7

US-09-848-754A-7985
; Sequence 7985, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7985
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-848-754A-7985

Query Match 70.6%; Score 12; DB 9; Length 48;

Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGC 12
||||| :||
Db 37 CGGGCCAGCAGC 48

RESULT 8

US-09-848-754A-8229
; Sequence 8229, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8229
; LENGTH: 48
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-848-754A-8229

Query Match 70.6%; Score 12; DB 9; Length 48;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCCAGCAGC 12
||||| :||
Db 37 CGGGCCAGCAGC 48

RESULT 9

US-09-943-722-5
; Sequence 5, Application US/09943722
; Publication No. US20020192860A1
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF ELIMINATING INHIBITORY/INSTABILITY REGIONS OF mRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,722
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,049
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,478
; FILING DATE: 26-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

us-08-770-564a-14.oligo.rnpb

Fri Jun 27 07:41:33 2003

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; APPLICATION NUMBER: PCT/US93/02908
; FILING DATE: 29-MAR-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,747
; FILING DATE: 27-MAR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-4006US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6849
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; US-09-943-722-5

Query Match      70.6%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CAGCAGCTGACA 17
Db      35 CAGCAGCTGACA 46

RESULT 10
US-09-943-722-9
; Sequence 9, Application US/09943722
; Publication No. US00020192660A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF ELIMINATING
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/943,722
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,049
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,478
; FILING DATE: 26-OCT-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: PCT/US93/02908
; APPLICATION NUMBER:
; FILING DATE: 29-MAR-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,747
; FILING DATE: 27-MAR-1992
; CLASSIFICATION:

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-4006US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)751-6849
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; US-09-943-722-9

Query Match      70.6%; Score 12; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 CAGCAGCTGACA 17
Db      35 CAGCAGCTGACA 46

RESULT 11
US-09-879-792-9
; Sequence 9, Application US/09879792
; Patent No. US0020061850A1
; GENERAL INFORMATION:
; APPLICANT: Xiao Yonghong
; TITLE OF INVENTION: Regulation of Human Transmembrane Serine
; TITLE OF INVENTION: Protease
; FILE REFERENCE: 02973.00035
; CURRENT APPLICATION NUMBER: US/09/879,792
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/211,224
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US 60/283,353
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/283,648
; PRIOR FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: PCT
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-879-792-9

Query Match      64.7%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GCCAGCAGCTG 14
Db      3 GCCAGCAGCTG 13

RESULT 12
US-09-942-374-4
; Sequence 4, Application US/09942374
; Patent No. US20020137063A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alessandra
; APPLICANT: Glucksmann, Maria Alessandra
; APPLICANT: White, David
; TITLE OF INVENTION: 57242, a Human G-Protein Coupled
; TITLE OF INVENTION: Receptor Family Member and Uses Therefor
; FILE REFERENCE: WPI2000-368P1R
; CURRENT APPLICATION NUMBER: US/09/942,374

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; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/228,409
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: murine 57242 primer sequence
US-09-942-374-4

Query Match          64.7%; Score 11; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 CAGCAGCTGAC 16
    |||||
Db   3 CAGCAGCTGAC 13

RESULT 13
US-10-181-846-121
; Sequence 121, Application US/10181846
; Publication No. US20030083297A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTSP-0383
; CURRENT APPLICATION NUMBER: US/10/181,846
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: PCT/US01/01416
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 09/490,692
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 121
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-846-121

Query Match          64.7%; Score 11; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  4 GCCAGCAGCTG 14
    |||||
Db   2 GCCAGCAGCTG 12

RESULT 14
US-09-949-427-318/c
; Sequence 318, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusia, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NPUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07

; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 318
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-318

Query Match          64.7%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

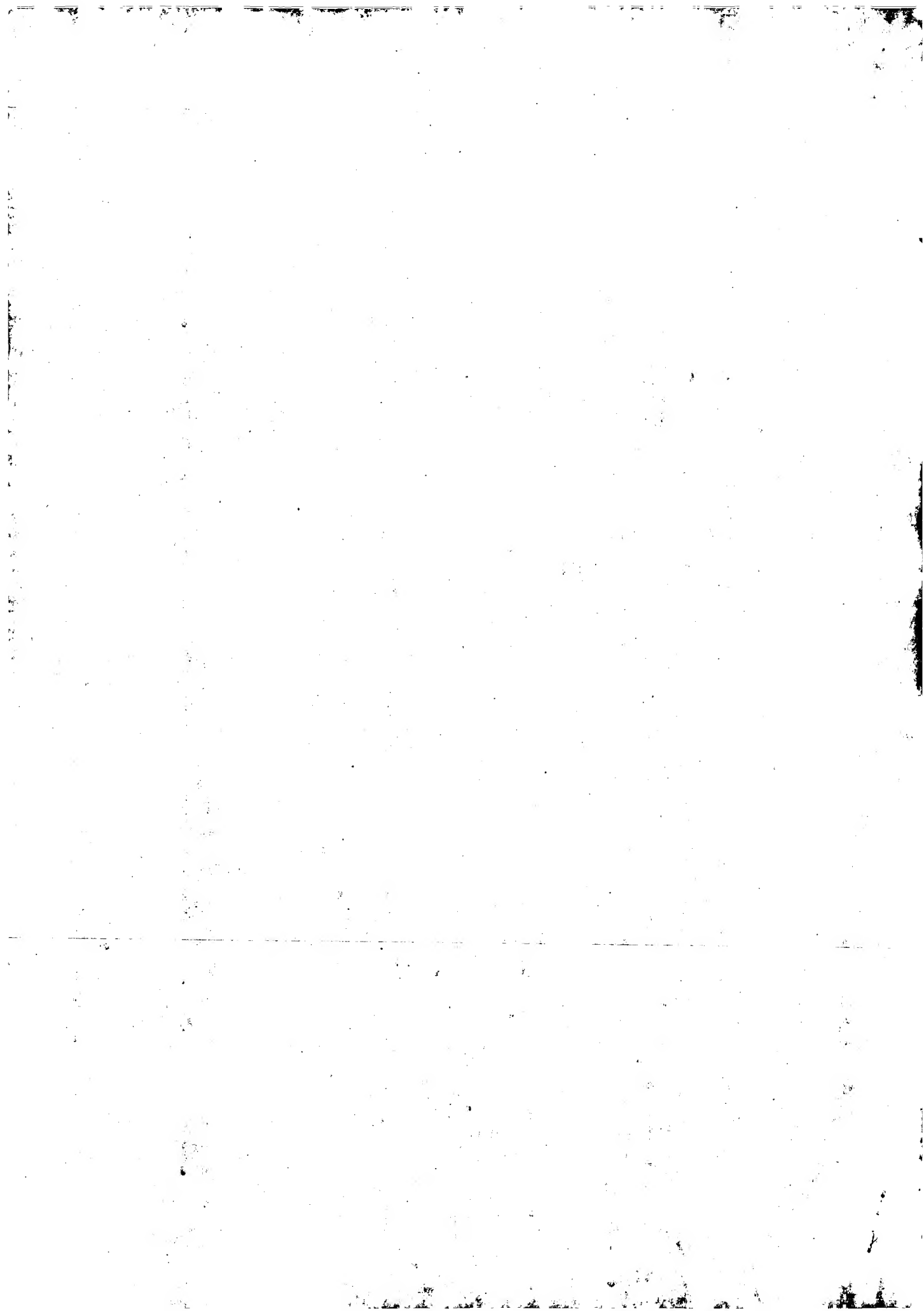
QY  4 GCCAGCAGCTG 14
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Db   16 GCCAGCAGCTG 6

RESULT 15
US-10-098-263B-32486/c
; Sequence 32486, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Mittman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 32486
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-32486

Query Match          64.7%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  7 AGCAGCTGACA 17
    |||||
Db   19 AGCAGCTGACA 9

Search completed: June 23, 2003, 20:01:35
Job time : 137.61 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 26.6175 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17
Sequence: 1 CGGGCCAGCAGCTGACA 17

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 15338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B COMB.seq.*
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4: /cgn2_6/prodata/2/ina/6B COMB.seq.*
5: /cgn2_6/prodata/2/ina/6C COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	US-08-770-565-14	Sequence 14, Appl
2	17	100.0	30	US-08-833-377-5	Sequence 5, Appl
3	15	88.2	25	US-08-482-115B-26	Sequence 26, Appl
4	15	88.2	25	US-08-472-802C-27	Sequence 27, Appl
5	12	70.6	18	US-08-584-040-8292	Sequence 8292, Ap
6	12	70.6	18	US-08-584-040-8293	Sequence 8293, Ap
7	12	70.6	48	US-07-720-222-41	Sequence 41, Appl
8	12	70.6	50	US-08-850-049-5	Sequence 5, Appl
9	12	70.6	50	US-08-850-049-9	Sequence 9, Appl
10	12	70.6	50	US-08-050-478-5	Sequence 5, Appl
11	12	70.6	50	US-08-050-478-9	Sequence 9, Appl
12	12	70.6	50	US-07-858-747B-5	Sequence 5, Appl
13	12	70.6	50	US-07-858-747B-9	Sequence 9, Appl
14	12	70.6	50	US-09-414-117-5	Sequence 5, Appl
15	12	70.6	50	US-09-414-117-9	Sequence 9, Appl
16	12	70.6	50	US-09-678-437-5	Sequence 5, Appl
17	12	70.6	50	US-09-678-437-9	Sequence 9, Appl
18	11	64.7	14	US-08-998-099-368	Sequence 368, App
19	11	64.7	17	US-08-257-784A-8	Sequence 8, Appl
20	11	64.7	17	US-08-489-066A-12	Sequence 12, Appl
21	11	64.7	17	US-08-489-072A-12	Sequence 12, Appl
22	11	64.7	17	US-08-489-071A-12	Sequence 12, Appl
23	11	64.7	17	US-08-584-040-7226	Sequence 7226, Ap
24	11	64.7	20	US-08-837-201C-19	Sequence 19, Appl
25	11	64.7	20	US-09-490-692-121	Sequence 121, Appl
26	11	64.7	22	US-09-364-416-19	Sequence 19, Appl
27	11	64.7	22	US-08-482-115B-32	Sequence 32, Appl

28	11	64.7	22	2	US-08-472-802C-37	Sequence 37, Appl
29	11	64.7	27	2	US-08-793-229-23	Sequence 23, Appl
30	11	64.7	27	3	US-09-285-957-23	Sequence 23, Appl
31	11	64.7	27	4	US-08-584-040-5244	Sequence 5244, Ap
32	11	64.7	31	4	US-08-679-645-417	Sequence 417, App
33	11	64.7	32	4	US-08-813-781-124	Sequence 124, App
34	11	64.7	33	3	US-08-816-346-52	Sequence 52, Appl
35	11	64.7	33	3	US-09-335-411-52	Sequence 52, Appl
36	11	64.7	36	2	US-08-292-620A-1158	Sequence 1158, Ap
37	11	64.7	36	2	US-08-925-708-4	Sequence 4, Appl
38	11	64.7	36	2	US-08-925-708-5	Sequence 5, Appl
39	11	64.7	36	3	US-09-071-845-1158	Sequence 1158, Ap
40	11	64.7	37	1	US-08-330-638D-9	Sequence 9, Appl
41	11	64.7	37	2	US-08-906-746A-9	Sequence 9, Appl
42	11	64.7	46	5	PCT-US91-02954-9	Sequence 9, Appl
43	11	64.7	48	1	US-08-066-961-2	Sequence 2, Appl
44	11	64.7	49	1	US-08-530-492-89	Sequence 89, Appl
45	11	64.7	49	4	US-08-906-517-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-08-770-565-14
; Sequence 14, Application US/08770565
; Patent No. 5846723
; GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; TITLE OF INVENTION: Telomerase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-002300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-770-565-14

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;
QY 1 CGGGCCAGCAGCTGACA 17

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,802C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000820
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-472-802C-27

Query Match 88.2%; Score 15; DB 2; Length 25;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGCACGAGCTGCA 17
DB 9 GGCACGAGCTGACA 23

RESULT 5
US-08-584-040-8292/C
Sequence 8292, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8292:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-8292

Query Match 70.6%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCAGCAGCTGAC 16
DB 15 CCAGCAGCTGAC 4

RESULT 6
US-08-584-040-8293/C
Sequence 8293, Application US/08584040
Patent No. 6346398
GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8293:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-8293

Query Match 70.6%; Score 12; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGAGCAGCTGAC 16
DB 12 CCGAGCAGCTGAC 1

RESULT 7
US-07-720-222-41
Sequence 41, Application US/07720222
Patent No. 5190873
GENERAL INFORMATION:
APPLICANT: Larnhardt, Waldeemar
APPLICANT: Bourdon, Mario
APPLICANT: Youderlian, Phil
TITLE OF INVENTION: HYBRID PROTEINS CONTAINING BINDING SITES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSER: Bingham & Fitting
STREET: 11230 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/720.222
FILING DATE: 19910621
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: CIB0012P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-587-3533
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-720-222-41

Query Match 70.6%; Score 12; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCCAGCAGCTGA 15
DB 8 GCCAGCAGCTGA 19

RESULT 8
US-08-850-049-5
Sequence 5, Application US/08850049
Patent No. 5965726

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,049
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-850-049-5

Query Match 70.6%; Score 12; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
DB 35 CAGCAGCTGACA 46

RESULT 9
US-08-850-049-9
Sequence 9, Application US/08850049
Patent No. 5965726
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE

CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/850,049
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-850-049-9

Query Match 70.6%; Score 12; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46

RESULT 10
US-08-050-478-5
Sequence 5, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-050-478-5

Query Match 70.6%; Score 12; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46

RESULT 11
US-08-050-478-9
Sequence 9, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & PINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398

REFERENCE/DOCKET NUMBER: 2026-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-050-478-9

Query Match 70.6%; Score 12; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
DB 35 CAGCAGCTGACA 46

RESULT 12
US-07-858-747B-5
Sequence 5, Application US/07858747B
Patent No. 617466
GENERAL INFORMATION:
APPLICANT: PAVLAKIS, GEORGE N.; FELBER, BARBARA
APPLICANT: K.
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,747B
FILING DATE: 19920327
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MARY J. MORRY
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 50
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: RNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: HIV-1
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:

CELL LINE:
ORGANELLE:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: CODING SEQUENCE SPANNING NT
OTHER INFORMATION: 654-703 OF THE REVISED NT SEQUENCE OF THE HIV-1
OTHER INFORMATION: MOLECULAR CLONE PHX82
US-07-858-747B-5

Query Match 70.6%; Score 12; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
DB 35 CAGCAGCTGACA 46

RESULT 13
US-07-858-747B-9
Sequence 9, Application US/07858747B
Patent No. 617466
GENERAL INFORMATION:
APPLICANT: PAVLAKIS, GEORGE N.; FELBER, BARBARA
APPLICANT: K.
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,747B
FILING DATE: 19920327
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MARY J. MORRY
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026-4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 50
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: OTHER
HYPOTHETICAL: YES
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: OLIGONUCLEOTIDE M4
US-07-858-747B-9

Query Match 70.6%; Score 12; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46

RESULT 14

US-09-414-117-5
; Sequence 5, Application US/09414117
; Patent No. 6291664
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF ELIMINATING
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,117
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,049
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02908
; FILING DATE: 29-MAR-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,747
; FILING DATE: 27-MAR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRIS, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-4006US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
US-09-414-117-5

Query Match 70.6%; Score 12; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46

RESULT 15

US-09-414-117-9
; Sequence 9, Application US/09414117

; Patent No. 6291664
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF ELIMINATING
; TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
; NUMBER OF SEQUENCES: 130
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/414,117
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/850,049
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/02908
; FILING DATE: 29-MAR-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/858,747
; FILING DATE: 27-MAR-1992
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRIS, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2026-4006US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
US-09-414-117-9

Query Match 70.6%; Score 12; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 CAGCAGCTGACA 17
Db 35 CAGCAGCTGACA 46

Search completed: June 23, 2003, 10:17:10
Job time : 27.6175 secs

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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 18:09:32 ; Search time 112.972 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-14

Perfect score: 17 CCGGCCAGCAGCTGACA 17

Sequence: 1 CCGGCCAGCAGCTGACA 17

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	19	AAV41181
2	17	100.0	25	20	AA207280
3	17	100.0	30	19	AAV63648
4	17	100.0	30	20	AA223630
5	17	100.0	30	22	AA509475
6	15	88.2	25	17	AA110302
7	14	82.4	24	22	AA556779
8	14	82.4	42	18	AA158806
9	13	76.5	14	20	AAV93815

10	12	70.6	17	21	AA265597
C 11	12	70.6	18	18	AA275542
C 12	12	70.6	18	18	AA275543
C 13	12	70.6	21	20	AA238106
C 14	12	70.6	21	20	AA231700
C 15	12	70.6	22	21	AA269270
C 16	12	70.6	22	22	AA293030
C 17	12	70.6	23	21	AA294606
C 18	12	70.6	47	22	AA209076
C 19	12	70.6	50	14	AA050205
C 20	12	70.6	50	22	AA228271
C 21	12	70.6	50	22	AA235675
C 22	12	70.6	50	22	AA209081
C 23	11	64.7	17	16	AA095628
C 24	11	64.7	17	16	AA080412
C 25	11	64.7	17	18	AA274476
C 26	11	64.7	17	23	AA223927
C 27	11	64.7	18	22	AA240858
C 28	11	64.7	19	24	AA239182
C 29	11	64.7	20	19	AA227732
C 30	11	64.7	20	19	AA269957
C 31	11	64.7	20	19	AA208229
C 32	11	64.7	20	20	AA222293
C 33	11	64.7	20	20	AA284046
C 34	11	64.7	20	22	AA258664
C 35	11	64.7	20	22	AA273020
C 36	11	64.7	21	24	AA271217
C 37	11	64.7	21	24	AA268313
C 38	11	64.7	22	11	AA204792
C 39	11	64.7	22	17	AA210308
C 40	11	64.7	22	22	AA203498
C 41	11	64.7	25	24	AA212839
C 42	11	64.7	26	24	AA230606
C 43	11	64.7	27	18	AA272494
C 44	11	64.7	27	21	AA261994
C 45	11	64.7	27	21	AA262044

ALIGNMENTS

RESULT 1	AAV41181	standard; DNA; 17 BP.
ID	AAV41181	
AC	AAV41181	
DT	08-OCT-1998	(first entry)
DE	RNA component of human telomerase (hTR) antisense oligo RP2.	
XX	RNA component; human telomerase; antisense oligonucleotide; infection; neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer; contraction; sterilisation; immunosuppression; therapeutic; hTR;	
KW	Immune system down-regulation; anti-inflammatory therapy; ss.	
OS	Synthetic.	
XX	Homo sapiens.	
XX	WO9828442-A1.	
XX	PD	
XX	02-JUL-1998.	
PF	19-DEC-1997;	97WO-US23619.
XX	20-DEC-1996;	96US-0770565.
PR	20-DEC-1996;	96US-0770564.
XX	(GERO-) GERON CORP.	
PA	Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;	
PI	WPI; 1998-37670/32.	
XX		
DR		

Immunosuppressant
Mouse flt-1-VEGF r
Mouse flt-1-VEGF r
Human FKHL7 gene s
Human FKHL7 gene P
Human ABC1 gene ex
Partial exon 2 cor
Matze cyclin D ZMC
Human oligonucleot
INS mutagenic olig
Human SNP oligonuc
Human SNP oligonuc
Human oligonucleot
Human c-fos target
Hu-IFN-alpha-001 p
Mouse flt-1 VEGF r
Human interferon H
SNP specific lower
Mouse 5742 DNA am
Human transmembran
Human c-fos protei
PCR primer ABCR-EX
Probe Seq ID No: 3
Primer used in met
Murine myostatin g
Human dxxx inhibit
Mouse HYP1P1 locu
Mouse HYP1P1 locu
5'-3' primer for c
RNA component of h
Human primer, Dp42
Oligonucleotide ad
(AT)4-5P13, 5' tai
Mouse flt-1 VEGF r
Hammerhead ribozym
Hammerhead ribozym

XX New polynucleotide(s) anti:sense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 11; Page 65; 80pp; English.
 XX
 CC Sequences shown in AAV1169 to AAV1181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridise to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridise to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting assembly
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 CC
 SQ Sequence 17 BP; 4 A; 6 C; 6 G; 1 T; 0 other;
 Query Match 100.0%; Score 17; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTGACA 17
 DB 1 CGGGCCAGCAGCTGACA 17
 RESULT 2
 AA207280
 ID AA207280 standard; DNA; 25 BP.
 XX
 AC AA207280;
 XX
 DT 22-OCT-1999 (first entry)
 XX
 DE Human telomerase RNA gene (hTR) specific primer TRC3R.
 XX
 KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
 KW gene therapy; thymidine kinase gene; anticancer therapy; human;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO938964-A2.
 XX
 PD 05-AUG-1999.
 XX
 PF 29-JAN-1999; 99WO-GB00308.
 XX
 PR 29-JAN-1998; 98GB-0001902.
 XX
 PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PI Keith WN;
 PT MPI; 1999-479183/40.
 DR Mouse and human telomerase RNA gene promoters, useful for tumor
 PT specific gene therapy

XX Disclosure; Fig 6; 10pp; English.
 PS
 XX
 CC The invention relates to promoter regions from mouse and human
 CC telomerase RNA (TR) component genes. The TR gene promoter can be linked
 CC to a heterologous gene, especially a gene encoding a cytotoxin, for
 CC therapy of cancer, especially neoplasias. The telomerase is necessary for
 CC the unrestricted proliferative capacity of many human cancers. Mutation
 CC or dysregulation of the telomerase repression pathway may cause
 CC substances, identified in the methods, can be used to block transcription
 CC from the TR gene promoter through interaction of the 5' regulatory
 CC sequences. These substances, e.g. antisense oligonucleotides,
 CC transcription factors, peptide nucleic acids and factors that disrupt
 CC signal transduction, are useful for cancer therapy. In particular, gene
 CC therapy vectors (especially pGR2-codAmp) comprising the promoter and a
 CC viral thymidine kinase gene can be used to convert or treated. Direct
 CC gene/cytovir, so that neoplasia can be controlled or treated. Direct
 CC down-regulation of telomerase RNA gene through manipulation of
 CC transcription factors may be effective anticancer therapy and the cloning
 CC of the hTR gene promoter allows the analysis of therapeutic molecules
 CC which modulate hTR promoter activity. Sequences AA20723-80 represents
 CC PCR primers for amplifying human TR gene (hTR) promoter sequence.
 XX
 SQ Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 other;
 Query Match 100.0%; Score 17; DB 20; Length 25;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTGACA 17
 DB 7 CGGGCCAGCAGCTGACA 23
 RESULT 3
 AAV63648
 ID AAV63648 standard; DNA; 30 BP.
 XX
 AC AAV63648;
 XX
 DT 15-FEB-1999 (first entry)
 XX
 DE Antisense oligonucleotide 13 for human telomerase RNA component.
 XX
 KW Human; telomerase RNA component; anticancer therapy; purification;
 KW assay; vaccine; cancer; antisense oligonucleotide; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "biotinylated"
 XX
 PN WO9845450-A1.
 XX
 PD 15-OCT-1998.
 XX
 PF 04-APR-1997; 97WO-US06012.
 XX
 PR 04-APR-1997; 97WO-US06012.
 XX
 PA (GERO-) GERON CORP.
 PI Atkinson EM, Kealey JT, Lichtsteiner SP, Pruzan RA;
 PI Vaeserot AP, Weinrich SL;
 PT MPI; 1998-59485/50.
 DR Purification of telomerase on affinity material - useful for, e.g.
 PT diagnosis and treatment of cancer

XX Disclosure; Page 24; 76pp; English.
 PS The present sequence represents an antisense oligonucleotide.
 XX CC directed against the human telomerase RNA component gene sequences.
 CC The oligonucleotide can be used as an affinity agent in the methods of
 CC the invention, which are used to purify human telomerase. The methods
 CC involve the use of several sequential steps, including the use of two
 CC matrices that bind molecules bearing negative charges, a matrix that
 CC binds molecules bearing positive charges, an affinity purification step
 CC and a size separation. Telomerase is a particular target of anticancer
 CC therapies, and is useful in assays for characterizing (pre)cancerous
 CC cells. Telomerase can also be used to screen for specific modulators,
 CC for biochemical analysis of its activity, and in preparation of
 CC antibodies. Fragments of telomerase, or nucleic acid encoding them,
 CC are used in vaccines, and for treating over expression of telomerase,
 CC particularly in cancer.
 XX SQ Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
 Query Match 100.0%; Score 17; DB 19; Length 30;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTGACA 17
 Db 4 CGGGCCAGCAGCTGACA 20
 RESULT 4
 ID AA223630 standard; DNA; 30 BP.
 XX AA223630;
 AC 07-JUN-2000 (first entry)
 XX
 DT Human clone 28-1, telomerase oligonucleotide oligo-13.
 XX
 DE
 XX
 KW Telomerase; human; immune response; cancer; vaccine; treatment;
 KM disease; primer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /note= "5'-biotinylated guanosine"
 FT
 PN US5968506-A.
 XX
 PN 19-OCT-1999.
 XX
 PD 04-APR-1997; 97US-0833377.
 XX
 PF 04-AUG-1995; 95US-0510736.
 XX
 PR (GERO-) GERON CORP.
 XX
 PA
 XX
 PI Ackinson EM, Lichtsteiner SP, Weinrich SL, Pruzan RA, Kealey JT;
 PI Vasserot AP;
 PI
 XX
 DR WPI; 1999-590379/50.
 XX
 XX Compositions comprising human telomerase, useful for treating diseases
 PT associated with overexpression of telomerase e.g. cancer -
 XX
 XX Disclosure; Column 45-46; 34pp; English.
 XX
 CC This invention describes a novel composition comprising human telomerase
 CC having at least 2000-fold (preferably at least 60000-fold) increased
 CC relative purity compared with crude extract of cells from

CC adenovirus-transformed kidney cell line. The composition is useful for
 CC eliciting an immune response in animals and may therefore be used as a
 CC vaccine for treating diseases associated with the overexpression of
 CC telomerase e.g. cancer. AA223626-223637 represent oligonucleotides used
 CC in the isolation of human clone 28-1 which contains a fragment of the
 CC human telomerase described in the method of the invention.
 XX SQ Sequence 30 BP; 6 A; 6 C; 8 G; 10 T; 0 other;
 Query Match 100.0%; Score 17; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTGACA 17
 Db 4 CGGGCCAGCAGCTGACA 20
 RESULT 5
 ID AA509475 standard; DNA; 30 BP.
 XX AA509475;
 AC 24-OCT-2001 (first entry)
 XX
 DT Antisense oligonucleotide for human telomerase, Oligo 13.
 XX
 DE
 XX
 KW Human; Telomerase; vaccine; antibody; cancer; E2H;
 KM nucleolin; antisense oligonucleotide; Oligo 13; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= G
 FT /note= "G is biotinylated"
 FT
 PN US6261556-B1.
 XX
 PN 17-JUL-2001.
 XX
 PD 18-OCT-1999; 99US-0420056.
 XX
 PF 04-APR-1997; 97US-0833377.
 XX
 PR 04-AUG-1995; 95US-0510736.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Weinrich SL, Ackinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;
 PI Kealey JT;
 PI
 XX
 DR WPI; 2001-450477/48.
 XX
 XX Purified human telomerase, useful for inducing immune response in
 PT animals, comprises several thousand folds increased purity compared
 PT with cytoplasmic crude cell preparations -
 XX
 XX Disclosure; Column 18; 29pp; English.
 XX
 CC The sequence represents a biotinylated antisense oligonucleotide
 CC used in the purification of human telomerase. The invention
 CC relates to a purified human telomerase core enzyme protein comprising
 CC 2000-fold increased purity compared with a crude extract of cells from
 CC adenovirus-transformed kidney cell line (293 cells) and when associated
 CC with telomerase RNA component has DNA polymerase activity and a molecular
 CC weight of 200-2000 kDa. The purified telomerase is useful
 CC for inducing a humoral or cell-mediated immune response in an animal.
 CC Purified telomerase or immunogenic fragments are useful as vaccines for
 CC treating diseases associated with over-expression of telomerase, such as
 CC cancer and for producing antibodies that recognize telomerase, which are
 CC useful as affinity agents in isolating the proteins and for detecting the

AA58806/c
 ID AAT58806 standard; DNA; 42 BP.
 XX
 AC AAT58806;
 XX
 DT 20-NOV-1997 (first entry)
 XX
 DE Human telomerase template PCR primer hTR170.
 XX
 KW Cancer; eukaryotic parasite; hTR; vertebrate telomerase; yeast;
 KW protozoa; tumour; antibody; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 PN WO9640868-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09517.
 XX
 PR 07-JUN-1995; 95US-0478352.
 XX
 XX (COLD-) COLD SPRING HARBOR LAB.
 PA
 XX Autexier C, Greider C;
 PI
 XX WPI; 1997-099928/09.
 XX
 XX DNA encoding essential RNA components of human telomerase - also
 PT truncated or recombinant telomerase, useful for diagnosis and
 PT treatment of cancer and infection by eukaryotic parasites
 XX
 XX Example 4; Page 30; 48pp; English.
 PS
 XX The present sequence represents PCR primer hTR170 used for amplifying
 CC the human telomerase (hTR) template. The RNA and DNA can be used in
 CC hybridisation assays to detect or quantify telomerase activity in cells,
 CC tissue or fluid samples, e.g. for diagnosis of eukaryotic parasites
 CC (yeast and protozoa) or tumours. It is also useful as primers for
 CC amplification assays. The truncated or recombinant vertebrate telomerase
 CC is used therapeutically to increase telomerase activity (also as
 CC reagents in the screening assay) while the RNA or other inhibitors such
 CC as antisense molecules, are used to reduce such activity. Typical
 CC applications are initiation/restoration of activity to cause senescence
 CC or to prevent immortalisation of cells in tumours or parasites. The DNA
 CC is also used to produce recombinant telomerase, which can then be used
 CC conventionally to raise antibodies for diagnostic detection of
 CC telomerase. Detecting telomerase allows early diagnosis of tumour or
 CC infection, before clinical signs manifest. Telomerase inhibitors
 CC directed against e.g. Trypanosoma should cause fewer side effects than
 CC drugs currently used to treat such infections. The DNA encodes those
 CC parts of hTR RNA essential for activity but are significantly shorter
 CC than the endogenous RNA component.
 XX
 SQ Sequence 42 BP; 8 A; 10 C; 12 G; 12 T; 0 other;
 Query Match 82.4%; Score 14; DB 18; Length 42;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCTG 14
 DB 39 CGGGCCAGCAGCTG 26
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 RESULT 9
 AAV93815/c
 ID AAV93815 standard; RNA; 14 BP.
 XX
 AC AAV93815;
 XX
 DT 18-FEB-1999 (first entry)
 XX

DE Human B-raf target sequence nucleotide position 2205.
 XX
 KW Human; c-raf; A-raf; B-raf; hammerhead ribozyme; hairpin ribozyme;
 KW target; substrate; catalyst; modulation; expression; Raf gene;
 KW delivery; screening; identification; synthesis; deprotection;
 KW purification; cancer; inflammation; psoriasis; non-hepatic ascites;
 KW infection; genetic drift; restenosis; rheumatoid arthritis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9850530-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 05-MAY-1998; 98WO-US09249.
 XX
 PR 19-DEC-1997; 97US-0068212.
 PR 09-MAY-1997; 97US-0046059.
 PR 09-JUN-1997; 97US-0049002.
 PR 03-JUL-1997; 97US-0051718.
 PR 22-AUG-1997; 97US-0056808.
 PR 02-OCT-1997; 97US-0061321.
 PR 02-OCT-1997; 97US-0061324.
 PR 05-NOV-1997; 97US-0064866.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Beaudry A, Beigelman L, Bellon L, Burgin A, Jarvis T;
 PI Karpeisky A, Kisch K, Matulic-Adamic J, McSwiggen JA;
 PI Parry T, Reynolds M, Svedler D, Thompson J, Workman CT;
 XX
 XX WPI; 1999-009494/01.
 DR
 XX Identifying new catalytic nucleic acid that modulates selected
 PT processes - especially ribozymes that cleave Raf RNA for treating
 PT cancer, restenosis, and also new ribozymes and modified nucleoside
 PT triphosphates used as antiviral agents and synthons
 PS
 XX Claim 179; Page 175; 259pp; English.
 CC
 XX A method has been developed for the identification of a nucleic acid
 CC capable of modulating a process in a biological system. The method
 CC comprises: (a) introducing into the system a random library of nucleic
 CC acid catalysts (NAC) having a substrate binding domain (SBD), comprising
 CC a random sequence, and a catalytic domain (CD); and (b) identifying NAC
 CC in systems where modulation has occurred and/or determining the sequence
 CC of at least part of the SBDs in such systems. Nucleic acid molecules
 CC with endonuclease activity and catalytic activity, from the present
 CC invention, are used to modulate gene expression in plant and mammalian
 CC cells and to cleave target nucleic acid, particularly for treating
 CC systemic diseases caused by specific RNA, e.g. cancer, inflammation,
 CC psoriasis, non-hepatic ascites and infection. They may also be used to
 CC detect genetic drift and mutations in diseased cells and to determine
 CC c-raf RNA. Specifically NACs with RNA-cleaving activity that modulate
 CC expression of the Raf gene, are used to treat cancer, restenosis,
 CC psoriasis or rheumatoid arthritis, or generally any condition associated
 CC with the level of c-raf. Introduction of sugar/phosphate modifications
 CC increases stability against nuclease and activity. AAV90922 to AAV93877
 CC represent NACs that can be used in the method, specifically for
 CC modulating the expression of a Raf gene.
 XX
 SQ Sequence 14 BP; 1 A; 5 C; 6 G; 2 U; 0 other;
 Query Match 76.5%; Score 13; DB 20; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGCT 13
 DB 14 CGGGCCAGCAGCT 2
 |||||
 RESULT 10

AAZ65597
 ID AAZ65597 standard; DNA; 17 BP.
 AC AAZ65597;
 XX
 DT 30-MAR-2000 (first entry)
 XX
 DE Immunosuppressant inhibitor oligonucleotide flt-rm-2115.
 XX
 XX Immunosuppressant inhibitor; transforming growth factor beta; TGF beta;
 KW vascular endothelial growth factor; VEGF; interleukin-10; IL-10; cancer;
 KW prostaglandin E2; PGE2; immune response; tumour; asthma; Crohn's disease;
 KW monocyte chemoattractant protein-1; MCP-1; ulcerative colitis; diabetes;
 KW glomerulonephritis; acute respiratory distress syndrome; ss;
 KW atherosclerosis.
 XX
 OS Unidentified.
 XX
 PN WO963975-A2.
 XX
 PD 16-DEC-1999.
 XX
 XX 10-JUN-1999; 99WO-EP04013.
 XX
 PF 10-JUN-1998; 98EP-0110709.
 PR 25-JUL-1998; 98EP-0113974.
 XX
 XX (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
 PA
 XX Schlingensiepen K, Schlingensiepen R, Brysch W;
 PI
 XX WPI; 2000-097470/08.
 DR
 XX Composition containing immune stimulant and inhibitor of agent that
 PT adversely affects the immune response, for treating cancers and
 PT infections.
 PS
 XX Claim 10; Figure 1; 30pp; English.
 CC This sequence is an immunosuppressant inhibitor oligonucleotide, which
 CC is used in the invention. The invention relates to a composition which
 CC contains at least one inhibitor (less than 100 kD) of a substance (e.g.
 CC transforming growth factor TGF-beta, vascular endothelial growth factor
 CC VEGF, interleukin-10, prostaglandin E2, PGE2, or their receptors)
 CC that adversely affects the immune response. The composition also includes
 CC at least one stimulant that positively affects the immune response. This
 CC oligonucleotide is an example of an inhibitor that is used in the
 CC composition. The composition is used as an immunostimulant for the
 CC treatment of neoplasms and infections, particularly hyperproliferation;
 CC leukaemia; (non-)Hodgkin's lymphoma; carcinoma (of oesophagus, bronchi,
 CC colon-rectum, stomach, intestine, gall bladder or duct, pancreas, anus,
 CC breast, ovary, cervix, endometrium, prostate or bladder), liver tumours,
 CC malignant melanoma, brain tumours and sarcomas. The oligonucleotides,
 CC most of which are directed against TGFbeta or VEGF, are inhibitors of
 CC monocyte chemoattractant protein-1 (MCP-1) and are useful as
 CC anti-inflammatory for treating e.g. asthma, Crohn's disease, ulcerative
 CC colitis, diabetes, glomerulonephritis, acute respiratory distress
 CC syndrome and the formation of atherosclerotic plaque.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 5 G; 2 T; 0 other;
 Query Match 70.6%; Score 12; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCAGCAGCTGAC 16
 Db 1 CCAGCAGCTGAC 12
 RESULT 11
 AAX75542/c
 ID AAX75542 standard; RNA; 18 BP.

XX AAX75542;
 AC
 XX 28-JUL-1999 (first entry)
 DT
 XX Mouse flt-1 VEGF receptor hairpin ribozyme substrate #1.
 DE
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 XX 25-OCT-1996; 96WO-US17480.
 XX
 PF 11-JAN-1996; 96US-0584040.
 PR 26-OCT-1995; 95US-0005974.
 XX
 XX (CHIR-) CHIRON CORP.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 PI
 XX WPI; 1997-259017/23.
 DR
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 4; Page 184; 218pp; English.
 CC The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient of the
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 SQ Sequence 18 BP; 3 A; 4 C; 7 G; 4 U; 0 other;
 Query Match 70.6%; Score 12; DB 18; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCAGCAGCTGAC 16
 Db 15 CCAGCAGCTGAC 4
 RESULT 12
 AAX75543/c
 ID AAX75543 standard; RNA; 18 BP.
 XX
 XX AAX75543;
 AC
 XX 28-JUL-1999 (first entry)
 DT
 XX Mouse flt-1 VEGF receptor hairpin ribozyme substrate #2.
 DE
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1;
 KW flk-1; KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW

KW foetal liver kinase 1; ss.
 XX Mus sp.
 XX WO9715662-A2.
 XX PD 01-MAY-1997.
 XX PF 25-OCT-1996; 96WO-US17480.
 XX PR 11-JAN-1996; 96US-0584040.
 XX PR 26-OCT-1995; 95US-0005974.
 XX PA (CHIR) CHIRON CORP.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Escobedo J, McSwiggen J, Pavco P, Stinchcomb D;
 XX WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or
 PT mRNA stability - useful for treating e.g. tumour angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX Claim 4; Page 184; 218pp; English.
 XX The present invention describes nucleic acid molecules which modulate
 CC the synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can
 CC be treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention.
 XX
 XX Sequence 18 BP; 3 A; 6 C; 6 G; 3 U; 0 other;
 Query Match 70.6%; Score 12; DB 18; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CCAGCAGCTGAC 16
 Db 12 CCAGCAGCTGAC 1
 RESULT 13
 AAZ38106/c
 ID AAZ38106 standard; DNA; 21 BP.
 AC AAZ38106;
 XX 22-FEB-2000 (first entry)
 DT Human FKHL7 gene specific reverse primer Fkh10-Rv.
 DE
 XX Forkhead transcription factor gene; FKHL7; treatment; glaucoma; human;
 KW transgenic animal; drug screening; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9953060-A2.
 PN 21-OCT-1999.
 XX 14-APR-1999; 99WO-US08148.
 PF 15-APR-1998; 98US-0081870.
 XX 22-MAY-1998; 98US-0083352.
 PR

PA (IOWA) UNIV IOWA RES FOUND.
 XX Sheffield VC, Alward WLM, Stone EM, Nishimura D, Patil S;
 XX WPI; 1999-620429/53.
 XX New isolated human forkhead transcription factor gene, FKHL7, used to,
 PT e.g. develop products for the diagnosis -
 XX Claim 31; Page 87; 99pp; English.
 XX The invention provides a human forkhead transcription factor gene,
 CC FKHL7. The FKHL7 protein can be produced by standard recombinant
 CC methodology. The products can be used for diagnosis, prognosis,
 CC monitoring, prevention and treatment of glaucoma. They can also be used
 CC for the production of transgenic animals and drug screening. Sequences
 CC AAZ38081-110 represent PCR primers specific for the human FKHL7 gene.
 XX
 XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 other;
 Query Match 70.6%; Score 12; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGC 12
 Db 12 CGGGCCAGCAGC 1
 RESULT 14
 AAZ31700/c
 ID AAZ31700 standard; DNA; 21 BP.
 AC AAZ31700;
 XX 17-JAN-2000 (first entry)
 DT Human FKHL7 gene PCR primer Fkh10-Rv.
 DE
 XX FKHL7; human; forkhead transcription factor gene; diagnosis; therapy;
 KW congenital heart disease; PCR primer; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9952415-A2.
 PN 21-OCT-1999.
 PD 14-APR-1999; 99WO-US08159.
 PF 15-APR-1998; 98US-0081870.
 XX 22-MAY-1998; 98US-0083351.
 PR (IOWA) UNIV IOWA RES FOUND.
 PA Sheffield VC, Alward WLM, Stone EM, Nishimura D, Patil S;
 XX WPI; 1999-620257/53.
 XX New isolated human forkhead transcription factor gene, FKHL7, used to
 PT develop products for the diagnosis, prognosis, monitoring, prevention
 PT or treatment of congenital heart disease -
 XX Claim 31; Page 85; 98pp; English.
 XX This sequence represents a PCR primer for DNA encoding the human forkhead
 CC transcription factor gene, designated FKHL7, of the invention. FKHL7 can
 CC be used in a novel method for treating or preventing the development of a
 CC congenital heart disease (CHD) in a subject. The FKHL7 sequences can be
 CC used for diagnosis, prognosis, monitoring, prevention and treatment of
 CC CHD. They can also be used for the production of transgenic animals and
 CC drug screening.

XX Sequence 21 BP; 1 A; 7 C; 9 G; 4 T; 0 other;
 SQ Query Match 70.6%; Score 12; DB 20; Length 21;
 Best Local Similarity 100.0%; Pred. NO. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGGCCAGCAGC 12
 DB 12 CGGGCCAGCAGC 1
 RESULT 15
 AAC69270/c
 ID AAC69270 standard; DNA; 22 BP.
 XX
 AC AAC69270;
 DT 29-JAN-2001 (first entry)
 XX
 DE Human ABC1 gene exon 2 fragment corrected sequence, SEQ ID NO:169.
 XX
 KW Human ABC1 cholesterol transporter; chromosome 9q31;
 KW ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TB; familial HDL deficiency; FHA; polymorphism;
 KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;
 KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
 KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
 KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200055318-A2.
 XX
 XX 21-SEP-2000.
 XX
 XX 15-MAR-2000; 2000WO-IB00532.
 XX
 XX 15-MAR-1999; 99US-0124702.
 XX 08-JUN-1999; 99US-0138048.
 XX 17-JUN-1999; 99US-0139600.
 XX 01-SEP-1999; 99US-0151977.
 XX
 XX (UYBR-) UNIV BRITISH COLUMBIA.
 XX (XENO-) XENON BIORESEARCH INC.
 XX
 XX Hayden MR, Wilson AR, Pimstone SN;
 XX
 XX WPI; 2000-587528/55.
 XX
 XX New ABC1 polypeptide is useful for treating diseases associated with
 PT ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
 PT disease and cancer -
 XX
 XX Example; Fig 11; 229pp; English.
 XX
 CC The invention relates to the human ABC1 cholesterol transporter protein
 CC (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
 CC a member of the ATP-binding cassette (ABC transporter) superfamily of
 CC proteins, and plays a crucial role in cholesterol transport, particularly
 CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
 CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
 CC located on chromosome 9q31, and mutations in this gene are associated
 CC with two genetic HDL (high density lipoprotein) deficiency disorders,
 CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
 CC are distinguishable in that TD is an autosomal recessive disorder, while
 CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
 CC cholesterol") in the blood correlate with a high risk of cardiovascular
 CC disease, particularly coronary artery disease, but also cerebrovascular
 CC disease, coronary restenosis, and peripheral vascular disease.
 CC Conversely, a high level of HDL has protective effects against
 CC cardiac/vascular disease. The invention provides genetic constructs and

CC transgenic cells and non-human animals comprising human ABC1 nucleic
 CC acids, and methods of gene therapy for the treatment or prevention of
 CC cardiovascular disease comprising the administration of an expression
 CC vector encoding ABC1 or an active fragment thereof. The invention also
 CC encompasses compounds which mimic ABC1 activity, compounds which
 CC stimulate ABC1 expression and methods of screening for such compounds.
 CC It further relates to methods for determining whether a patient has an
 CC increased risk for cardiovascular disease due to polymorphisms in the
 CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat
 CC or prevent cardiovascular disease, especially coronary artery disease,
 CC cerebrovascular disease, coronary restenosis or peripheral vascular
 CC disease. They may also be used in the treatment of diseases associated
 CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
 CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
 CC The invention specifically excludes proteins with the exact amino acid
 CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
 CC acid with the exact sequence as GenBank Accession No: AJ012376.1.
 CC Sequences C69269-C69282 represent published and corrected versions
 CC of human ABC1 gene exon fragments.

XX
 SQ Sequence 22 BP; 3 A; 4 C; 9 G; 6 T; 0 other;

Query Match 70.6%; Score 12; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. NO. 3.5e+03;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CAGCAGCTGACA 17
 DB 12 CAGCAGCTGACA 1

Search completed: June 23, 2003, 05:43:42
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OM nucleic - nucleic search, using SW model

Run on: June 24, 2003, 22:19:40 ; Search time 933.379 Seconds
(without alignments)
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2	11	100.0	11	US-08-770-564A-11	Sequence 11, Appl
3	11	100.0	11	US-09-540-119B-11	Sequence 11, Appl
4	11	100.0	13	US-09-540-119B-12	Sequence 12, Appl
5	11	100.0	15	PCT-US97-23619-10	Sequence 10, Appl
6	11	100.0	15	US-08-770-564A-10	Sequence 10, Appl
7	11	100.0	18	US-08-974-549-543	Sequence 543, App
8	11	100.0	18	US-09-402-181A-543	Sequence 543, App
9	11	100.0	18	US-09-402-181B-543	Sequence 543, App
10	11	100.0	18	US-09-432-503-543	Sequence 543, App
11	11	100.0	18	US-09-721-477-543	Sequence 543, App
12	11	100.0	18	US-09-721-506-543	Sequence 543, App
13	11	100.0	19	PCT-US97-23619-9	Sequence 9, Appl
14	11	100.0	19	US-08-770-564A-9	Sequence 9, Appl
15	11	100.0	21	US-07-887-265A-13	Sequence 13, Appl
16	11	100.0	21	US-08-244-121-13	Sequence 13, Appl
17	11	100.0	21	US-09-997-868A-13	Sequence 13, Appl
18	11	100.0	22	US-09-765-873A-5	Sequence 5, Appl
19	11	100.0	22	US-60-147-719-5	Sequence 5, Appl
20	11	100.0	23	US-09-952-522B-9	Sequence 9, Appl
21	11	100.0	23	US-09-952-522B-17	Sequence 17, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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22 11 100.0 23 36 US-09-952-522B-31 Sequence 31, Appl
23 11 100.0 24 31 US-09-807-809-5 Sequence 5, Appl
24 11 100.0 25 42 US-10-245-813-2 Sequence 2, Appl
25 11 100.0 26 16 US-09-250-336A-4 Sequence 4, Appl
26 11 100.0 27 35 US-09-642-177-4 Sequence 4, Appl
27 11 100.0 28 36 US-09-956-604-135337 Sequence 135337,
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29 11 100.0 30 36 US-09-956-604B-135337 Sequence 135337,
30 11 100.0 31 62 US-10-215-112-6862 Sequence 6862, A
31 11 100.0 32 67 US-60-333-620-66031 Sequence 140656,
32 11 100.0 33 67 US-60-334-049-140656 Sequence 333144,
33 11 100.0 34 79 US-60-353-987-396066 Sequence 396066,
34 11 100.0 35 79 US-60-353-987-924166 Sequence 924166,
35 11 100.0 36 1 PCT-US96-14679A-27 Sequence 27, Appl
36 11 100.0 37 26 PCT-US96-14679A-27 Sequence 27, Appl
37 11 100.0 38 26 PCT-US97-15394-16 Sequence 16, Appl
38 11 100.0 39 26 PCT-US99-03302-4 Sequence 4, Appl
39 11 100.0 40 26 PCT-US99-07533-4 Sequence 4, Appl
40 11 100.0 41 26 PCT-US98-07533-4 Sequence 4, Appl
41 11 100.0 42 26 US-08-272-102-23 Sequence 23, Appl
42 11 100.0 43 26 US-08-387-524-19 Sequence 19, Appl
43 11 100.0 44 26 US-08-405-496-16 Sequence 16, Appl
44 11 100.0 45 26 US-08-422-711-16 Sequence 16, Appl

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ALIGNMENTS

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RESULT 1
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Sequence 11, Application PC/RUS9723619
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Scirella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

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LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..11
OTHER INFORMATION: /note="oligo 21ab2"
PCT-US97-23619-11

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Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

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RESULT 2
US-08-770-564A-11
Sequence 11, Application US/0870564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinlich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND AND TOWNSEND AND CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Scirella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-11

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Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 11;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

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RESULT 3
US-09-540-119B-11

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; Sequence 11, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-11

Query Match      100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 4
US-09-540-119B-12
; Sequence 12, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-12

Query Match      100.0%; Score 11; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 5
PCT-US97-23619-10
; Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
```

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ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..15
; OTHER INFORMATION: /note="oligo 21ab3"
PCT-US97-23619-10

Query Match      100.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GCTCTAGATG 11
Db      1 GCTCTAGATG 11

RESULT 6
US-08-770-564A-10
; Sequence 10, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
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REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-10

Query Match 100.0%; Score 11; DB 11; Length 15;
Best Local Similarity 100.0%; Pred No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 7
US-08-974-549-543
Sequence 543, Application US/08974549
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTR molecule"
US-08-974-549-543

Query Match 100.0%; Score 11; DB 13; Length 18;
Best Local Similarity 100.0%; Pred No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 8
US-09-402-181A-543
Sequence 543, Application US/09402181A
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181A
FILING DATE: 29-SEP-1997
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-402-181A-543
Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 9
US-09-402-181B-543
Sequence 543, Application US/09402181B
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/402,181B
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-402-181B-543
Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 10
US-09-432-503-543
Sequence 543, Application US/09432503
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-432-503-543
Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11
RESULT 11
US-09-721-477-543
Sequence 543, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
CORRESPONDENCE ADDRESSES:
NUMBER OF SEQUENCES: 727
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-477-543
Query Match 100.0%; Score 11; DB 29; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11
RESULT 12
US-09-721-506-543
Sequence 543, Application US/09721506
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,506
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note= "antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-506-543

Query Match 100.0%; Score 11; DB 29; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 1 GCTCTAGATG 11

RESULT 13
PCT-US97-23619-9
; Sequence 9, Application PC/TUS9723619
; GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methode for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Scorella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note= "oligo 21ab"
PCT-US97-23619-9

Query Match 100.0%; Score 11; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 1 GCTCTAGATG 11

RESULT 14
US-08-770-564a-9
; Sequence 9, Application US/08770564a
; GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor

Fri Jun 27 07:41:11 2003

us-08-770-564a-11.inpm

Page 8

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Paten in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-9

Query Match 100.0%; Score 11; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 15
US-07-887-265A-13/c
Sequence 13, Application US/07887265A
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
APPLICANT: Mariott, Dave,
APPLICANT: Groskreutz, Debyra J
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/887,265A
FILING DATE: 19920522
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 748P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-887-265A-13

Query Match 100.0%; Score 11; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

Search completed: June 25, 2003, 06:20:27
Job time : 934.994 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:54 ; Search time 33.4382 Seconds
(without alignments)
482.732 Million cell updates/sec

Title: US-08-770-564a-11
Perfect score: 11
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 832576

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	11	100.0	21	9	US-09-997-868-13
2	11	100.0	22	10	US-09-765-873A-5
3	11	100.0	23	9	US-09-952-522B-9
4	11	100.0	23	9	US-09-952-522B-17
5	11	100.0	23	9	US-09-952-522B-31
6	11	100.0	25	9	US-10-245-813-2
7	11	100.0	24	9	US-10-215-112-6862
8	11	100.0	26	9	US-10-011-366-16
9	11	100.0	26	9	US-10-118-495-11
10	11	100.0	26	9	US-10-118-495-13
11	11	100.0	26	9	US-09-952-522B-19
12	11	100.0	26	9	US-10-044-692-312
13	11	100.0	26	9	US-10-044-539-312
14	11	100.0	27	10	US-09-057-351-23
15	11	100.0	28	10	US-09-784-508-8
16	11	100.0	28	10	US-09-844-006A-3
17	11	100.0	29	9	US-10-162-223-2
18	11	100.0	34	10	US-09-784-508-10
19	11	100.0	36	9	US-10-166-183-14

C 20	11	100.0	36	9	US-10-127-816-18	Sequence 18, Appl
21	11	100.0	36	10	US-09-784-508-11	Sequence 11, Appl
22	10	90.9	21	8	US-08-913-322-3	Sequence 3, Appl
23	10	90.9	21	10	US-09-767-479-15	Sequence 15, Appl
24	10	90.9	22	9	US-09-981-648-11	Sequence 11, Appl
25	10	90.9	23	9	US-09-989-706-2	Sequence 2, Appl
26	10	90.9	23	9	US-10-071-485-49	Sequence 49, Appl
C 27	10	90.9	25	9	US-10-098-263B-8894	Sequence 8894, Ap
28	10	90.9	25	9	US-10-098-263B-44593	Sequence 44593, A
29	10	90.9	25	9	US-10-098-263B-44594	Sequence 44594, A
C 30	10	90.9	25	9	US-10-098-263B-80109	Sequence 80109, A
C 31	10	90.9	25	9	US-10-098-263B-80110	Sequence 80110, A
C 32	10	90.9	25	9	US-10-098-263B-104702	Sequence 104702,
C 33	10	90.9	26	10	US-09-954-695-10	Sequence 30, Appl
C 34	10	90.9	26	10	US-09-954-695-13	Sequence 34, Appl
35	10	90.9	26	10	US-09-954-695-18	Sequence 38, Appl
36	10	90.9	26	10	US-09-954-695-42	Sequence 42, Appl
C 37	10	90.9	26	10	US-09-954-695-40	Sequence 30, Appl
C 38	10	90.9	26	10	US-09-954-586-34	Sequence 34, Appl
39	10	90.9	26	10	US-09-954-586-38	Sequence 38, Appl
40	10	90.9	26	10	US-09-954-586-42	Sequence 42, Appl
41	10	90.9	29	9	US-10-117-846-27	Sequence 27, Appl
42	10	90.9	29	9	US-10-083-590-4	Sequence 4, Appl
C 43	10	90.9	30	9	US-09-987-021-13	Sequence 13, Appl
C 44	10	90.9	30	9	US-09-987-021-17	Sequence 17, Appl
C 45	10	90.9	30	10	US-09-957-485-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-997-868-13/c
; Sequence 13, Application US/09997868
; Publication No. US20030031654A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.,
; Groskreutz, Debbyra J.
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,868
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/887265
; FILING DATE: 22-May-1992
; APPLICATION NUMBER: 07/803631
; FILING DATE: 06-Dec-1992
; APPLICATION NUMBER: PCT/US92/10621
; FILING DATE: 04-Dec-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0748P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 US-09-997-868-13

Query Match 100.0%; Score 11; DB 9; Length 21;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
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 DB 11 GCTCTAGATG 1

RESULT 2
 US-09-765-873A-5
 ; Sequence 5, Application US/09765873A
 ; Patent No. US20010053847A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Xiao-Song
 ; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
 ; FILE REFERENCE: BCI009 US CIP
 ; CURRENT APPLICATION NUMBER: US/09/765,873A
 ; CURRENT FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: US 09/627,216
 ; PRIOR FILING DATE: 2000-07-27
 ; PRIOR APPLICATION NUMBER: US 60/147,719
 ; PRIOR FILING DATE: 1999-08-06
 ; NUMBER OF SEQ ID NOS: 38
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO: 5
 ; LENGTH: 22
 ; TYPE: DNA
 ; ORGANISM: Primer
 ; US-09-765-873A-5

Query Match 100.0%; Score 11; DB 10; Length 22;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 3 GCTCTAGATG 13

RESULT 3
 US-09-952-522B-9
 ; Sequence 9, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benham, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448, 77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 9
 ; LENGTH: 23

TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: human
 OTHER INFORMATION: osteocalcin forward primer
 US-09-952-522B-9

Query Match 100.0%; Score 11; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 11 GCTCTAGATG 11

RESULT 4
 US-09-952-522B-17
 ; Sequence 17, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benham, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448, 77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B
 ; CURRENT FILING DATE: 2001-09-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/06232
 ; PRIOR FILING DATE: 2000-03-10
 ; PRIOR APPLICATION NUMBER: 60/123,711
 ; PRIOR FILING DATE: 1999-03-10
 ; PRIOR APPLICATION NUMBER: 60/162,462
 ; PRIOR FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 17
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
 ; US-09-952-522B-17

Query Match 100.0%; Score 11; DB 9; Length 23;
 Best Local Similarity 100.0%; Pred. No. 9.9e+02;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 11 GCTCTAGATG 11

RESULT 5
 US-09-952-522B-31
 ; Sequence 31, Application US/09952522B
 ; Publication No. US20030082152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Katz, Adam J.
 ; APPLICANT: Liull, Ramon
 ; APPLICANT: Futrell, J. William
 ; APPLICANT: Hedrick, Marc H.
 ; APPLICANT: Benham, Prosper
 ; APPLICANT: Lorenz, Hermann Peter
 ; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
 ; FILE REFERENCE: 30448, 77US11
 ; CURRENT APPLICATION NUMBER: US/09/952,522B


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; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
; US-09-952-522B-31

Query Match      100.0%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTGAATG 11
DB      1 GCTCTGAATG 11

RESULT 6
US-10-245-813-2
; Sequence 2, Application US/10245813
; Publication No. US2003006043A1
; GENERAL INFORMATION:
; APPLICANT: Gyun Min Lee
; APPLICANT: No. US2003006043A1Soo Kim
; TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE
; TITLE OF INVENTION: EXPRESSION OF ANTISENSE RNA OF CASPASE-2
; FILE REFERENCE: 118.19-US-01
; CURRENT APPLICATION NUMBER: US/10/245,813
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 2001-57353
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: casp3L primer
; US-10-245-813-2

Query Match      100.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTGAATG 11
DB      1 GCTCTGAATG 11

RESULT 7
US-10-215-112-6862/c
; Sequence 6862, Application US/10215112
; Publication No. US20030082596A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltman
; TITLE OF INVENTION: Method of Genetic Analysis of Probes:
; FILE REFERENCE: 3119
; CURRENT APPLICATION NUMBER: US/10/215,112
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 14936
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 6862
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
; US-10-215-112-6862

Query Match      100.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTGAATG 11
DB      15 GCTCTGAATG 5

RESULT 8
US-10-011-366-16
; Sequence 16, Application US/10011366
; Publication No. US20030054493A1
; GENERAL INFORMATION:
; APPLICANT: Williams, James A.
; APPLICANT: Kink, John A.
; TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
; OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
; DISEASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/011,366
; FILING DATE: 16-No. US20030054493A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,310
; FILING DATE: 23-OCT-1997
; APPLICATION NUMBER: US 08/329,154
; FILING DATE: 24-OCT-1994
; APPLICATION NUMBER: US 08/161,907
; FILING DATE: 02-DEC-1993
; APPLICATION NUMBER: US 07/985,321
; FILING DATE: 04-DEC-1992
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPFD-01121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16

Query Match      100.0%; Score 11; DB 9; Length 26;
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 5 GCTCTAGATG 15

RESULT 13
US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US20030100093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 5 GCTCTAGATG 15

RESULT 14
US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Vailleponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 11; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
|||
Db 5 GCTCTAGATG 15

RESULT 15
US-09-784-508-8
Sequence 8, Application US/09784508
Patent No. US20020046417A1
GENERAL INFORMATION:
APPLICANT: Martin, Robert R.
APPLICANT: Mathews, Helena
APPLICANT: Keller, Karen
APPLICANT: Kellogg, Jill A.
APPLICANT: Wagner, Ry
TITLE OF INVENTION: Development of Resistance to Raspberry
TITLE OF INVENTION: Bushy Dwarf Virus
FILE REFERENCE: 4257-0024.31
CURRENT APPLICATION NUMBER: US/09/784,508
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/737,719
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,018
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-784-508-8

Query Match 100.0%; Score 11; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
|||
Db 2 GCTCTAGATG 12

Search completed: June 25, 2003, 22:25:08
Job time : 34.4382 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:17:30 ; Search time 16.6972 Seconds
(without alignments)
202.036 Million cell updates/sec

Title: US-08-770-564A-11
Perfect score: 11
Sequence: 1 GCTCTAGATG 11

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/prodata/2/ina/5A_COMB.seq: *
4: /cgn2_6/prodata/2/ina/5B_COMB.seq: *
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/prodata/2/ina/backfillseq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	2	US-08-770-565-11
2	11	100.0	15	2	US-08-770-565-10
3	11	100.0	18	4	US-08-974-549A-543
4	11	100.0	19	2	US-08-770-565-9
5	11	100.0	21	4	US-08-026-143B-13
6	11	100.0	21	5	PCT-US92-10621-13
7	11	100.0	21	5	PCT-US94-02233-13
8	11	100.0	22	4	US-09-627-216A-5
9	11	100.0	22	3	US-08-973-068-46
10	11	100.0	23	1	US-08-330-123A-23
11	11	100.0	26	1	US-08-480-604A-16
12	11	100.0	26	1	US-08-482-115B-23
13	11	100.0	26	2	US-08-660-678A-23
14	11	100.0	26	2	US-08-710-249-26
15	11	100.0	26	2	US-08-485-778-19
16	11	100.0	26	2	US-08-405-496A-16
17	11	100.0	26	2	US-08-472-802C-24
18	11	100.0	26	3	US-08-520-550A-19
19	11	100.0	26	3	US-08-598-443-23
20	11	100.0	26	4	US-08-974-549A-598
21	11	100.0	26	4	US-09-060-523-23
22	11	100.0	26	4	US-08-915-136-16
23	11	100.0	26	4	US-09-220-157A-26
24	11	100.0	26	4	US-09-286-959B-4
25	11	100.0	26	4	US-09-580-517-23
26	11	100.0	26	4	US-09-153-310-4
27	11	100.0	26	4	US-08-957-310-16

28	11	100.0	27	2	US-08-770-565-26	Sequence 26, Appl
29	11	100.0	27	3	US-08-630-172-24	Sequence 24, Appl
30	11	100.0	27	4	US-09-375-419-24	Sequence 24, Appl
31	11	100.0	30	2	US-08-770-565-8	Sequence 8, Appl
32	11	100.0	30	2	US-08-995-927-7	Sequence 7, Appl
33	11	100.0	30	4	US-09-349-627-5	Sequence 5, Appl
34	11	100.0	30	4	US-09-582-096-7	Sequence 7, Appl
35	11	100.0	33	3	US-08-630-172-22	Sequence 22, Appl
36	11	100.0	33	4	US-09-375-419-22	Sequence 22, Appl
37	11	100.0	37	3	US-08-815-190A-3	Sequence 3, Appl
38	11	100.0	39	4	US-09-091-305-3	Sequence 3, Appl
39	11	100.0	40	1	US-08-395-800A-12	Sequence 12, Appl
40	11	100.0	15	2	US-08-624-601-13	Sequence 13, Appl
41	10	90.9	16	4	US-08-687-580B-9	Sequence 9, Appl
42	10	90.9	20	4	US-08-964-722-7	Sequence 7, Appl
43	10	90.9	21	1	US-07-956-700B-114	Sequence 114, App
44	10	90.9	21	1	US-08-476-537-114	Sequence 114, App
45	10	90.9	21	1	US-08-485-607-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-08-770-565-11
; Sequence 11, Application US/08770565
; Patent No. 5846723
GENERAL INFORMATION:
; APPLICANT: Kim, Nam Woo
; APPLICANT: Wu, Fred
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Methods for Detecting the RNA Component of
; NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
; MEDIUM TYPE: PC floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,565
; FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
; NAME: Scorella, John R.
; REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-770-565-11
Query Match 100.0%; Score 11; DB 2; Length 11;
Best local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11

Db 1 GCTCTAGATG 11

RESULT 2
US-08-770-565-10
Sequence 10, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinlich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 01589-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-10
Query Match 100.0%; Score 11; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 3
US-08-974-549A-543
Sequence 543, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
US-08-974-549A-543
Query Match 100.0%; Score 11; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 4
US-08-770-565-9
Sequence 9, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 1 GCTCTAGATG 11

RESULT 5
US-08-026-143B-13/C
Sequence 13, Application US/08026143B
Patent No. 6348327
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
Groskreutz, Debya J.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
Polypeptide Synthesis
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,143B
FILING DATE: 01-Mar-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-026-143B-13

Query Match 100.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 11 GCTCTAGATG 1

RESULT 6
PCT-US92-10621-13/C
Sequence 13, Application PC/TUS9210621
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Gorman, Cornelia M.,
APPLICANT: Mariotte, Dave,
APPLICANT: Groskreutz, Debya J.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 19921204
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 748P2.PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9814
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US92-10621-13

Query Match 100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

RESULT 7
PCT-US94-02233-13/c
Sequence 13, Application PC/TUS9402233
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 748P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-02233-13

Query Match 100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

RESULT 8
US-09-627-216A-5
Sequence 5, Application US/09627216A
Patent No. 6168837
GENERAL INFORMATION:
APPLICANT: Sarsisani, Sima F
APPLICANT: Tang, Xiao-Song
APPLICANT: Qi, Wei Wei
APPLICANT: Vannelli, Todd
APPLICANT: Gatenby, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BC1009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO: 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-627-216A-5

Query Match 100.0%; Score 11; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
Db 3 GCTCTAGATG 13

RESULT 9
US-08-973-068-46
Sequence 46, Application US/08973068
Patent No. 6127604
GENERAL INFORMATION:
APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
APPLICANT: Hafner, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
EARLIER FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO: 46
LENGTH: 23
TYPE: DNA
ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-46

Query Match 100.0%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 10
US-08-330-123A-23

Sequence 23, Application US/08330123A
Patent No. 5583016
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 5 GCTCTAGATG 15

RESULT 11
US-08-480-604A-16
Sequence 16, Application US/08480604A
Patent No. 5736139
GENERAL INFORMATION:
APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPND-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-480-604A-16

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 12
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

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Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 5 GCTCTAGATG 15

RESULT 13
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 5 GCTCTAGATG 15

RESULT 14
US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26

Job time : 17.6972 secs

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
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DB 5 GCTCTAGATG 15

RESULT 15

US-08-485-778-19
; Sequence 19, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Biasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSH94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-778-19

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 5 GCTCTAGATG 15

Search completed: June 25, 2003, 00:24:40

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:47:09 ; Search time 567.135 Seconds
(without alignments)
314.123 Million cell updates/sec

Title: US-08-770-564A-11
Perfect score: 11
Sequence: 1 GCTCTAGAATG 11

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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16: em_estom:*
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24: em_gse_mus:*
25: em_gse_other:*
26: em_gse_pro:*
27: em_gse_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
C 1	10	90.9	19 17	AZ471573 1M0286G13
C 2	10	90.9	34 10	AV964763 AV964763
C 3	10	90.9	49 17	BH791685 SALK_0608
C 4	9	81.8	27 17	BH812447 SALK_0617
C 5	9	81.8	27 17	BH849811 SALK_0703
C 6	9	81.8	27 17	TA349802P
C 7	9	81.8	27 17	TA349802P

Result No.	Score	Query Match length	ID	Description
C 7	9	81.8	30 9	AU257604
C 8	9	81.8	31 9	A1032592
C 9	9	81.8	36 17	A2812974
C 10	9	81.8	38 17	A2786040
C 11	9	81.8	40 12	B563012
C 12	9	81.8	41 9	AU258962
C 13	9	81.8	41 17	A275318
C 14	9	81.8	42 12	BF732142
C 15	9	81.8	42 12	B613445
C 16	9	81.8	43 17	A2456311
C 17	9	81.8	44 17	BH624958
C 18	9	81.8	46 17	A2812338
C 19	9	81.8	49 10	AM100845
C 20	9	81.8	50 9	AU103413
C 21	9	81.8	50 14	BM889496
C 22	9	81.8	50 17	A2478817
C 23	9	81.8	18 14	BQ790001
C 24	9	81.8	19 17	A2309082
C 25	9	81.8	19 17	A2659092
C 26	9	81.8	24 17	A2325427
C 27	9	81.8	25 9	A1763346
C 28	9	81.8	26 17	A2787926
C 29	9	81.8	26 17	BH791427
C 30	9	81.8	26 17	TA107C03P
C 31	9	81.8	28 9	A1006312
C 32	9	81.8	28 17	BH848015
C 33	9	81.8	28 17	BH848015
C 34	9	81.8	29 17	TA888080
C 35	9	81.8	30 17	A2588091
C 36	9	81.8	31 9	AA885849
C 37	9	81.8	31 14	R68337
C 38	9	81.8	33 17	A2806504
C 39	9	81.8	33 17	BH792618
C 40	9	81.8	34 9	AA921704
C 41	9	81.8	35 17	AA623189
C 42	9	81.8	36 13	BQ045071
C 43	9	81.8	36 17	A2430239
C 44	9	81.8	37 17	A2787295
C 45	9	81.8	38 14	R82106

ALIGNMENTS

RESULT 1
LOCUS AZ471573 19 bp DNA
DEFINITION IM0286G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION AZ471573
VERSION AZ471573.1 GI:10629698
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

BH812447
 LOCUS BH812447 27 bp DNA linear GSS 02-MAY-2002
 DEFINITION SALK_061781 Arabidopsis thaliana TDNA insertion lines Arabidopsis
 thaliana genomic clone SALK_061781, DNA sequence.
 ACCESSION BH812447
 VERSION BH812447.1 GI:20390902
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 27)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,
 C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-indexed library of insertion mutations in the
 Arabidopsis Genome
 JOURNAL Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 FEATURES
 source Location/Qualifiers
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 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_061781"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 12 a 3 c 5 g 7 t
 ORIGIN
 Query Match 81.8%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CTCTAGAT 10
 Db 18 CTCTAGAT 26

RESULT 5
 BH849811 27 bp DNA linear GSS 13-JUN-2002
 LOCUS BH849811
 DEFINITION Arabidopsis thaliana genomic clone SALK_070310.38.90.x, DNA
 SALK_070310.38.90.x Arabidopsis thaliana TDNA insertion lines
 Arabidopsis thaliana genomic clone SALK_070310.38.90.x, DNA
 sequence.
 ACCESSION BH849811
 VERSION BH849811.1 GI:21420682
 KEYWORDS GSS.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 27)
 REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadriab,
 C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.,
 Zimmerman,J. and Ecker,J.R.
 TITLE A Sequence-indexed library of insertion mutations in the

Arabidopsis Genome
 Unpublished (2001)
 COMMENT Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of
 TDNA.
 Class: TDNA tagged.
 FEATURES
 source Location/Qualifiers
 1..27
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone="SALK_070310.38.90.x"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TDNA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/tdna_protocols.html"
 BASE COUNT 7 a 2 c 8 g 10 t
 ORIGIN
 Query Match 81.8%; Score 9; DB 17; Length 27;
 Best Local Similarity 100.0%; Pred. No. 7.9e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TCTAGATG 11
 Db 8 TCTAGATG 16

RESULT 6
 TA349B02P 27 bp DNA linear GSS 13-DEC-2000
 LOCUS TA349B02P
 DEFINITION T. Brucei sheared genomic DNA clone 349B02, forward sequence,
 genomic survey sequence.
 ACCESSION AL493641
 VERSION AL493641.1 GI:11869420
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei.
 Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 REFERENCE Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
 Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
 Melville,S.E., Rajandream,W.A. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhs@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + l method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.
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 source Location/Qualifiers
 1..27
 /organism="Trypanosoma brucei"

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Best Local Similarity 100.0%; Pred. No. 7; ge+04;
Matches      9; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
Qy      1 GCTCTGAA 9
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Db      7 GCTCTGAA 15

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RESULT	7
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LOCUS	
DEFINITION	AU257604 30 bp mRNA linear EST 25-APR-2002
ACCESSION	AU257604.3 -directed mouse cDNA library Mus musculus cDNA clone
VERSION	BED0011024.3, mRNA sequence.
KEYWORDS	AU257604
SOURCE	AU257604.1 GI:2032287
ORGANISM	EST.
REFERENCE	house mouse,
AUTHORS	Mus musculus
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
COMMENT	1 (bases 1 to 30)
	Kato,K. and Matsuda,R.
	Generation of expressed sequence tags from mouse brain
	Unpublished (2002).
	Contact: Kikuya Kato

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FEATURES
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    /organism="Mus musculus"
    /db_xref="taxon:10090"
    /clone="BED0011024"
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    /tissue_type="brain"
    /note="Vector: pGEM-T-easy"
BASE COUNT
  13 a      6 c      4 g      7 t
ORIGIN

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Query_Match		81.8%;	Score 9;	DB 9;	Length 30;
Best Local Similarity		100.0%;	Pred.No. 8.1e+04;		
Matches	9; Conservative	0;	Mismatches	0;	Gaps 0;
OY	2 CTCAGAAAT 10 				
Dd	5 CTCAGAAAT 13				
RESULT 8					
A1032592/c					
LOCUS	A1032592	31 bp	mRNA	linear	EST 25-JUN-1996
DEFINITION	ow73g08.f1 Soares fetal liver spleen JNLS S1 Homo sapiens cDNA clone IMAGE1562510 3, similar to TR.O15102 O15102 HYPOTHETICAL 40.0 KD PROTEIN., mRNA sequence.				
ACCESSION	A1032592				
VERSION	A1032592.1	GI:3253718			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 31)				

AUTHORS	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
JOURNAL	Tumor Gene Index
COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: ccgapsb@email.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Seq primer: ~40m3 fwd. RT from Amersham High quality sequence stop: 1. Location/Qualifiers 1..31 chr:- "Homo sapiens"
FEATURES	
source	

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/clone="IMAGE:1652510"
/clone_1ib="Soares_fetal_liver_spleen_INFLS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/name="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI.
This is a subcloned version of The original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AAGCGAAGAGATTATATTAAGACATCTTTTTTTTTTTTTTTT 3'].
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia)" digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Patima Bonaldo."

```

Query Match	81.8%	Score 9;	DB 9;	Length 31;
Best Local Similarity	100.0%;	Prod. No. 8.1e+04;		
Matches	9;	Conservative 0;	Mismatches 0;	Indels 0;
OY	3 TCTAGATG 11			
Db	28 TCTAGATG 20			
RESULT 9				
LOCUS	AZ812974	36 bp	DNA	linear
DEFINITION	2M08080101F Mouse 10kb plasmid UNGC1M library Mus musculus genomic			SSS 20-FEB-2001
ACCESSION	Clone UNGC0M080101 F, DNA sequence.			
VERSION	AZ812974			
KEYWORDS	AZ812974.1 GI:12982751			
SOURCE	SSS.			
ORGANISM	house mouse.			
	Mus musculus			
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 36)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,			
	Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly			
	,M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.			
	and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb			
	plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss			
	University of Utah Genome Center			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT			
	84112 USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000 Std Error: 0.00			
	Plate: 0080 Row: 1 Column: 01			

Seq primer: CATTGTAAAACGACGCCACT
 Class: plasmid ends
 High quality sequence stop: 36.
 Location/Qualifiers

Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 38.
 Location/Qualifiers

1.36
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0080101"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"

1.38
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCG2M0030822"
 /clone_1ib="Mouse 10kb plasmid UUCG1M library"
 /sex="Male"

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PWD42uv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 ORIGIN
 Query Match
 Best Local Similarity 81.8%; Score 9; DB 17; Length 36;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT
 ORIGIN
 Query Match
 Best Local Similarity 81.8%; Score 9; DB 17; Length 38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GCTCTAGAA 9
 |||||
 3 GCTCTAGAA 11

RESULT 10
 A2786040/c
 LOCUS
 DEFINITION 38 bp DNA linear GSS 16-FEB-2001
 2M0030822R Mouse 10kb plasmid UUCG1M library Mus musculus genomic
 clone UUCG2M0030822 R, DNA sequence.
 ACCESSION
 A2786040
 A2786040.1 GI:12923402
 GSS.
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 38)
 Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,
 M., Rose,M., Rose,R., Stokes,R., Tinney,A., von Niederhausern,A.
 and Wright,D., Weis,R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0030 row: B column: 22

JOURNAL
 COMMENT

RESULT 11
 BG563012/c
 LOCUS
 DEFINITION 40 bp mRNA linear EST 10-APR-2001
 602581189F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4708895 5',
 mRNA sequence.
 ACCESSION
 BG563012
 BG563012.1 GI:13570664
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 40)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-rc@mail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ULNL at:
 http://image.llnl.gov
 Plate: LCM1545 row: a column: 24
 High quality sequence stop: 40.
 Location/Qualifiers
 1.40
 /organism="Homo sapiens"

/db_xref="taxon:9606"
 /clone="IMAGE:4708895"
 /clone_lib="NIH MGC 76"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggccgctcggcc); Site 2: SfiI (ggccattatggcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CAGCGCCATTATGGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCCGAGCGCGCAGATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH MGC library."

BASE COUNT

6 a 8 c 9 g 17 t

Query Match 81.8%; Score 9; DB 12; Length 40;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAAAT 10
 |||||
 Db 9 CTCTAGAAAT 1

RESULT 12 41 bp mRNA linear EST 25-APR-2002
 AU258962
 LOCUS BED0014206 3', mRNA sequence.
 DEFINITION
 AU258962 3'-directed mouse cDNA library Mus musculus cDNA clone
 BED0014206 3', mRNA sequence.
 ACCESSION
 AU258962
 VERSION
 AU258962.1 GI:20325030
 KEYWORDS
 EST
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Kato, K. and Matoda, R.
 TITLE 1 (bases 1 to 41)
 JOURNAL Generation of expressed sequence tags from mouse brain
 COMMENT Unpublished (2002)
 CONTACT: Kikuya Kato
 Graduate School of Biological Sciences
 Nara Institute of Science and Technology
 8916-5 Takeyama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72-5581
 Fax: 81-743-72-5589
 Email: kkatodbs.aist-nara.ac.jp,
 URL: http://love2.aist-nara.ac.jp/BD/index.html.
 FEATURES
 source
 1..41
 Location/Qualifiers

BASE COUNT 14 a 10 t 1 others
 ORIGIN
 Query Match 81.8%; Score 9; DB 9; Length 41;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CTCTAGAAAT 10
 |||||
 Db 4 CTCTAGAAAT 12

RESULT 13 41 bp DNA linear GSS 16-FEB-2001
 AZ775318/c
 LOCUS

DEFINITION 2M0007B12R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
 clone UGCG2M0007B12 R, DNA sequence.
 ACCESSION
 A2775318
 VERSION
 A2775318.1 GI:12901677
 KEYWORDS
 SOURCE
 house mouse.
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Dunn, P., Aoyagi, A., Barber, M., Beacons, T., Duval, B., Hamil, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 TITLE
 Unpublished (2000)
 JOURNAL
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0007 row: B column: 12
 Seq primer: CACACAGAAACAGCATGATGACC
 Class: plasmid ends
 High quality sequence stop: 41.
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 1..41
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG2M0007B12"
 /clone_lib="Mouse 10kb plasmid UGCGIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
 /note="Vector: pMD22; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/shares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (gil47321149b/AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 10 a 11 c 11 g
 ORIGIN

Query Match 81.8%; Score 9; DB 17; Length 41;
 Best Local Similarity 100.0%; Pred. No. 8.6e+04;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGAA 9
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 Db 41 GCTTAGAA 33

RESULT 14 42 bp mRNA linear EST 30-MAY-2001
 BF732142/c
 LOCUS

```

DEFINITION EST-NGR-1-20 mouse GR-1+ myeloid progenitor cells cDNA Library Mus
ACCESSION musculus cDNA 3', mRNA sequence.
VERSION BF732142
KEYWORDS BF732142.1 GI:14249762
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 42)
JOURNAL Chen, J., Rowley, D.A., Clark, T., Lee, S., Zhou, G., Beer, C., Rowley
COMMENT J.D. and Wang, S.M.
Pattern of gene expression in mouse GR-1+ myeloid progenitor cells
Unpublished (2001)
CONTACT: Wang SM
Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swang@midway.uchicago.edu
This EST fragment was amplified from mouse GR-1+ myeloid progenitor
cells cDNA library with GIGI technique (generation of longer cDNA
fragments from SAGE tags for Gene Identification, Proc. Natl. Acad.
Sci. USA 97, 349, 2000), which starts from the 3' end till the last
CATG site of the target cDNA sequence.
Seq primer: M13 Forward.
FEATURES
source
1..42
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="mouse GR-1+ myeloid progenitor cells cDNA
library"
/sex="female"
/cisue_type="bone marrow"
/notes="CDNA was identified and isolated from Mus musculus
benzo(a)pyrene-downregulated total RNA pool by
differential display Polymerase Chain Reaction using
indicated anchor and arbitrary primer (Hiroglyn mRNA
Profile Kit 3, Genomix Corporation, Foster City, CA) and
sequenced directly from PCR products."
BASE COUNT 4 a 7 c 6 g 25 t
ORIGIN
Query Match 81.8%; Score 9; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAA 9
| | | | |
| | | | |
Db 28 GCTCTAGAA 20
| | | | |
| | | | |

RESULT 15
BG613445 42 bp mRNA linear EST 18-APR-2001
LOCUS 602641351F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772341 5',
DEFINITION mRNA sequence.
ACCESSION BG613445
VERSION BG613445
KEYWORDS BG613445.1 GI:13664816
SOURCE EST.
ORGANISM human.
REFERENCE Homo sapiens
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
JOURNAL NIH-MGC http://mgs.nci.nih.gov/
Unpublished (1999)
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Straubeberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```

```

Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10C1642 row: e column: 14
High quality sequence stop: 29.
FEATURES
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1..42
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:4772341"
/clone_lib="NIH MGC 61"
/tissue_type="embryonal carcinoma"
/lab_note="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgcctcgcc); Site 2: SfiI (ggccatcgcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dT(30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 9 a 6 c 11 g 16 t
ORIGIN
Query Match 81.8%; Score 9; DB 12; Length 42;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 CTCTAGAA 10
| | | | |
| | | | |
Db 10 CTCTAGAA 2
| | | | |
| | | | |

Search completed: June 23, 2003, 10:10:29
Job time : 569.289 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:45:21 / Search time 482.861 Seconds
(without alignments)
158.668 Million cell updates/sec

Title: US-08-770-564a-11
Perfect score: 11
Sequence: 1 GCTTAGAATG 11

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 7820798 seqs, 3482471992 residues

Word size: 0

Total number of hits satisfying chosen parameters: 8653682

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Database:

Pending_Patents_NA_New: *
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq: *
2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq: *
3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq: *
4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq: *
5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
6: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq: *
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12: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *
13: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	18	US-09-721-456-543	Sequence 543, App
2	11	100.0	18	US-10-325-810-543	Sequence 543, App
3	11	100.0	21	PCT-US03-05708-27	Sequence 27, Appl
4	11	100.0	21	PCT-US03-05708-202	Sequence 202, App
5	11	100.0	21	PCT-US03-04088-539	Sequence 539, App
6	11	100.0	21	PCT-US03-04088-543	Sequence 543, App
7	11	100.0	21	PCT-US03-04088-547	Sequence 547, App
8	11	100.0	21	PCT-US03-04088-551	Sequence 551, App
9	11	100.0	21	PCT-US03-04088-555	Sequence 555, App
10	11	100.0	21	PCT-US03-04088-559	Sequence 559, App
11	11	100.0	21	US-10-374-366-27	Sequence 27, Appl
12	11	100.0	21	US-10-374-366-202	Sequence 202, App
13	11	100.0	22	US-10-188-5238-5	Sequence 5, Appl
14	11	100.0	22	US-10-188-5238-5	Sequence 5, Appl
15	11	100.0	23	PCT-US03-04088-520	Sequence 520, App
16	11	100.0	23	PCT-US03-04088-521	Sequence 521, App
17	11	100.0	23	US-10-310-188-36216	Sequence 36216, A
18	11	100.0	24	US-09-807-809A-5	Sequence 5, Appl
19	11	100.0	25	US-09-954-445A-66031	Sequence 66031, A
20	11	100.0	25	US-10-355-577-393144	Sequence 393144, A

21	11	100.0	25	US-10-355-577-396066	Sequence 396066, A
22	11	100.0	25	US-10-355-577-924166	Sequence 924166, A
23	11	100.0	25	US-60-427-808-6866	Sequence 6866, App
24	11	100.0	25	US-60-427-808-62369	Sequence 62369, A
25	11	100.0	25	US-60-427-808-104137	Sequence 104137, A
26	11	100.0	25	US-60-427-808-115885	Sequence 115885, A
27	11	100.0	25	US-60-427-808-137579	Sequence 137579, A
28	11	100.0	25	US-60-427-808-301228	Sequence 301228, A
29	11	100.0	25	US-60-427-808-397410	Sequence 397410, A
30	11	100.0	25	US-60-427-808-420914	Sequence 420914, A
31	11	100.0	25	US-60-427-808-425838	Sequence 425838, A
32	11	100.0	25	US-60-427-808-469846	Sequence 469846, A
33	11	100.0	25	US-60-427-808-666732	Sequence 666732, A
34	11	100.0	25	US-60-427-808-681847	Sequence 681847, A
35	11	100.0	25	US-60-427-808-681848	Sequence 681848, A
36	11	100.0	25	US-60-427-808-887509	Sequence 887509, A
37	11	100.0	25	US-60-427-808-952728	Sequence 952728, A
38	11	100.0	25	US-60-427-836-248462	Sequence 248462, A
39	11	100.0	25	US-60-427-836-248463	Sequence 248463, A
40	11	100.0	25	US-60-427-836-280388	Sequence 280388, A
41	11	100.0	25	US-60-427-836-506901	Sequence 506901, A
42	11	100.0	25	US-60-427-836-612340	Sequence 612340, A
43	11	100.0	25	US-60-427-836-612342	Sequence 612342, A
44	11	100.0	26	PCT-US02-11134-11	Sequence 11, Appl
45	11	100.0	26	PCT-US02-11134-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-721-456-543
Sequence 543, Application US/09721456
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
SERVER: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312

FILED DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-456-543

Query Match 100.0%; Score 11; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

RESULT 2
US-10-325-810-543
Sequence 543, Application US/10325810
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Hartley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-10-325-810-543

Query Match 100.0%; Score 11; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

RESULT 3
PCT-US03-05708-27
Sequence 27, Application PCT/TUS0305708
GENERAL INFORMATION:
APPLICANT: E.I. DuPont de Nemours and Company, Inc.
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
FILE REFERENCE: CL1794 PCT
CURRENT APPLICATION NUMBER: PCT/US03/05708
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/360,279
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 203
SOFTWARE: Patent In version 3.2
SEQ ID NO 27
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer 18-5'
PCT-US03-05708-27

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11

Db 3 GCTCTGAATG 13

RESULT 4
PCT-US03-05708-202
; Sequence 202, Application PC/TUS0305708
; GENERAL INFORMATION:
; APPLICANT: E.I. Dupont de Nemours and Company, Inc.
; TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
; FILE REFERENCE: CL1794 PCT
; CURRENT APPLICATION NUMBER: PCT/US03/05708
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 60/360,279
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 202
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Rhodospiridium glutinis
PCT-US03-05708-202

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGAATG 11
|||
Db 3 GCTCTGAATG 13

RESULT 5
PCT-US03-04088-539/c
; Sequence 539, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 539
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE: Artificial
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-539

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGAATG 11
|||
Db 19 GCTCTGAATG 9

RESULT 6
PCT-US03-04088-543
; Sequence 543, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 543
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE: Artificial
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
; NAME/KEY: misc feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
PCT-US03-04088-543

Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGAATG 11
|||
Db 1 GCTCTGAATG 11

RESULT 7
PCT-US03-04088-547/c
; Sequence 547, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600

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PCT-US03-04088-551
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent version 3.2
; SEQ ID NO 547
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE: Description of Artificial Sequence: siRNA sense region
; NAME/KEY: misc_feature
; LOCATION: (1)..(2)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5'-3' attached terminal deoxyabasic moiety
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(5)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (21)..(21)
; OTHER INFORMATION: 3'-3' attached terminal deoxyabasic moiety
PCT-US03-04088-547
Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTGAGATG 11
DB 19 GCTCTGAGATG 9
RESULT 8
PCT-US03-04088-551
; Sequence 551, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
```

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; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
; FILE REFERENCE: 02-708-A (400/080)
; CURRENT APPLICATION NUMBER: PCT/US03/04088
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US 60/396,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 626
; SOFTWARE: Patent version 3.2
; SEQ ID NO 551
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE: Description of Artificial Sequence: Target sequence/siRNA
; NAME/KEY: misc_feature
; LOCATION: (2)..(5)
; OTHER INFORMATION: antisense region
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: 2'-deoxy-2'-fluoro
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(21)
; OTHER INFORMATION: n stands for thymidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: Phosphorothioate 3'-internucleotide linkage
PCT-US03-04088-551
Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTGAGATG 11
DB 1 GCTCTGAGATG 11
RESULT 9
PCT-US03-04088-555/c
; Sequence 555, Application PC/TUS0304088
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
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/ TITLE OF INVENTION: Expression Using Short Interfering RNA (siRNA)
/ FILE REFERENCE: 02-708-A (400/080)
/ CURRENT APPLICATION NUMBER: PCT/US03/04088
/ CURRENT FILING DATE: 2003-04-28
/ PRIOR APPLICATION NUMBER: US 60/396,600
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 60/386,782
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/406,784
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US 60/408,378
/ PRIOR FILING DATE: 2002-09-05
/ PRIOR APPLICATION NUMBER: US 60/409,293
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: US 60/440,129
/ PRIOR FILING DATE: 2003-01-15
/ NUMBER OF SEQ ID NOS: 626
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 555
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA sense
/ OTHER INFORMATION: region
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(2)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: 5'-3' attached terminal deoxyribose moiety
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(5)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (6)..(6)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (7)..(9)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (11)..(14)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (15)..(18)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (19)..(19)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (20)..(21)
/ OTHER INFORMATION: n stands for thymidine

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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (21)..(21)
/ OTHER INFORMATION: 3'-3' attached terminal deoxyribose moiety
/ PCT-US03-04088-555
Query Match 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTGATG 11
Db 19 GCTCTGATG 9
RESULT 10
PCT-US03-04088-559
/ Sequence 559, Application PC/TUS0304088
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: McSwigen, James
/ APPLICANT: Beigelman, Leonid
/ TITLE OF INVENTION: RNA Interference Mediated Inhibition of Telomerase Gene
/ FILE REFERENCE: 02-708-A (400/080)
/ CURRENT APPLICATION NUMBER: PCT/US03/04088
/ PRIOR FILING DATE: 2003-04-28
/ PRIOR APPLICATION NUMBER: US 60/396,600
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: US 60/358,580
/ PRIOR FILING DATE: 2002-02-20
/ PRIOR APPLICATION NUMBER: US 60/363,124
/ PRIOR FILING DATE: 2002-03-11
/ PRIOR APPLICATION NUMBER: US 60/386,782
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/406,784
/ PRIOR FILING DATE: 2002-08-29
/ PRIOR APPLICATION NUMBER: US 60/408,378
/ PRIOR FILING DATE: 2002-09-05
/ PRIOR APPLICATION NUMBER: US 60/409,293
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: US 60/440,129
/ PRIOR FILING DATE: 2003-01-15
/ NUMBER OF SEQ ID NOS: 626
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 559
/ LENGTH: 21
/ TYPE: RNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siRNA
/ OTHER INFORMATION: antisense region
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (2)..(5)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (6)..(9)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (10)..(10)
/ OTHER INFORMATION: 2'-deoxy-2'-fluoro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (11)..(13)
/ OTHER INFORMATION: 2'-deoxy
/ FEATURE:

```

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NAME/KEY: misc_feature
LOCATION: (14)..(14)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15)..(16)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17)..(17)
OTHER INFORMATION: 2'-deoxy-2'-fluoro
FEATURE:
NAME/KEY: misc_feature
LOCATION: (18)..(19)
OTHER INFORMATION: 2'-deoxy
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(20)
OTHER INFORMATION: Phosphorothioate 3'-internucleotide linkage
FEATURE:
NAME/KEY: misc_feature
LOCATION: (20)..(21)
OTHER INFORMATION: n strands for thymidine
PCT-US03-04088-559
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Query Match
Best Local Similarity 100.0%; Score 11; DB 1; Length 21;
Best Local Similarity 72.7%; Pred. No. 4.1e+03;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATG 11
Db 1 GCCTAGATG 11
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```
RESULT 11
US-10-374-366-27
Sequence 27, Application US/10374366
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
APPLICANT: Milano, Joseph
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
FILE REFERENCE: CL1794 US NA
CURRENT APPLICATION NUMBER: US/10/374,366
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/360,279
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer 18-5'
US-10-374-366-27
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Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
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```
RESULT 12
US-10-374-366-202
Sequence 202, Application US/10374366
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
APPLICANT: Milano, Joseph
TITLE OF INVENTION: METHOD FOR THE RECOMBINATION OF GENETIC ELEMENTS
FILE REFERENCE: CL1794 US NA
```

```
CURRENT APPLICATION NUMBER: US/10/374,366
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: 60/360,279
PRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 203
SOFTWARE: PatentIn version 3.2
SEQ ID NO 202
LENGTH: 21
TYPE: DNA
ORGANISM: Rhodospiridium glutinis
US-10-374-366-202
```

```
Query Match
Best Local Similarity 100.0%; Score 11; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
```

```
RESULT 13
US-10-188-523B-5
Sequence 5, Application US/10188523B
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009 US DIVCIP
CURRENT APPLICATION NUMBER: US/10/188,523B
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-10-188-523B-5
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Query Match
Best Local Similarity 100.0%; Score 11; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GCTCTAGATG 11
Db 3 GCCTAGATG 13
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RESULT 14
US-10-188-523C-5
Sequence 5, Application US/10188523C
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BC1009-CIP
CURRENT APPLICATION NUMBER: US/10/188,523C
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: MICROSOFT OFFICE 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: primer
US-10-188-523C-5

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Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

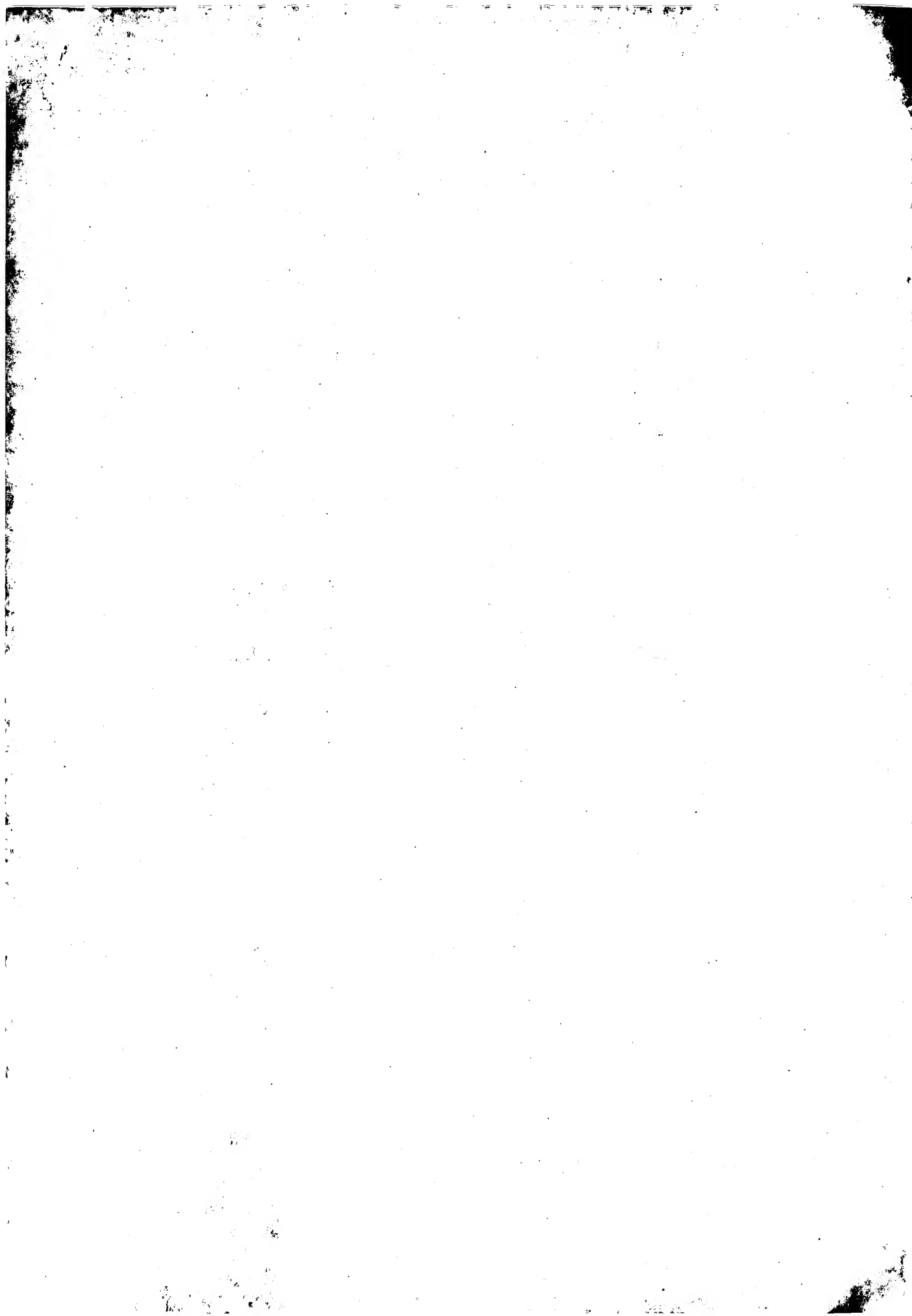
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Db 3 GCTCTAGAATG 13

RESULT 15
PCT-US03-04088-520/c
Sequence 520, Application PC/TUS0304088
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: RNA interference Mediated Inhibition of Telomerase Gene
FILE REFERENCE: 02-708-A (400/080)
CURRENT APPLICATION NUMBER: PCT/US03/04088
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/396,600
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/358,580
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124
PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 60/386,782
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/406,784
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/408,378
PRIOR FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/409,293
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: US 60/440,129
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 626
SOFTWARE: Patent version 3.2
SEQ ID NO 520
LENGTH: 23
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense
PCT-US03-04088-520

Query Match 100.0%; Score 11; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGAATG 11
|||
Db 23 GCTCTAGAATG 13

Search completed: June 23, 2003, 19:12:13
Job time: 483.861 secs



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 05:20:00 ; Search time 922.598 Seconds
(without alignments)
299.770 Million cell updates/sec

Title: US-08-770-564A-11
Perfect score: 11
Sequence: 1 GCTCTGAAATG 11

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 24791104 seqs, 12571243825 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Pending Patents_NA_Main:*

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3	11	100.0	11	US-09-540-119B-11	Sequence 11, Appl
4	11	100.0	13	US-09-540-119B-12	Sequence 12, Appl
5	11	100.0	15	PCT-US97-23619-10	Sequence 10, Appl
6	11	100.0	15	US-08-770-564A-10	Sequence 10, Appl
7	11	100.0	18	US-08-974-549-543	Sequence 543, App
8	11	100.0	18	US-09-402-181A-543	Sequence 543, App
9	11	100.0	18	US-09-402-181B-543	Sequence 543, App
10	11	100.0	18	US-09-432-503-543	Sequence 543, App
11	11	100.0	18	US-09-721-477-543	Sequence 543, App
12	11	100.0	18	US-09-721-506-543	Sequence 543, App
13	11	100.0	19	PCT-US97-23619-9	Sequence 9, Appl
14	11	100.0	19	US-08-770-564A-9	Sequence 9, Appl
15	11	100.0	21	US-07-887-265A-13	Sequence 13, Appl
16	11	100.0	21	US-08-244-121-13	Sequence 13, Appl
17	11	100.0	21	US-09-997-868-13	Sequence 13, Appl
18	11	100.0	22	US-09-765-873A-5	Sequence 5, Appl
19	11	100.0	22	US-60-147-719-5	Sequence 5, Appl
20	11	100.0	23	US-09-952-522B-9	Sequence 9, Appl
21	11	100.0	23	US-09-952-522B-17	Sequence 17, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 11 100.0 23 36 US-09-952-532B-31 Sequence 31, Appl
23 11 100.0 24 31 US-09-807-809-5 Sequence 5, Appl
24 11 100.0 24 31 US-10-245-813-2 Sequence 2, Appl
25 11 100.0 25 16 US-09-250-336A-4 Sequence 4, Appl
26 11 100.0 25 16 US-09-642-177-4 Sequence 4, Appl
27 11 100.0 25 36 US-09-956-604-135337 Sequence 135337
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30 11 100.0 25 42 US-10-215-112-6862 Sequence 6862, Ap
31 11 100.0 25 67 US-60-233-620-66031 Sequence 66031, A
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33 11 100.0 25 79 US-60-353-987-393144 Sequence 393144
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37 11 100.0 26 1 PCT-US96-14678A-27 Sequence 27, Appl
38 11 100.0 26 1 PCT-US97-15394-16 Sequence 16, Appl
39 11 100.0 26 1 PCT-US99-03302-4 Sequence 4, Appl
40 11 100.0 26 1 PCT-US99-07533-4 Sequence 4, Appl
41 11 100.0 26 1 PCT-US99-07533-4 Sequence 4, Appl
42 11 100.0 26 6 US-08-272-102-23 Sequence 23, Appl
43 11 100.0 26 7 US-08-387-524-19 Sequence 19, Appl
44 11 100.0 26 8 US-08-405-496-16 Sequence 16, Appl
45 11 100.0 26 8 US-08-422-711-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
PCT-US97-23619-11
Sequence 11, Application PC/TUS9723619
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
TITLE OF INVENTION: RNA Component of Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..11
OTHER INFORMATION: /note="oliigo 21ab2"
PCT-US97-23619-11
Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-08-770-564A-11
Sequence 11, Application US/08770564A
GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
TITLE OF INVENTION: Against the RNA Component of Telomerase
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: DNA
US-08-770-564A-11
Query Match 100.0%; Score 11; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 11, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-11

Query Match      100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
DB      1 GCTCTAGATG 11

RESULT 4
US-09-540-119B-12
; Sequence 12, Application US/09540119B
; GENERAL INFORMATION:
; APPLICANT: Gryaznov, Sergei
; APPLICANT: Pruzan, Ronald
; APPLICANT: Weinrich, Scott
; TITLE OF INVENTION: Telomerase Inhibitor Polynucleotides
; FILE REFERENCE: 029/001
; CURRENT APPLICATION NUMBER: US/09/540,119B
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-540-119B-12

Query Match      100.0%; Score 11; DB 21; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
DB      1 GCTCTAGATG 11

RESULT 5
PCT-US97-23619-10
; Sequence 10, Application PC/TUS9723619
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: Methods for Detecting and Inhibiting the
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/23619
; FILING DATE: Not yet assigned
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,564
; FILING DATE: 20-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/770,565
; FILING DATE: 20-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 15389-27PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY:
; LOCATION: 1..15
; OTHER INFORMATION: /note="oligo 21ab3"
PCT-US97-23619-10

Query Match      100.0%; Score 11; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTCTAGATG 11
DB      1 GCTCTAGATG 11

RESULT 6
US-08-770-564A-10
; Sequence 10, Application US/08770564A
; GENERAL INFORMATION:
; APPLICANT: Kealey, James T.
; APPLICANT: Pruzan, Ron
; APPLICANT: Weinrich, Scott L.
; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
; TITLE OF INVENTION: Against the RNA Component of Telomerase
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/770,564A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
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REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564a-10

Query Match 100.0%; Score 11; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 7

US-08-974-549-543

Sequence 543, Application US/08974549

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 726
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549

FILING DATE: 19-NOV-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTR molecule"
US-08-974-549-543

Query Match 100.0%; Score 11; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 8

US-09-402-181A-543

Sequence 543, Application US/09402181A

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181A

FILING DATE: 29-SEP-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-402-181A-543

Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 9
US-09-402-181B-543
; Sequence 543, Application US/09402181B
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-402-181B-543

Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 1 GCTCTAGATG 11

RESULT 10
US-09-432-503-543
; Sequence 543, Application US/09432503
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30

Fri Jun 27 07:41:06 2003

us-08-770-564a-11.01go.rnrm

Page 6

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,503
FILING DATE: 02-Nov-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /notes "antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-432-503-543
Query Match 100.0%; Score 11; DB 18; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 11
US-09-721-477-543
Sequence 543, Application US/09721477
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.;
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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COUNTRY: USA
ZIP: 94111-3634
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,477
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/974,549
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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LOCATION: 1..18
OTHER INFORMATION: /notes "antisense hTRT molecule"
SEQUENCE DESCRIPTION: SEQ ID NO: 543:
US-09-721-477-543
Query Match 100.0%; Score 11; DB 29; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11
RESULT 12
US-09-721-506-543
Sequence 543, Application US/09721506
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.;
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
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TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,506
FILING DATE: 22-Nov-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17865
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 543:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..18
OTHER INFORMATION: /note="antisense hTERT molecule"
US-09-721-506-543

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATG 11

RESULT 13
PCT-US97-23619-9
; Sequence 9, Application PC/TUS9723619
; GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: Methods for Detecting and Inhibiting the
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/23619
FILING DATE: Not yet assigned
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,564
FILING DATE: 20-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/770,565
FILING DATE: 20-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 15389-27PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..19
OTHER INFORMATION: /note="oligo 21ab"
PCT-US97-23619-9

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATG 11

RESULT 14
US-08-770-564a-9
; Sequence 9, Application US/08770564A
; GENERAL INFORMATION:
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ron
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Inhibitory Polynucleotides Directed
AGAINST THE RNA COMPONENT OF TELOMERASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor

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Page 8

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,564A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-564A-9

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Best Local Similarity 100.0%; Score 11; DB 11; Length 19;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GCTTAGATG 11

RESULT 15
US-07-887-265A-13/C
Sequence 13, Application US/07887265A
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
APPLICANT: Maxfield, Dave,
APPLICANT: Groskreutz, Debyra J
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/887,265A
FILING DATE: 19920522
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 748P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881

TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-887-265A-13

Query Match
Best Local Similarity 100.0%; Score 11; DB 3; Length 21;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTAGATG 11
DB 11 GCTTAGATG 1

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Job time : 923.675 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 06:41:29 ; Search time 88.3944 Seconds
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Title: US-08-770-564a-11

Perfect score: 11

Sequence: 1 GCTTACGATG 11

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Searched: 1042519 seqs, 733713590 residues

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Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database: Published Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	11	100.0	22	10	US-09-765-873A-5
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4	11	100.0	23	9	US-09-952-522B-17
5	11	100.0	23	9	US-09-952-522B-31
6	11	100.0	24	9	US-10-245-813-2
7	11	100.0	25	9	US-10-215-112-6862
8	11	100.0	26	9	US-10-011-366-16
9	11	100.0	26	9	US-10-118-495-11
10	11	100.0	26	9	US-10-118-495-13
11	11	100.0	26	9	US-09-952-522B-19
12	11	100.0	26	9	US-10-044-539-312
13	11	100.0	26	10	US-09-057-351-23
14	11	100.0	27	10	US-09-784-508-8
15	11	100.0	28	10	US-09-844-006A-3
16	11	100.0	29	9	US-10-162-223-2
17	11	100.0	34	10	US-09-784-508-10
18	11	100.0	36	9	US-10-166-183-14
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23	10	90.9	21	10	US-09-767-479-15
24	10	90.9	22	9	US-09-981-648-11
25	10	90.9	23	9	US-09-989-706-2
26	10	90.9	23	9	US-10-071-488-49
27	10	90.9	25	9	US-10-098-263B-8894
28	10	90.9	25	9	US-10-098-263B-44593
29	10	90.9	25	9	US-10-098-263B-44594
30	10	90.9	25	9	US-10-098-263B-80109
31	10	90.9	25	9	US-10-098-263B-80110
32	10	90.9	26	10	US-10-098-263B-104702
33	10	90.9	26	10	US-09-954-695-10
34	10	90.9	26	10	US-09-954-695-14
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36	10	90.9	26	10	US-09-954-695-42
37	10	90.9	26	10	US-09-954-695-10
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40	10	90.9	26	10	US-09-954-586-18
41	10	90.9	26	10	US-09-954-586-42
42	10	90.9	29	9	US-10-117-846-27
43	10	90.9	29	9	US-10-083-590-4
44	10	90.9	30	9	US-09-987-021-13
45	10	90.9	30	9	US-09-987-021-17
C 45	10	90.9	30	10	US-09-957-485-13

ALIGNMENTS

RESULT 1
US-09-997-868-13/C
Sequence 13, Application US/09997868
Publication No. US20030031654A1
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
Groskreutz, Debora J.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/997,868
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-May-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-Dec-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-Dec-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-997-868-13

Query Match 100.0%; Score 11; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

RESULT 2

US-09-765-873A-5
Sequence 5, Application US/09765873A
Patent No. US20010053847A1
GENERAL INFORMATION:
APPLICANT: Tang, Xiao-Song
TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
FILE REFERENCE: BCI009 US CIP
CURRENT APPLICATION NUMBER: US/09/765,873A
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: US 09/627,216
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: primer
US-09-765-873A-5

Query Match 100.0%; Score 11; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 3 GCTCTAGATG 13

RESULT 3

US-09-952-522B-9
Sequence 9, Application US/09952522B
Publication No. US20030082152A1
GENERAL INFORMATION:
APPLICANT: Ketz, Adam J.
APPLICANT: Lull, Ramon
APPLICANT: Futrell, J. William
APPLICANT: Hedrick, Marc H.
APPLICANT: Benham, Prosper
APPLICANT: Lorenz, Hermann Peter
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
FILE REFERENCE: 30448, 77US11
CURRENT APPLICATION NUMBER: US/09/952,522B
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US00/06232
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/123,711
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/162,462
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 9
LENGTH: 23

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: osteocalcin forward primer
US-09-952-522B-9

Query Match 100.0%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 4

US-09-952-522B-17
Sequence 17, Application US/09952522B
Publication No. US20030082152A1
GENERAL INFORMATION:
APPLICANT: Ketz, Adam J.
APPLICANT: Lull, Ramon
APPLICANT: Futrell, J. William
APPLICANT: Hedrick, Marc H.
APPLICANT: Benham, Prosper
APPLICANT: Lorenz, Hermann Peter
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
FILE REFERENCE: 30448, 77US11
CURRENT APPLICATION NUMBER: US/09/952,522B
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US00/06232
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/123,711
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/162,462
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 17
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Osteopontin
OTHER INFORMATION: forward primer
US-09-952-522B-17

Query Match 100.0%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 5

US-09-952-522B-31
Sequence 31, Application US/09952522B
Publication No. US20030082152A1
GENERAL INFORMATION:
APPLICANT: Ketz, Adam J.
APPLICANT: Lull, Ramon
APPLICANT: Futrell, J. William
APPLICANT: Hedrick, Marc H.
APPLICANT: Benham, Prosper
APPLICANT: Lorenz, Hermann Peter
TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
FILE REFERENCE: 30448, 77US11
CURRENT APPLICATION NUMBER: US/09/952,522B

CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: PCT/US00/06232
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 60/123,711
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/162,462
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: PPAR gamma 1
US-09-952-522B-31

Query Match 100.0%; Score 11; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 6
US-10-245-813-2
Sequence 2, Application US/10245813
Publication No. US20030060443A1
GENERAL INFORMATION:
APPLICANT: Gyun Min Lee
TITLE OF INVENTION: INHIBITION OF APOPTOSIS BY THE
EXPRESSION OF ANTISENSE RNA OF CASPASE-2
FILE REFERENCE: 118-19-US-01
CURRENT APPLICATION NUMBER: US/10/245,813
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 2001-57353
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: casp3L primer
US-10-245-813-2

Query Match 100.0%; Score 11; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 7
US-10-215-112-6862/c
Sequence 6862, Application US/10215112
Publication No. US20030082596A1
GENERAL INFORMATION:
APPLICANT: Michael Wittmann
TITLE OF INVENTION: Method of Genetic Analysis of Probes:
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/10/215,112
CURRENT FILING DATE: 2002-08-08
NUMBER OF SEQ ID NOS: 14936
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 6862
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-10-215-112-6862

Query Match 100.0%; Score 11; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
Db 15 GCTCTAGATG 5

RESULT 8
US-10-011-366-16
Sequence 16, Application US/10011366
Publication No. US20030054493A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
DISEASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,366
FILING DATE: 16-NO. US20030054493A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/957,310
FILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 08/329,154
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPND-01121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-011-366-16
Query Match 100.0%; Score 11; DB 9; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 1 GCTCTAGATG 11

RESULT 9
US-10-118-495-11
; Sequence 11, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Kling, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-118-495-11

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 1 GCTCTAGATG 11

RESULT 10
US-10-118-495-13
; Sequence 13, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Kling, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-118-495-13

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 1 GCTCTAGATG 11

RESULT 11
US-09-952-522B-19
; Sequence 19, Application US/09952522B
; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Adam J.
; APPLICANT: Llull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benham, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bone
; OTHER INFORMATION: stalooprotein forward primer
US-09-952-522B-19

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 1 GCTCTAGATG 11

RESULT 12
US-10-044-692-312
; Sequence 312, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 335
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/044,692
; FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-692-312

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 5 GCTCTAGATG 15

RESULT 13
US-10-044-539-312
Sequence 312, Application US/10044539
Publication No. US2003010093A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: THERAPEUTIC METHODS
DIAGNOSTIC AND
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539
FILING DATE: 11-Jan-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 312:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 312:
US-10-044-539-312

Query Match 100.0%; Score 11; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
DB 5 GCTCTAGATG 15

RESULT 14
US-09-057-351-23
Sequence 23, Application US/09057351
Patent No. US20010034439A1
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
Feng, Junli
APPLICANT: Funk, Walter
Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,351
FILING DATE: 08-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,802
FILING DATE: 07-JUN-1995

Fri Jun 27 07:41:05 2003

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Page 6

ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000821US.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-057-351-23

Query Match 100.0%; Score 11; DB 10; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 5 GCTCTAGATG 15

RESULT 15
US-09-784-508-8
Sequence 8, Application US/09784508
Patent No. US20020046417A1
GENERAL INFORMATION:
APPLICANT: Martin, Robert R.
APPLICANT: Mathews, Helena
APPLICANT: Keller, Karen
APPLICANT: Kellogg, Jill A.
APPLICANT: Wagner, Ry
TITLE OF INVENTION: Development of Resistance to Raspberry
FILE REFERENCE: 4257-0024.31
CURRENT APPLICATION NUMBER: US/09/784,508
PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/737,719
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,018
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-784-508-8

Query Match 100.0%; Score 11; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
Db 2 GCTCTAGATG 12

Search completed: June 23, 2003, 20:01:33
Job time : 89.3944 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 04:53:08 ; Search time 17.2231 Seconds
(without alignments)
195.867 Million cell updates/sec

Title: US-08-770-564a-11

Perfect score: 11
Sequence: 1 GCTCTAGATG 11

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 609818

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA:*
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	100.0	11	2	US-08-770-565-11
2	11	100.0	15	2	US-08-770-565-10
3	11	100.0	18	4	US-08-974-549A-543
4	11	100.0	19	2	US-08-770-565-9
5	11	100.0	21	4	US-08-026-143B-13
6	11	100.0	21	5	PCT-US92-10621-13
7	11	100.0	21	5	PCT-US94-02233-13
8	11	100.0	22	4	US-09-627-216A-5
9	11	100.0	23	3	US-08-973-068-46
10	11	100.0	26	1	US-08-330-123A-23
11	11	100.0	26	1	US-08-480-604A-16
12	11	100.0	26	1	US-08-482-115B-23
13	11	100.0	26	2	US-08-660-678A-23
14	11	100.0	26	2	US-08-710-249-26
15	11	100.0	26	2	US-08-485-778-19
16	11	100.0	26	2	US-08-405-496A-16
17	11	100.0	26	2	US-08-472-802C-24
18	11	100.0	26	3	US-08-520-550A-19
19	11	100.0	26	3	US-08-998-443-23
20	11	100.0	26	4	US-08-974-549A-558
21	11	100.0	26	4	US-09-060-523-23
22	11	100.0	26	4	US-08-915-136-16
23	11	100.0	26	4	US-09-220-157A-26
24	11	100.0	26	4	US-09-286-959B-4
25	11	100.0	26	4	US-09-580-517-23
26	11	100.0	26	4	US-09-153-310-4
27	11	100.0	26	4	US-08-957-310-16

28	11	100.0	27	2	US-08-770-565-26	Sequence 26, Appl
29	11	100.0	27	3	US-08-630-172-24	Sequence 24, Appl
30	11	100.0	27	4	US-09-375-419-24	Sequence 8, Appl
31	11	100.0	30	2	US-08-770-565-8	Sequence 7, Appl
32	11	100.0	30	2	US-08-995-927-7	Sequence 5, Appl
33	11	100.0	30	4	US-09-349-627-5	Sequence 22, Appl
34	11	100.0	30	4	US-08-582-096-7	Sequence 22, Appl
35	11	100.0	33	3	US-08-630-172-22	Sequence 3, Appl
36	11	100.0	33	4	US-09-375-419-22	Sequence 12, Appl
37	11	100.0	37	3	US-08-815-190A-3	Sequence 9, Appl
38	11	100.0	39	4	US-09-091-305-3	Sequence 11, App
39	11	100.0	40	1	US-08-395-800A-12	Sequence 11, App
40	10	90.9	15	2	US-08-624-601-13	Sequence 14, App
41	10	90.9	16	4	US-08-687-580B-9	Sequence 14, App
42	10	90.9	20	4	US-08-964-722-7	Sequence 11, App
43	10	90.9	21	1	US-07-956-700B-114	Sequence 11, App
44	10	90.9	21	1	US-08-476-537-114	Sequence 11, App
45	10	90.9	21	1	US-08-485-607-114	Sequence 11, App

ALIGNMENTS

RESULT 1
US-08-770-565-11
; Sequence 11, Application US/08770565
; Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-11
Query Match 100.0%; Score 11; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. NO. 2.8e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGATG 11

RESULT 4
US-08-770-565-9
Sequence 9, Application US/08770565
Patent No. 5846723
GENERAL INFORMATION:
APPLICANT: Kim, Nam Woo
APPLICANT: Wu, Fred
APPLICANT: Kealey, James T.
APPLICANT: Pruzan, Ronald
APPLICANT: Weinrich, Scott L.
TITLE OF INVENTION: Methods for Detecting the RNA Component of
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,565
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-002300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-770-565-9

Query Match 100.0%; Score 11; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
|||||
Db 1 GCTCTAGATG 11

RESULT 5
US-08-026-143B-13/c
Sequence 13, Application US/08026143B
Patent No. 6348327
GENERAL INFORMATION:
APPLICANT: Gorman, Cornelia M.,
Groskreutz, Debyra J.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
Polypeptide Synthesis
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/026,143B
FILING DATE: 01-Mar-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-026-143B-13

Query Match 100.0%; Score 11; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTAGATG 11
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Db 11 GCTCTAGATG 11

RESULT 6
PCT-US92-10621-13/c
Sequence 13, Application PC/TUS9210621
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Gorman, Cornelia M.,
APPLICANT: Mariotte, Dave,
APPLICANT: Groskreutz, Debyra J.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 19921204
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
ATTORNEY/AGENT INFORMATION:

NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 748P2.PCT
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
TELEX: 914371-1168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-10621-13

Query Match 100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

RESULT 7
PCT-US94-02233-13/C
Sequence 13, Application PC/TUS9402233
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Prohormone Convertase Transformed Cells and Polypeptide Synthe
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02233
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 748P3PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910371-7168
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-02233-13

Query Match 100.0%; Score 11; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11
Db 11 GCTCTAGATG 1

RESULT 8
US-09-627-216A-5
Sequence 5, Application US/09627216A
Patent No. 646837
GENERAL INFORMATION:
APPLICANT: Sarisanti, Sima F
APPLICANT: Wang, Xue-song
APPLICANT: Qi, Wei Wei
APPLICANT: Vannelli, Todd
APPLICANT: Garshey, Anthony
TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
FILE REFERENCE: BCI009 US NA
CURRENT APPLICATION NUMBER: US/09/627,216A
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/147,719
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-627-216A-5

Query Match 100.0%; Score 11; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11
Db 3 GCTCTAGATG 13

RESULT 9
US-08-973-068-46
Sequence 46, Application US/08973068
Patent No. 6127604
GENERAL INFORMATION:
APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
APPLICANT: Hafner, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INTERGENIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/NU96/00335
EARLIER FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 46
LENGTH: 23
TYPE: DNA
ORGANISM: Banana Bunchy Top Virus (BBTV)
US-08-973-068-46

Query Match 100.0%; Score 11; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCTCTAGATG 11
Db 1 GCTCTAGATG 11

RESULT 10
US-08-330-123A-23

Sequence 23, Application US/08330123A
Patent No. 5583016
GENERAL INFORMATION:
APPLICANT: VILLEPONTEAU, Bryant
APPLICANT: FENG, Junli
APPLICANT: FUNK, Walter
APPLICANT: ANDREWS, William H.
TITLE OF INVENTION: HUMAN TELOMERASE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,123A
FILING DATE: 27-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15389-000810
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-330-123A-23

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 5 GCTCTAGATG 15

RESULT 11
US-08-480-604A-16
Sequence 16, Application US/08480604A
Patent No. 5736139
GENERAL INFORMATION:
APPLICANT: KIRK, JOHN A.
APPLICANT: THALLEY, BRUCE S.
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
APPLICANT: STAFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPMD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-480-604A-16

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
|||||
DB 1 GCTCTAGATG 11

RESULT 12
US-08-482-115B-23
Sequence 23, Application US/08482115B
Patent No. 5776679
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Assays for the RNA Component of Human
TITLE OF INVENTION: Telomerase
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,115B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000830US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-115B-23

Query Match 100.0%; Score 11; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTAGATG 11
Db 5 GCTCTAGATG 15

RESULT 13
US-08-660-678A-23
Sequence 23, Application US/08660678A
Patent No. 5837857
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Funk, Walter
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Mammalian Telomerase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,678A
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,123
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,102
FILING DATE: 07-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.

REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-000811US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-660-678A-23

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTCTAGATG 11
Db 5 GCTCTAGATG 15

RESULT 14
US-08-710-249-26
Sequence 26, Application US/08710249
Patent No. 5858777
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Peng, Junli
APPLICANT: Andrews, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015389-001220US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-710-249-26

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 17.2231 secs

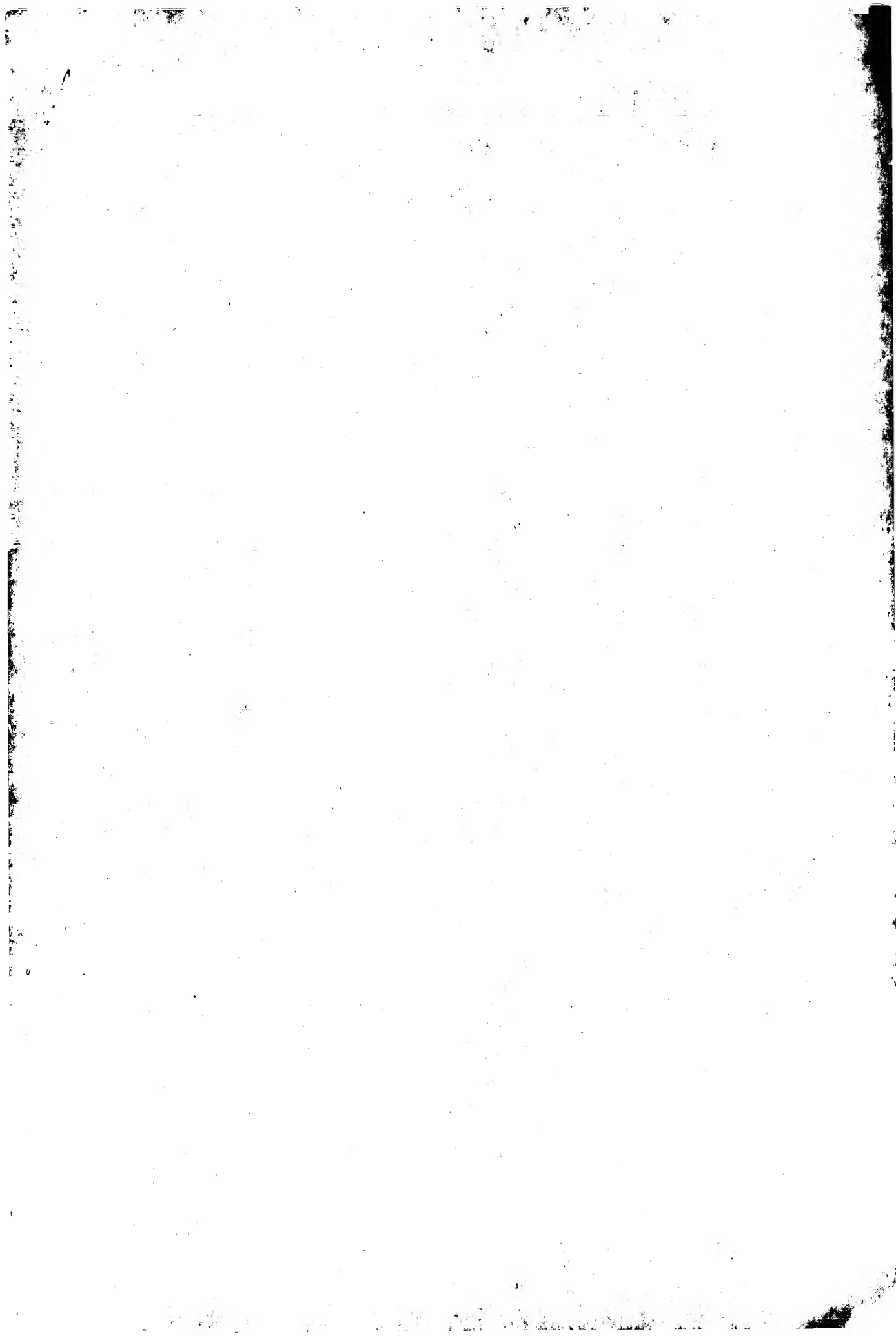
QY 1 GCTCTGAATG 11
|||||
Db 5 GCTCTGAATG 15

RESULT 15
US-08-485-778-19
; Sequence 19, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avillion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHJ94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-778-19

Query Match 100.0%; Score 11; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11
|||||
Db 5 GCTCTGAATG 15

Search completed: June 23, 2003, 10:17:07



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OM nucleic - nucleic search, using bw model

Run on: June 22, 2003, 18:09:32 ; Search time 73.0996 Seconds
(without alignments)
338.880 Million cell updates/sec

Title: US-08-770-564A-11
Perfect score: 11
Sequence: 1 GCTCTAGCATG 11

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 2185239 seqs, 112599159 residues

Word size: 0
Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database:

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17:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24:	/SIDS2/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	19	AAV41178
2	11	100.0	11	23	AA515929
3	11	100.0	13	23	AA515930
4	11	100.0	15	19	AAV41177
5	11	100.0	17	22	AA57369
6	11	100.0	19	19	AAV41176
7	11	100.0	19	22	AAH43421
8	11	100.0	21	14	AAQ43258
9	11	100.0	21	14	AAQ43257

C	10	11	100.0	21	15	AAQ71457
	11	11	100.0	22	24	AAD33073
	12	11	100.0	22	24	AAD26921
	13	11	100.0	23	18	AAT49421
	14	11	100.0	24	20	AA563470
	15	11	100.0	25	20	AAZ08704
	16	11	100.0	26	17	AAT10304
	17	11	100.0	26	17	AAT10299
	18	11	100.0	26	17	AAT29258
	19	11	100.0	26	17	AAT11044
	20	11	100.0	26	18	AAT58811
	21	11	100.0	26	19	AAV30567
	22	11	100.0	26	19	AAV19489
	23	11	100.0	26	19	AAV17033
	24	11	100.0	26	20	AAV90788
	25	11	100.0	26	20	AAV77402
	26	11	100.0	26	20	AAV01542
	27	11	100.0	26	21	ABK09963
	28	11	100.0	26	21	AAA88250
	29	11	100.0	26	21	AAA08601
	30	11	100.0	26	24	ABK48024
	31	11	100.0	26	24	AAD24246
	32	11	100.0	27	18	AAT97049
	33	11	100.0	27	19	AAV41193
	34	11	100.0	27	22	AAH22533
	35	11	100.0	27	24	ABA95497
	36	11	100.0	28	17	AAT43859
	37	11	100.0	28	19	AAV57587
	38	11	100.0	28	21	AAV95720
	39	11	100.0	28	24	ABA04366
	40	11	100.0	29	21	AAV66568
	41	11	100.0	29	22	AAH45090
	42	11	100.0	29	24	ABK89026
	43	11	100.0	30	18	AAT91844
	44	11	100.0	30	19	AAV63649
	45	11	100.0	30	19	AAV41175

ALIGNMENTS

RESULT 1	
AAV41178	
ID	AAV41178 standard; DNA; 11 BP.
XX	
AC	AAV41178;
XX	
DT	08-OCT-1998 (first entry)
XX	
DE	RNA component of human telomerase (hTR) antisense oligo 21ab2.
XX	
KW	RNA component; human telomerase; antisense oligonucleotide; infection;
KW	neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW	contraction; sterilisation; immunosuppression; therapeutic; hTR;
KW	immune system down-regulation; anti-inflammatory therapy; ss.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO9828442-A1.
XX	
PD	02-JUL-1998.
XX	
PF	19-DEC-1997; 97WO-US23619.
XX	
PR	20-DEC-1996; 96US-0770565.
PR	20-DEC-1996; 96US-0770564.
XX	
PA	(GERO-) GERON CORP.
XX	
PI	Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
XX	
DR	WPI; 1998-377670/32.

Rx 2,4 protelaxin
Phenylalanine ammo
Rhodoporphyrin for
Banana bunchy top
Oligonucleotide Cl
Human telomerase R
RNA component of h
C. difficile toxin
Primer for product
Human telomerase P
Clostridium difficile
Human hTR gene RT-
Telomerase PCR pri
Human telomerase R
Human telomerase R
PCR primer for Hum
Novel recombinant
Human telomerase R
PCR primer #4 to a
Human telomerase-a
Human telomerase (S
Sense primer for h
RNA component of h
RBDV movement prot
Human telomerase R
Mouse ob gene forw
HER-A cDNA amplify
B. subtilis KatB g
Crt C-domain-green
Human FGFR-1 PCR p
Murine interleukin
PCR primer, pF83H,
Human inhibitory k
Antisense oligonuc
RNA component of h

```

XX New polynucleotide(s) anti-sense to human telomerase - used for
PT detecting or inhibiting human telomerase, e.g. for treating cancers,
PT contrereption, immuno-suppression or treating infection
XX
XX Claim 11; Page 65; 80pp; English.
XX
XX Sequences shown in AAV41169 to AAV41181 represent antisense
CC oligonucleotides to the RNA component of human telomerase (hTR). These
CC antisense oligonucleotides specifically hybridise to a nucleotide
CC sequence within an accessible region of the hTR, but that does not
CC hybridise to a sequence within the template region of hTR. These
CC oligonucleotides may specifically be used for detection of an RNA
CC component of human telomerase in a sample. This is useful for diagnosing
CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
CC and providing prognosis for a cancer patient. The inhibitory
CC oligonucleotides can inhibit the telomerase activity level in a cell by
CC interfering with transcription of the RNA component, decreasing the
CC half-life of the telomerase RNA component transcript, inhibiting assembly
CC of the RNA component into the telomerase holoenzyme, or inhibiting the
CC polymerase activity of telomerase. These antisense oligonucleotides can
CC be used for inhibiting telomerase activity in both cultured cells and in
CC cells in vivo. They can be used in therapeutics for treating or
CC preventing cancer, for contraception or sterilisation, for
CC immunosuppression, and for selectively down-regulating specific branches
CC of the immune system, e.g. a specific subset of T-cells, in
CC anti-inflammatory therapies or for treating infections by, e.g. Yeast,
CC parasites or fungi.
XX
XX Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 other;
SQ
Query Match 100.0%; Score 11; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAGATG 11
DB 1 GCTCTAGAGATG 11

```

RESULT 2

AA515929
ID AA515929 standard; DNA; 11 BP.

XX AA515929;

XX 27-FEB-2002 (first entry)

XX Human telomerase polynucleotide inhibitor #10.

XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;

XX breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;

XX fertility; inflammatory condition; tumour; cancer; veterinary;

XX immunosuppression; telomerase inhibitor; ss.

XX Homo sapiens.

XX Synthetic.

XX Key

XX modified_base 1..11

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10476.

XX 31-MAR-2000; 2000US-0540119.

XX (GERO-) GERON CORP.

```

XX Gryaznov SM, Pruzan R, Weinrich SL;
XX WPI; 2001-656955/75.
XX
XX New polynucleotide useful for inhibiting telomerase activity in cells,
PT or for treating telomerase-mediated condition or disease, such as
PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
XX
XX Example 3; Page 32; 48pp; English.
XX
XX The invention relates to polynucleotide inhibitors (I) and methods for
CC inhibiting telomerase activity. (II) are useful in inhibiting telomerase
CC activity and proliferation of a telomerase positive cell, and in
CC manufacturing a medicament for inhibiting telomerase activity in a cell
CC and in treating telomerase-mediated condition or disease, such as
CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
CC useful in treating a tumour or in manufacturing a medicament for the
CC treatment of tumour. The polynucleotide inhibitors may also be used in
CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
CC activity in cells in vivo is useful in prophylactic and therapeutic
CC methods of treating cancer and other disorders involving inappropriate
CC expression of telomerase, and in treating veterinary proliferative
CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
CC for immunosuppression and for selectively down-regulating specific
CC branches of the immune system. The present sequence represents
CC human telomerase polynucleotide inhibitor #10, as described in the
CC method of the invention.
XX
XX Sequence 11 BP; 3 A; 2 C; 3 G; 3 T; 0 other;
SQ
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTCTAGAGATG 11
DB 1 GCTCTAGAGATG 11

```

RESULT 3

AA515930
ID AA515930 standard; DNA; 13 BP.

XX AA515930;

XX 27-FEB-2002 (first entry)

XX Human telomerase polynucleotide inhibitor #11.

XX Human; telomerase; hTR; cytostatic; anti-inflammatory; adenocarcinoma;

XX breast; prostate; colon; mixed cell leukaemia; Hodgkin's disease;

XX fertility; inflammatory condition; tumour; cancer; veterinary;

XX immunosuppression; telomerase inhibitor; ss.

XX Homo sapiens.

XX Synthetic.

XX Key

XX modified_base 1..13

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US10476.

XX 31-MAR-2000; 2000US-0540119.

XX

PA (GERO-) GERON CORP.
 XX
 PI Gryaznov SM, Pruzan R, Weinrich SL;
 XX
 DR WPI; 2001-656955/75.
 XX
 PT New polynucleotide useful for inhibiting telomerase activity in cells,
 PT or for treating telomerase-mediated condition or disease, such as
 PT cancers, tumours, Hodgkin's disease, or inflammatory conditions -
 XX
 PS Example 3; Page 32; 48pp; English.
 XX
 CC The invention relates to polynucleotide inhibitors (I) and methods for
 CC inhibiting telomerase activity. (I) are useful in inhibiting telomerase
 CC activity and proliferation of a telomerase positive cell, and in
 CC manufacturing a medicament for inhibiting telomerase activity in a cell
 CC and in treating telomerase-mediated condition or disease, such as
 CC adenocarcinoma of breast, prostate or colon, mixed cell leukaemia,
 CC Hodgkin's disease, fertility and inflammatory conditions. (I) are also
 CC useful in treating a tumour or in manufacturing a medicament for the
 CC treatment of tumour. The polynucleotide inhibitors may also be used in
 CC diagnostic assays for detecting RNA or DNA. Inhibition of telomerase
 CC activity in cells in vivo is useful in prophylactic and therapeutic
 CC methods of treating cancer and other disorders involving inappropriate
 CC expression of telomerase, and in treating veterinary proliferative
 CC diseases. Inhibition of telomerase in haematopoietic stem cells is useful
 CC for immunosuppression and for selectively down-regulating specific
 CC branches of the immune system. The present sequence represents
 CC human telomerase polynucleotide inhibitor #11, as described in the
 CC method of the invention.
 XX
 SQ Sequence 13 BP; 5 A; 2 C; 3 G; 3 T; 0 other;
 XX
 Query Match 100.0%; Score 11; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATG 11
 Db 1 GCTCTAGATG 11

RESULT 4
 AAV41177
 ID AAV41177 standard; DNA; 15 BP.
 XX
 AC AAV41177;
 XX
 DT 08-OCT-1998 (first entry)
 XX
 DE RNA component of human telomerase (hTR) antisense oligo 21ab3.
 XX
 KW RNA component; human telomerase; antisense oligonucleotide; infection;
 KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
 KW contraception; sterilisation; immunosuppression; therapeutic; hTR;
 KW immune system down-regulation; anti-inflammatory therapy; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9828442-A1.
 XX
 PD 02-JUL-1998.
 XX
 PF 19-DEC-1997; 97WO-US23619.
 XX
 XX 20-DEC-1996; 96US-0770565.
 PR 20-DEC-1996; 96US-0770564.
 XX
 PA (GERO-) GERON CORP.
 XX
 PI Kealey JT, Kim NW, Pruzan R, Weinrich SL, Wu F;
 PT

DR WPI; 1998-377670/32.
 XX
 PT New polynucleotide(s) antisense to human telomerase - used for
 PT detecting or inhibiting human telomerase, e.g. for treating cancers,
 PT contraception, immuno-suppression or treating infection
 XX
 PS Claim 11; Page 65; 80pp; English.
 XX
 CC Sequences shown in AAV41169 to AAV41181 represent antisense
 CC oligonucleotides to the RNA component of human telomerase (hTR). These
 CC antisense oligonucleotides specifically hybridise to a nucleotide
 CC sequence within an accessible region of the hTR, but that does not
 CC hybridise to a sequence within the template region of hTR. These
 CC oligonucleotides may specifically be used for detection of an RNA
 CC component of human telomerase in a sample. This is useful for diagnosing
 CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),
 CC and providing prognosis for a cancer patient. The inhibitory
 CC oligonucleotides can inhibit the telomerase activity level in a cell by
 CC interfering with transcription of the RNA component, decreasing the
 CC half-life of the telomerase RNA component transcript, inhibiting assembly
 CC of the RNA component into the telomerase holoenzyme, or inhibiting the
 CC polymerase activity of telomerase. These antisense oligonucleotides can
 CC be used for inhibiting telomerase activity in both cultured cells and in
 CC cells in vivo. They can be used in therapeutics for treating or
 CC preventing cancer, for contraception or sterilisation, for
 CC immunosuppression, and for selectively down-regulating specific branches
 CC of the immune system, e.g. a specific subset of T-cells, in
 CC anti-inflammatory therapies or for treating infections by, e.g. yeast,
 CC parasites or fungi.
 XX
 SQ Sequence 15 BP; 5 A; 3 C; 4 G; 3 T; 0 other;
 XX
 Query Match 100.0%; Score 11; DB 19; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGATG 11
 Db 1 GCTCTAGATG 11

RESULT 5
 AAF57369
 ID AAF57369 standard; DNA; 17 BP.
 XX
 AC AAF57369;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Murine Cdc25A intron 7/exon 8 splice junction sequence.
 XX
 KW Cdc25; Cdc25 phosphatase; transcription; modulator; murine; CDC25A;
 KW exon; intron; ds.
 XX
 OS Mus sp.
 XX
 PN WO200120034-A2.
 XX
 PD 22-MAR-2001.
 XX
 PF 11-SEP-2000; 2000WO-US24838.
 XX
 PR 13-SEP-1999; 99US-0153639.
 XX
 PA (BADI) BASF AG.
 XX
 PI Voss J, Timm J;
 XX
 DR WPI; 2001-244825/25.
 XX
 PT Assay for screening modulators of Cdc25 activity by using a cell having
 PT a recombinant Cdc25 phosphatase gene whose expression alters the
 PT transcription of a selected gene in the presence of a modulator -

XX Example 1; Page 15; 55pp; English.

CC The invention relates to a method of identifying a modulator of Cdc25

CC activity that comprises contacting a test cell having a recombinant Cdc25

CC phosphatase gene whose expression alters transcription of a selected

CC gene, with a compound under conditions where recombinant Cdc25

CC phosphatase gene is expressed and alters the transcription of a selected

CC gene as an indication of the compound being a modulator of Cdc25-mediated

CC transcription. The method is useful for identifying modulators of Cdc25

CC activity. Sequences AAF57363-376 represent intron/exon splice junction

CC sequences of the murine Cdc25A gene.

XX

SQ Sequence 17 BP; 4 A; 3 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 11; DB 22; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGGAATG 11

Db 4 GCTCTGGAATG 14

RESULT 6

AAV41176

ID AAV41176 standard; DNA; 19 BP.

XX

AC AAV41176;

XX

DT 08-OCT-1998 (first entry)

XX

DE RNA component of human telomerase (hTR) antisense oligo 21ab.

XX

KW RNA component; human telomerase; antisense oligonucleotide; infection;

KW neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;

KW contraction; sclerolacton; immunosuppression; therapeutic; hTR;

KW immune system down-regulation; anti-inflammatory therapy; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN MO9828442-A1.

XX

PD 02-JUL-1998.

XX

PF 19-DEC-1997; 97MO-US23619.

XX

PR 20-DEC-1996; 96US-0770565.

PR 20-DEC-1996; 96US-0770564.

XX

PA (GERO-) GERON CORP.

XX

PI Kealey JT, Klm JW, Pruzan R, Weinrich SL, Wu F;

XX

DR WPI; 1998-377670/32.

XX

PT New polynucleotide(s) anti-sense to human telomerase - used for

PT detecting or inhibiting human telomerase, e.g. for treating cancers,

PT contraception, immuno-suppression or treating infection

XX

PS Claim 11; Page 65; 80pp; English.

XX

CC Sequences shown in AAV41169 to AAV41181 represent antisense

CC oligonucleotides to the RNA component of human telomerase (hTR). These

CC antisense oligonucleotides specifically hybridize to a nucleotide

CC sequence within an accessible region of the hTR, but that does not

CC hybridize to a sequence within the template region of hTR. These

CC oligonucleotides may specifically be used for detection of an RNA

CC component of human telomerase in a sample. This is useful for diagnosing

CC cancer (especially neuroblastoma, bladder, colon and prostate cancer),

CC and providing prognosis for a cancer patient. The inhibitory

CC oligonucleotides can inhibit the telomerase activity level in a cell by

CC interfering with transcription of the RNA component, decreasing the

CC half-life of the telomerase RNA component transcript, inhibiting assembly

CC of the RNA component into the telomerase holoenzyme, or inhibiting the

CC polymerase activity of telomerase. These antisense oligonucleotides can

CC be used for inhibiting telomerase activity in both cultured cells and in

CC cells in vivo. They can be used in therapeutics for treating or

CC preventing cancer, for contraception or sterilisation, for

CC immunosuppression, and for selectively down-regulating specific branches

CC of the immune system, e.g. a specific subset of T-cells, in

CC anti-inflammatory therapies or for treating infections by, e.g. yeast,

CC parasites or fungi.

XX

SQ Sequence 19 BP; 5 A; 3 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 11; DB 19; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTCTGGAATG 11

Db 1 GCTCTGGAATG 11

RESULT 7

AAH43421

ID AAH43421 standard; DNA; 19 BP.

XX

AC AAH43421;

XX

DT 04-DEC-2001 (first entry)

XX

DE ISAs reverse primer.

XX

KW European; infectious Salmon anaemia; ISA; antigen; RNA segment 3;

KW virus; ISA; nucleoprotein; vaccine; fish; infection; primer; amplify;

KW polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN WO200165659-A1.

XX

PD 13-SEP-2001.

XX

PF 08-MAR-2001; 2001WO-GB01013.

XX

PR 08-MAR-2000; 2000GB-0005457.

PR 14-MAR-2000; 2000GB-0005960.

PR 01-DEC-2000; 2000GB-0029409.

XX

PA (UYAB-) UNIV ABERDEEN.

XX

PI Melvin WT, Breeman S, Labus MB;

XX

DR WPI; 2001-589927/66.

XX

PT Vaccinating fish against Infectious Salmon Anemia (ISA) virus infection

PT using European ISA virus antigen polypeptides -

XX

PS Claim 34; Page 34; 41pp; English.

XX

CC The sequences given in AAH43407-21 are primers which were used in

CC the amplification and cloning of the cDNA encoding the European

CC infectious Salmon anaemia (ISA) antigen polypeptide. The antigen is

CC cloned from RNA segment 3 of ISA virus (ISAV) and is believed to be

CC a major cell culture antigen of the virus, which may be a nucleoprotein.

CC The ISA antigen, or a fragment of it, may be used to vaccinate fish

CC against ISAV infection. It may also be used to screen fish for ISA

CC virus infection.

XX

SQ Sequence 19 BP; 5 A; 4 C; 4 G; 6 T; 0 other;

Query Match 100.0%; Score 11; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 1 GCTCTAGATG 11

RESULT 8
 AAQ43258/c
 ID AAQ43258 standard; DNA; 21 BP.

XX AC AAQ43258;

XX DT 24-SEP-1993 (first entry)

DE Sequence encoding the C-chain/A-chain junction prorelaxin (Rx)
 DE mutant Rx 2.4 at the prohormone convertase cleavage site.

XX KW Prohormone convertase; enzyme; cleavage; prorelaxin; hormone; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT CDS 1..21

XX FT /*tag= a

XX PN MO9311247-A.

XX PD 10-JUN-1993.

XX PF 04-DEC-1992; 92WO-US10621.

XX PR 06-DEC-1991; 91US-0803631.

XX PR 22-MAY-1992; 92US-0887265.

XX PA (GETH) GENENTECH INC.

XX PI Gorman CM, Groskreutz DJ, Marriot D;

XX DR WPI; 1993-197065/24.

XX DR P-PSDB; AAR37621.

XX PT Heterologous polypeptide factor prepn. - by introducing into

XX PT polypeptide factor dependent host cell nucleic acid, and then

XX PT culturing host cell, etc.

XX PS Example; Page 54; 134pp; English.

XX CC The inventors describe the production of mammalian cells expressing

XX CC prohormone convertase which facilitates the processing of prohormone

XX CC precursors to active hormones. More specifically the cleavage site

XX CC is the prohormone convertase cleavage site given in AAR37632-35. In

XX CC order to define murine prohormone convertase 1 specifically

XX CC prorelaxin alanine mutations of the basic residues K and R were

XX CC constructed. The following mutations were tested for substrate

XX CC specificity to murine prohormone convertase: 1.4, 2.4, 3.2, 4.3,

XX CC 7.2 and 8.6 (see AAQ43256-63; AAR37619-26).

XX CC Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

AC AAQ43257;
 XX XX
 XX DT 24-SEP-1993 (first entry)
 XX XX
 DE Sequence encoding the C-chain/A-chain junction prorelaxin (Rx)
 DE mutant Rx 1.4 at the prohormone convertase cleavage site.
 XX KW Prohormone convertase; enzyme; cleavage; prorelaxin; hormone; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT CDS 1..21
 XX FT /*tag= a

XX PN MO9311247-A.
 XX PD 10-JUN-1993.
 XX PF 04-DEC-1992; 92WO-US10621.
 XX PR 06-DEC-1991; 91US-0803631.
 XX PR 22-MAY-1992; 92US-0887265.
 XX PA (GETH) GENENTECH INC.
 XX PI Gorman CM, Groskreutz DJ, Marriot D;
 XX DR WPI; 1993-197065/24.
 XX DR P-PSDB; AAR37620.
 XX PT Heterologous polypeptide factor prepn. - by introducing into
 XX PT polypeptide factor dependent host cell nucleic acid, and then
 XX PT culturing host cell, etc.
 XX PS Example; Page 54; 134pp; English.

XX CC The inventors describe the production of mammalian cells expressing
 XX CC prohormone convertase which facilitates the processing of prohormone
 XX CC precursors to active hormones. More specifically the cleavage site
 XX CC is the prohormone convertase cleavage site given in AAR37632-35. In
 XX CC order to define murine prohormone convertase 1 specifically
 XX CC prorelaxin alanine mutations of the basic residues K and R were
 XX CC constructed. The following mutations were tested for substrate
 XX CC specificity to murine prohormone convertase: 1.4, 2.4, 3.2, 4.3,
 XX CC 7.2 and 8.6 (see AAQ43256-63; AAR37619-26).

XX CC Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

RESULT 10
 AAQ71457/c
 ID AAQ71457 standard; DNA; 21 BP.

XX AC AAQ71457;

XX DT 26-APR-1995 (first entry)

DE Rx 2.4 prorelaxin C/A chain junction mutant cleavage site.

XX KW prohormone; convertase; insulin; proinsulin; factor; growth;

XX KW precursors; transgenic; mammal; prorelaxin; cleavage; ss.

XX OS Synthetic.

PN WO9420624-A.
 XX 15-SEP-1994.
 PD
 XX
 PF 01-MAR-1994; 94WO-US02233.
 XX
 PR 01-MAR-1993; 93US-0026143.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Gorman CM, Grosekrentz DJ,
 XX
 DR WPI; 1994-303031/37.
 DR P-PSDB; AAR60585.
 XX
 PT Treating insulin-dependent disorders in mammals - by introducing
 PT a nucleic acid encoding a variant proinsulin into a host cell,
 PT with a constitutive pathway of protein secretion, or a plasmid,
 PT and introducing the cell or plasmid to the mammal
 XX
 XX Example 3; Page 52, 117pp; English.
 PS
 CC A series of natural or mutated cDNAs for the prohormone convertase (PC)
 CC cleavage sites in human proinsulin protein between the C and A chains
 CC (AAQ7455-59 corresponding to AAR60583-7) or in the B and C chains
 CC (AAQ7460-63 corresponding to AAR60588-90). The natural cleavage sites
 CC contain two dibasic residues, Lys-Arg, both of which are required for
 CC cleavage. The mutant sites have replacements of either residues with an
 CC Ala. This confers specificity to murine PC1. In this particular mutant,
 CC the Lys residue at the fourth position of the cleavage site has been
 CC replaced by a Ala residue. Relaxin is an ovarian hormonal peptide
 CC responsible for remodelling the reproductive tract prior to parturition.
 CC The cells containing both the prohormone convertase gene and the required
 CC precursor to be expressed can be injected into a mammal.
 CC
 SQ Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 11; DB 15; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 11 GCTCTAGATG 1

RESULT 11

AAD33073
 ID AAD33073 standard; DNA; 22 BP.

AC AAD33073;
 XX

DT 01-JUN-2002 (first entry)
 XX

DE Phenylalanine ammonia lyase (PAL) gene amplifying forward PCR primer.
 XX

XX Para-hydroxycinnamic acid; PHCA; food packaging; electronic connector;
 KW phenylalanine ammonia lyase; PAL; glucose; tyrosine ammonia lyase; TAL;
 KW cytochrome P-450; cytochrome P-450 reductase; liquid crystal polymer;
 KW LCP; telecommunication; medical device; aerospace application;
 KW biocatalyst; PCR; primer; ss.

XX
 OS unidentified.
 XX

XX WO200210407-A1.
 PN

XX 07-FEB-2002.
 PD

XX 23-JAN-2001; 2001MO-US02099.
 XX

XX 27-JUL-2000; 2000US-0627216.
 XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX

PA

XX Gatenby AA, Sariafani FS, Tang X, Qi WW, Vannelli T;
 PI
 XX WPI; 2002-280635/32.
 DR
 XX
 PT Novel nucleic acid encoding truncated mutant tyrosine ammonia lyase
 PT (PAL) polypeptide, or mutant TAL polypeptide, useful for producing
 PT parahydroxycinnamic acid in recombinant host cell lacking cinamate
 PT hydroxylase
 XX
 XX Example 9; Page 51, 139pp; English.
 PS

CC The invention relates to methods for biological production of para-
 CC hydroxycinnamic acid (PHCA). The invention relates to developing of a new
 CC biocatalyst for conversion of glucose to PHCA by incorporation of the
 CC wild type phenylalanine ammonia lyase (PAL; EC 4.3.1.5) from the yeast
 CC Rhodotorula glutinis into Escherichia coli underlying the ability of the
 CC wildtype PAL to convert tyrosine to PHCA. The invention is also directed
 CC to developing a new biocatalyst for conversion of glucose to PHCA by
 CC incorporation of the wildtype PAL which possesses enhanced tyrosine
 CC ammonia lyase (TAL) activity from the yeast Rhodotorula glutinis plus the
 CC plant cytochrome P-450 and the cytochrome P-450 reductase into E. coli.
 CC Nucleic acid encoding mutant TAL enzyme is useful for producing PHCA by
 CC recombinant techniques. The recombinantly produced PHCA may be used as a
 CC monomer for production of liquid crystal polymers (LCP). LCP may be used
 CC in electronic connectors and telecommunication and aerospace
 CC applications. LCP resistance to sterilizing radiation has also enabled
 CC these materials to be used in medical devices as well as chemical, and
 CC food packaging applications. The present sequence is a PCR primer used
 CC to amplify PAL gene.
 CC
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 11; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
 |||||
 DB 3 GCTCTAGATG 13

RESULT 12

AAD26921
 ID AAD26921 standard; DNA; 22 BP.

AC AAD26921;
 XX

DT 09-APR-2002 (first entry)
 XX

DE Rhodospiridium toruloides PAL gene amplifying PCR primer A.
 XX

XX para-hydroxycinnamic acid; tyrosine ammonia-lyase; TAL; medical device;
 KW liquid crystal Polymer; LCP; electronic connector; telecommunication;
 KW aerospace application; chemical; red yeast; PCR primer; ss.

XX Rhodospiridium toruloides.
 OS

XX WO200111071-A2.
 PN

XX 15-FEB-2001.
 PD

XX 03-AUG-2000; 2000WO-US21156.
 XX

XX 06-AUG-1999; 99US-147719P.
 XX

XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX

XX Tang X, Vannelli TM, Qi WW, Sariafani S, Gatenby AA;
 PI

XX WPI; 2002-121549/16.
 XX

XX

DR

PT Producing para-hydroxycinnamic acid for producing liquid crystal
 PT polymer, comprises converting cinnamate to PHCA, glucose to PHCA by
 PT phenyl ammonia-lyase route, or generating a biocatalyst with tyrosine
 PT ammonia-lyase activity -
 XX
 PS Example 9; Page 45; 75pp; English.
 CC The invention relates to a method for producing para-hydroxycinnamic
 CC acid (PHCA). The method comprises converting cinnamate to PHCA by
 CC converting glucose to phenylalanine to PHCA through the phenyl
 CC ammonia-lyase (PAL) route or by generating a new biocatalyst possessing
 CC enhanced tyrosine ammonia-lyase (TAL) activity. The method is useful for
 CC the biological production of PHCA which is useful as a monomer for the
 CC production of liquid crystal polymers (LCP), where the LCP is used in
 CC electronic connectors, telecommunications and aerospace applications.
 CC LCP is also useful in medical devices, as well as chemical, and food
 CC packing applications due to its resistance to sterilising radiation. The
 CC present sequence is a PCR primer used for amplifying red yeast
 CC (Rhodospiridium toruloides) PAL gene.
 CC
 SQ Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 other;
 Query Match 100.0%; Score 11; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 |||||
 DB 3 GCTCTAGAATG 13
 |||||
 RESULT 13
 AAT49421
 ID AAT49421 standard; DNA; 23 BP.
 AC AAT49421;
 XX
 XX AAT49421;
 DT 24-AUG-1997 (first entry)
 XX
 DE Banana bunchy top virus DNA component 4 promoter PCR primer BT4.1.
 XX
 KW Banana bunchy top virus; BRTV; intergenic region; promoter;
 KW transgenic plant; polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9638554-A1.
 XX
 PD 05-DEC-1996.
 XX
 PF 31-MAY-1996; 96MO-AU00335.
 XX
 PR 31-MAY-1995; 95AU-0003285.
 XX
 PA (UYOU-) UNIV QUEENSLAND TECHNOLOGY.
 XX
 PI Becker DK, Beetham PR, Dale JL, Dugdale B, Hafner GJ,
 PI Harding RM;
 XX
 DR WPI; 1997-034368/03.
 XX
 PT DNA from intergenic region of banana bunchy top virus DNA component
 PT - useful for promoting, enhancing, regulating or modifying
 PT transcription of a non-BRTV gene in transgenic plants
 XX
 PS Example 2; Page 22; 80pp; English.
 CC PCR primers BT4.1 (+662) (AAT49421) and BT4.2 (+278) (AAT49422) were
 CC used to amplify the intergenic region of banana bunchy top virus
 CC (BRTV) DNA component 4 (see also AAT49386) from BRTV infected banana
 CC nucleic extract. The 659 bp intergenic region was subcloned as a
 CC XbaI and BamHI fragment into pGEM4.1 (+). It was then
 CC cloned from pGEM4.1 as a XbaI and BamHI fragment into pBI101.3

CC (pBT4.1). The component 4 intergenic region insert in pBT4.1 is
 CC given in AAT49400.
 XX
 SQ Sequence 23 BP; 6 A; 2 C; 7 G; 8 T; 0 other;
 Query Match 100.0%; Score 11; DB 18; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 |||||
 DB 1 GCTCTAGAATG 11
 |||||
 RESULT 14
 AAF63470
 ID AAF63470 standard; DNA; 24 BP.
 AC AAF63470;
 XX
 XX AAF63470;
 DT 11-MAY-2001 (first entry)
 XX
 DE Oligonucleotide CLH3.
 XX
 KW Baculovirus expression system; ss.
 XX
 OS Unidentified.
 XX
 PN WO200112829-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 14-AUG-2000; 2000WO-GB03144.
 XX
 PR 18-AUG-1999; 99GB-0019409.
 XX
 PA (UYOX-) UNIV OXFORD BROOKES.
 PA (NATU-) NATURAL ENVIRONMENT RES COUNCIL.
 XX
 PI Possee RD, King LA;
 XX
 DR WPI; 2001-202870/20.
 XX
 PT Method for cloning a gene, especially useful for expressing thousands
 PT of genes in alternative hosts, comprises employing a
 PT replication-deficient baculovirus vector and a rescue vector and
 PT causing the vectors to recombine -
 XX
 PS Disclosure; Page 14; 54pp; English.
 XX
 CC The present invention relates to a method for cloning a gene. The method
 CC comprises employing a replication-deficient baculovirus vector and a
 CC rescue vector, and causing the vectors to recombine to produce a
 CC replication-enabled baculovirus vector having at least one gene to be
 CC cloned. The present sequence is an oligonucleotide used in the present
 CC invention. The method of the present invention is especially useful for
 CC expressing thousands of genes in alternative hosts (e.g. insect cells) to
 CC derive sufficient material for determining protein function.
 CC
 SQ Sequence 24 BP; 6 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 100.0%; Score 11; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 |||||
 DB 3 GCTCTAGAATG 13
 |||||
 RESULT 15
 AAZ08704
 ID AAZ08704 standard; DNA; 25 BP.

```
XX AA08704;
XX 20-OCT-1999 (first entry)
XX
XX Human telomerase RNA template PCR primer R3C.
XX
XX Telomerase; body fluid; cancer; tumour; screening; TRAP; diagnosis;
XX telomeric repeat amplification protocol; detection; PCR primer; ss.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX M09941406-A1.
XX
XX 19-AUG-1999.
XX
XX 16-FEB-1999; 99MO-US03302.
XX
XX 16-FEB-1998; 98US-0074793.
XX
XX (UYMA-) UNIV MARYLAND BALTIMORE.
XX
XX Abruzzo LV, Highsmith E, Stenberg J, Strovel JW;
XX WPI; 1999-508655/42.
XX
XX Detecting telomerase activity in non-cellular body fluid using a
XX modified telomeric repeat amplification protocol
XX
XX Disclosure; Page 16; 32pp; English.
XX
XX A method has been developed for detecting telomerase activity in a
XX non-cellular portion of body fluid from a cancer patient using a
XX modified telomeric repeat amplification protocol (TRAP). A method for
XX detecting cancer comprises: (a) removing the cellular portion of a body
XX fluid specimen from the patient; (b) preparing a protein extract from
XX the body fluid remainder; (c) assaying the extract for the presence and
XX quantity of telomerase RNA or telomerase activity; and (d) comparing the
XX results with normal levels, to determine the presence of cancer. The
XX methods are used in cancer diagnosis and prognosis, and also to monitor
XX cancer therapy effectiveness. Unlike prior art telomerase activity
XX assays in cancer patients, the method allows noninvasive sample
XX collection. The methods are also more reliable and less tumour specific
XX than other methods which detect circulating tumour markers. The present
XX sequence represents a human telomerase RNA template PCR primer used in
XX the exemplification of the present invention.
XX
XX
XX SQ Sequence 25 BP; 7 A; 3 C; 9 G; 6 T; 0 other;
XX
XX Query Match 100.0%; Score 11; DB 20; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GCTTAGATG 11
XX |||||
XX 4 GCTTAGATG 14
XX
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Search completed: June 23, 2003, 05:43:39
Job time : 73.4073 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 01:05:28 ; Search time 127.924 Seconds
(without alignments)
2502.502 Million cell updates/sec

Title: US-08-770-564A-11

Perfect score: 11
Sequence: 1 GCTCTAGATG 11

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Gapop 60.0, Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

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Minimum DB seq length: 0
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Post-processing: listing first 45 summaries

Database:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	100.0	11	6	AR063835
2	11	100.0	15	6	AR063834
3	11	100.0	17	6	AX099957
4	11	100.0	18	6	BD011244
5	11	100.0	18	6	E36993
6	11	100.0	19	6	AR063833
7	11	100.0	19	6	AX244257
8	11	100.0	21	6	AR193717
9	11	100.0	22	6	AR205029
10	11	100.0	22	6	AX082540
11	11	100.0	22	6	AX370655
12	11	100.0	23	6	AR112025
13	11	100.0	24	6	AX085592
14	11	100.0	26	6	A94988
15	11	100.0	26	6	AR000025
16	11	100.0	26	6	AR016055
17	11	100.0	26	6	AR028786
18	11	100.0	26	6	AR059216
19	11	100.0	26	6	AR075527
20	11	100.0	26	6	AR161925
21	11	100.0	26	6	AR169136
22	11	100.0	26	6	AR179447
23	11	100.0	26	6	AR202623
24	11	100.0	26	6	AX022187
25	11	100.0	26	6	AX033377
26	11	100.0	26	6	AX036237
27	11	100.0	26	6	AX468455
28	11	100.0	26	6	BD011297
29	11	100.0	26	6	E36508
30	11	100.0	26	6	E37046
31	11	100.0	26	6	I31770
32	11	100.0	27	6	AR063850
33	11	100.0	27	6	AX175102
34	11	100.0	27	6	AX317989
35	11	100.0	28	6	AX298137
36	11	100.0	30	6	AR063832
37	11	100.0	30	6	AR134697
38	11	100.0	30	6	AX465471
39	11	100.0	34	6	AX175104
40	11	100.0	36	6	AX175105
41	11	100.0	39	6	A63531
42	11	100.0	39	6	AR122907
43	11	100.0	40	6	AR039082
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45	10	90.9	15	6	I07861

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLES	JOURNAL	FEATURES
AR063835	AR063835	Sequence 11 from patent US 5846723.	AR063835	AR063835.1	GI:5993143	Unknown.	Unknown.	1 (bases 1 to 11)	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.	Methods for detecting the RNA component of telomerase	Patent: US 5846723-A 11 08-DEC-1998;	Location/Qualifiers
AR063835	AR063835	Sequence 11 from patent US 5846723.	AR063835	AR063835.1	GI:5993143	Unknown.	Unknown.	1 (bases 1 to 11)	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.	Methods for detecting the RNA component of telomerase	Patent: US 5846723-A 11 08-DEC-1998;	Location/Qualifiers

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Query Match 100.0%; Score 11; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATG 11

RESULT 2
AR063834 15 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 10 from patent US 5846723.
ACCESSION AR063834
VERSION AR063834.1 GI:5933142
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 15)
TITLE Kim, N.Woo, Wu, F., Kealey, J.T., Pruzan, R. and Weinrich, S.L.
JOURNAL Methods for detecting the RNA component of telomerase
FEATURES
    source 1.115
    /organism="unknown"
BASE COUNT 5 a 3 c 4 g 3 t
ORIGIN
Query Match 100.0%; Score 11; DB 6; Length 15;
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Db 1 GCTCTAGATG 11

RESULT 3
AX099957 17 bp DNA linear PAT 02-APR-2001
LOCUS
DEFINITION Sequence 17 from Patent WO0120034.
ACCESSION AX099957
VERSION AX099957.1 GI:13538967
KEYWORDS
SOURCE
ORGANISM Mus musculus.
REFERENCE Mus musculus.
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
JOURNAL 1 (bases 1 to 17)
Voss, J. and Timm, J.
METHODS Methods and compositions for the screening of cell cycle modulators
PATENT: WO 0120034-A 17 22-MAR-2001,
FEATURES
    source 1.117
    /organism="Mus musculus"
    /db_xref="taxon:10090"
BASE COUNT 4 a 3 c 4 g 6 t
ORIGIN
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCTCTAGATG 11
    |||||
Db 4 GCTCTAGATG 14

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RESULT 4
BD011244 18 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Human telomerase catalytic subunit.
ACCESSION BD011244
VERSION BD011244.1 GI:18639617
KEYWORDS JP 2001081042-A/201.
SOURCE
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sechi, T.R., Lingner, J., Nakamura, T., Chapman, K.B., Mori, G.B.,
TITLE Harley, C.B. and Andrews, W.H.
JOURNAL Human telomerase catalytic subunit
PATENT: JP 2001081042-A 201 27-MAR-2001;
COMMENT GERON CORP, UNIVERSITY TECHNOLOGY CORP
OS Unidentified
PN JP 2001081042-A/201
PD 27-MAR-2001
PF 27-JUL-2000 JP 2000227474
PR 01-OCT-1996 US 08/724643, 18-APR-1997 US 08/844419 PR
25-APR-1997 US 08/846017, 06-MAY-1997 US 08/851843 PR
14-AUG-1997 US 08/854050, 14-AUG-1997 US 08/91312 PR
R SECHI, JOACHIM LINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI THOMAS
MORIN.
PI CALVIN B HARLEY WILLIAM H ANDREWS
PC A61K39/00, A61K31/7088, A61K39/00, A61P35/00, A61P43/00,
PC C07K5/10, C07K5/107, C07K5/117, C07K7/06, C07K16/40, C12N9/12, PC
C12N15/08, C12N15/02, C12N14/8, C12N16/68, G01N33/15, G01N33/53, PC
G01N33/53, G01N33/56, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC
PC G01N33/53, G01N33/56, G01N33/573//C12P21/08, A61K37/02, C12N15/00 CC
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CC Topology: Linear;
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTCTAGATG 11

RESULT 5
E36993 18 bp DNA linear PAT 18-JUN-2001
LOCUS
DEFINITION Human telomerase catalytic subunit promoter.
ACCESSION E36993
VERSION E36993.1 GI:13022956
KEYWORDS JP 1999253177-A/201.
SOURCE
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Thomas, R.S., Jochimu, R., Toru, N., Karen, B.C., Greg, B.M.,
TITLE Calvin, B.H. and William, H.A.
JOURNAL Human telomerase catalytic subunit promoter
PATENT: JP 1999253177-A 201 21-SEP-1999;
JERON CORP, UNIVERSITY TECHNOLOGY CORP

```

COMMENT OS Unidentified
 PN JP 1999253177-A/201
 PD 21-SEP-1999
 PR 15-OCT-1998 JP 1998320169
 PR 01-OCT-1998 US 08/722,643,18-APR-1997 US 08/844,419, PR
 25-APR-1997 US 08/846,017,06-MAY-1997 US 08/851,843, PR
 09-MAY-1997 US 08/854,050,14-AUG-1997 US 08/911,312, PR
 14-AUG-1997 US 08/912,951,14-AUG-1997 US 08/915,503, PI THOMAS
 R SECHI, JOCHIMU RINGNER, TORU NAKAMURA, KAREN B CHAPMAN, PI GREG B
 MORIN,
 PI CALVIN B HARRI, WILLIAM H ANDREWS
 PC C12N15/09,A61K31/70,A61K38/55,A61K39/395,A61K39/395,A61K48/00,
 PC C12Q1/02,
 PC C12Q1/48,C12Q1/68,G01N33/15,G01N33/48,G01N33/50//C07K14/47, PC
 C07K16/40,
 PC C12N1/19,C12N1/21,C12N5/10,C12N9/12,C12P21/08,C12N1/19, PC
 C12R1/84),
 PC (C12N1/21,C12R1/19),(C12N9/12,C12R1/19),(C12N9/12,C12R1/84),
 PC (C12N9/12,C12R1/91),C12N15/00,A61K37/64,C12N5/00 CC
 Strandedness: Single;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT source 1..18
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 /db_xref="taxon:32644"
 BASE COUNT 5 a 2 c 7 g 4 t
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 Query Match 100.0%; Score 11; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 9.9e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 Db 1 GCTCTAGAATG 11
 RESULT 6
 AR063833
 LOCUS AR063833 19 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 9 from patent US 5846723.
 ACCESSION AR063833
 VERSION AR063833.1 GI:5993141
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Kim,N.Woo., Wu,F., Kealey,J.T., Prizan,R. and Weinrich,S.L.
 TITLE Methods for detecting the RNA component of telomerase
 JOURNAL Patent: US 5846723-A 9 08-DEC-1998;
 FEATURES Location/Qualifiers
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 QY 1 GCTCTAGAATG 11
 Db 1 GCTCTAGAATG 11
 RESULT 7
 AX244257
 LOCUS AX244257 19 bp DNA linear PAT 28-SEP-2001
 DEFINITION Sequence 19 from Patent WO0166569.

ACCESSION AX244257
 VERSION AX244257.1 GI:15859305
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Melvin,W.T., Breeman,S. and Labus,M.B.
 TITLE Viral antigen and vaccine against isav (infectious salmon anaemia virus)
 JOURNAL Patent: WO 0166569-A 19 13-SEP-2001;
 The University Court of The University of Aberdeen (GB)
 FEATURES Location/Qualifiers
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 /db_xref="taxon:32630"
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 BASE COUNT 5 a 4 c 4 g 6 t
 ORIGIN
 Query Match 100.0%; Score 11; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 Db 1 GCTCTAGAATG 11
 RESULT 8
 AR193717/c
 LOCUS AR193717 21 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 13 from patent US 6348327.
 ACCESSION AR193717
 VERSION AR193717.1 GI:20240309
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Gorman,C.M. and Groskreutz,D.J.
 TITLE Non-endocrine animal host cells capable of expressing variant
 proinsulin and processing the same to form active, mature insulin
 and methods of culturing such cells
 JOURNAL Patent: US 6348327-A 13 19-FEB-2002;
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTCTAGAATG 11
 Db 11 GCTCTAGAATG 1
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 AR205029
 LOCUS AR205029 22 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 5 from patent US 6368837.
 ACCESSION AR205029
 VERSION AR205029.1 GI:21502506
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 22)
 AUTHORS Gatenby,A.A., Sarrafian,S., Tang,X.-S., Qi,W.Wei. and Vannelli,T.
 TITLE Bioproduction of para-hydroxycinnamic acid

JOURNAL Patent: US 6368937-A 5 09-APR-2002;
 FEATURES Location/Qualifiers
 source 1..22
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 BASE COUNT 5 a 7 c 5 g 5 t
 ORIGIN

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QY 1 GCTCTAGATG 11
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 3 GCTCTAGATG 13

RESULT 10
 AX082540 22 bp DNA linear PAT 28-FEB-2001
 LOCUS
 DEFINITION Sequence 5 from Patent WO011071.
 AX082540
 ACCESSION
 VERSION AX082540.1 GI:13184654
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 1 (bases 1 to 22)
 AUTHORS Tang,X.S., Vannelli,T.M., Qi,W.W., Sarislan,I.S. and Gatenby,A.A.
 TITLE Bioproduction of para-hydroxycinnamic acid
 JOURNAL Patent: WO 011071-A 5 15-FEB-2001;
 E.I. DU PONT DE NEMOURS & COMPANY INCORPORATED (US)
 Location/Qualifiers
 source 1..22
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 /db_xref="taxon:32630"
 /note="primer"

BASE COUNT 5 a 7 c 5 g 5 t
 ORIGIN

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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
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 3 GCTCTAGATG 13

RESULT 11
 AX370655 22 bp DNA linear PAT 01-MAR-2002
 LOCUS
 DEFINITION Sequence 5 from Patent WO0210407.
 AX370655
 ACCESSION
 VERSION AX370655.1 GI:19188820
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 REFERENCE
 1
 AUTHORS Gatenby,A.A., Sarislan,I.S., Tang,X.S., Qi,W.W. and Vannelli,T.
 TITLE Bioproduction of para-hydroxycinnamic acid
 JOURNAL Patent: WO 0210407-A 5 07-FEB-2002;
 E.I. DUPONT DE NEMOURS AND COMPANY (US)
 Location/Qualifiers
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 /note="primer"

BASE COUNT 5 a 7 c 5 g 5 t
 ORIGIN

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QY 1 GCTCTAGATG 11
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 3 GCTCTAGATG 13

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 3 GCTCTAGATG 13
 Db

RESULT 12
 AR112025 23 bp DNA linear PAT 14-FEB-2001
 LOCUS
 DEFINITION Sequence 46 from patent US 6127604.
 AR112025
 ACCESSION
 VERSION AR112025.1 GI:12828873
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 REFERENCE
 1 (bases 1 to 23)
 AUTHORS Dale,U.Langham.,Harding,R.Maxwell., Dugdale,B., Beetham,P.Ronald.,
 Halner,G.John. and Becker,D.Kenneth.
 TITLE Intergenic regions of banana bunchy top virus
 JOURNAL Patent: US 6127604-A 46 03-OCT-2000;
 Location/Qualifiers
 source 1..23
 /organism="unknown"
 BASE COUNT 6 a 2 c 7 g 8 t
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 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTAGATG 11
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 1 GCTCTAGATG 11
 Db

RESULT 13
 AX085592 24 bp DNA linear PAT 09-MAR-2001
 LOCUS
 DEFINITION Sequence 5 from Patent WO0112829.
 AX085592
 ACCESSION
 VERSION AX085592.1 GI:13275601
 KEYWORDS
 SOURCE unidentified baculovirus.
 ORGANISM
 REFERENCE
 1 (bases 1 to 24)
 AUTHORS Posee,R.D. and King,L.A.
 TITLE Replication deficient baculovirus expression system
 JOURNAL Patent: WO 0112829-A 5 22-FEB-2001;
 OXFORD BROOKS UNIVERSITY (GB) ; NATURAL ENVIRONMENT RESEARCH COUNCIL (GB)
 Location/Qualifiers
 source 1..24
 /organism="unidentified baculovirus"
 /db_xref="taxon:10469"
 ORIGIN

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QY 1 GCTCTAGATG 11
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 3 GCTCTAGATG 13
 Db

RESULT 14
 A94988 26 bp DNA linear PAT 26-JAN-2000
 LOCUS
 DEFINITION Sequence 2 from Patent EP0926245.
 A94988

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ACCESSION      A94988
VERSION        A94988.1 GI:6779168
KEYWORDS
SOURCE         unidentified.
ORGANISM       unidentified.
REFERENCE      1 (bases 1 to 26)
AUTHORS        Emrich,T.D.
TITLE          Method for detection of carcinoma of the urinary bladder within a
               urine sample
JOURNAL        Patent: EP 0926245-A 2 30-JUN-1999;
               ROCHE DIAGNOSTICS GMBH (DE)
FEATURES
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               /db_xref="taxon:32644"
BASE COUNT    7 a 3 c 9 g 7 t
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Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11
    |||||
Db 5 GCTCTGAATG 15

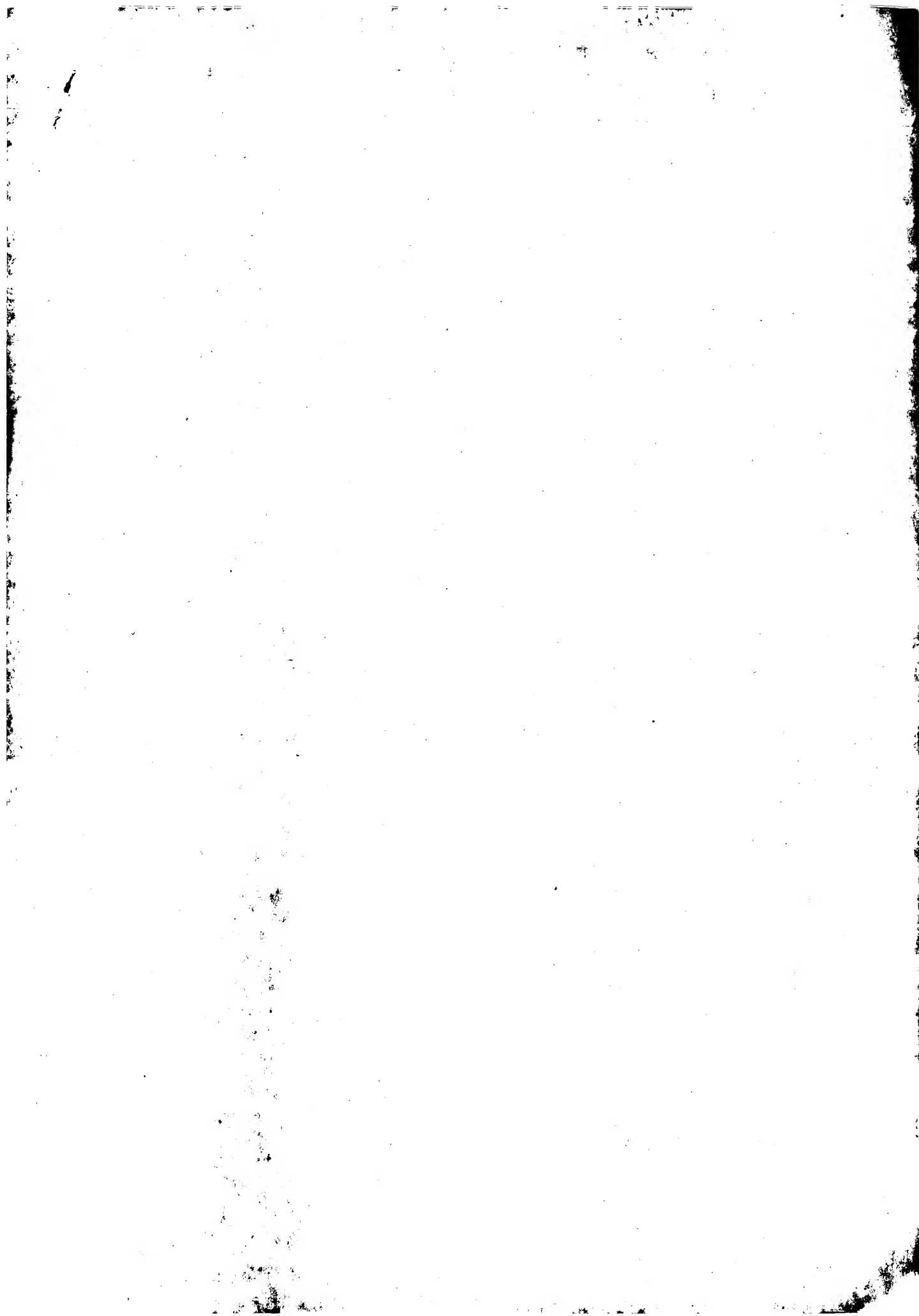
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LOCUS          AR000025
DEFINITION     Sequence 16 from patent US 5736139.
ACCESSION      AR000025
VERSION        AR000025.1 GI:3962556
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 26)
AUTHORS        Kink,J.A., Thalley,B.S., Stafford,D.C., Pirca,J.R. and Padhye,N.V.
TITLE          Treatment of Clostridium difficile induced disease
JOURNAL        Patent: US 5736139-A 16 07-APR-1998;
               Location/Qualifiers
FEATURES
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               /organism="unknown"
BASE COUNT    9 a 7 c 5 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTCTGAATG 11
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Db 1 GCTCTGAATG 11

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Search completed: June 23, 2003, 06:34:21
 Job time : 128.386 secs



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OM nucleic - nucleic search, using sw model

Run on: June 25, 2003, 13:28:55 ; Search time 167.219 Seconds
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Title: US-08-770-564A-12
Perfect score: 7
Sequence: 1 GCTTCAG 7

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Gapop 10.0, Gapext 1.0

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Listing first 45 summaries

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SUMMARIES

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C 1	7	100.0	10	US-10-329-465-53	Sequence 53, Appl
C 2	7	100.0	10	US-10-293-222-131	Sequence 131, Appl
C 3	7	100.0	11	US-10-314-322-34	Sequence 34, Appl
C 4	7	100.0	12	US-10-240-580-38	Sequence 38, Appl
C 5	7	100.0	13	US-10-106-799-13	Sequence 13, Appl
C 6	7	100.0	13	US-10-106-799-14	Sequence 14, Appl
C 7	7	100.0	13	US-10-146-505-84	Sequence 84, Appl
C 8	7	100.0	14	US-10-303-778-13859	Sequence 13859, A
C 9	7	100.0	15	US-10-294-035-747	Sequence 747, Appl
C 10	7	100.0	15	US-10-294-035-748	Sequence 748, Appl
C 11	7	100.0	15	US-10-294-035-940	Sequence 940, Appl
C 12	7	100.0	15	US-10-294-038-1008	Sequence 1008, Appl
C 13	7	100.0	15	US-10-294-038-2682	Sequence 2682, Appl
C 14	7	100.0	15	US-10-294-038-4251	Sequence 4251, Appl
C 15	7	100.0	15	US-10-287-822-1580	Sequence 1580, Appl
C 16	7	100.0	15	US-10-310-188-33324	Sequence 33324, A
C 17	7	100.0	15	US-10-310-188-72013	Sequence 72013, A
C 18	7	100.0	15	US-10-305-273-169	Sequence 169, Appl
C 19	7	100.0	15	US-10-305-273-1191	Sequence 1191, Appl
C 20	7	100.0	15	US-10-305-275-550	Sequence 550, Appl

C 21	7	100.0	15	US-10-316-956-1230	Sequence 1230, Appl
C 22	7	100.0	15	US-10-316-956-1239	Sequence 1239, Appl
C 23	7	100.0	15	US-10-316-956-1250	Sequence 1250, Appl
C 24	7	100.0	15	US-10-316-956-1251	Sequence 1251, Appl
C 25	7	100.0	15	US-10-316-956-1252	Sequence 1252, Appl
C 26	7	100.0	15	US-10-316-954-413	Sequence 413, Appl
C 27	7	100.0	15	US-10-316-954-1307	Sequence 1307, Appl
C 28	7	100.0	15	US-10-316-954-2852	Sequence 2852, Appl
C 29	7	100.0	15	US-10-316-954-2853	Sequence 2853, Appl
C 30	7	100.0	15	US-10-316-954-3393	Sequence 3393, Appl
C 31	7	100.0	15	US-10-316-954-4902	Sequence 4902, Appl
C 32	7	100.0	15	US-10-316-954-4903	Sequence 4903, Appl
C 33	7	100.0	15	US-10-321-854-1864	Sequence 1864, Appl
C 34	7	100.0	15	US-10-321-854-3261	Sequence 3261, Appl
C 35	7	100.0	15	US-10-310-157-1213	Sequence 1213, Appl
C 36	7	100.0	15	US-10-310-157-1214	Sequence 1214, Appl
C 37	7	100.0	15	US-10-310-157-3289	Sequence 3289, Appl
C 38	7	100.0	15	US-10-310-157-4486	Sequence 4486, Appl
C 39	7	100.0	15	US-10-310-157-55923	Sequence 55923, Appl
C 40	7	100.0	15	US-10-310-157-55935	Sequence 55935, Appl
C 41	7	100.0	15	US-10-310-157-6009	Sequence 6009, Appl
C 42	7	100.0	15	US-10-305-273A-169	Sequence 169, Appl
C 43	7	100.0	15	US-10-305-273A-1191	Sequence 1191, Appl
C 44	7	100.0	15	US-10-305-275A-550	Sequence 550, Appl
C 45	7	100.0	15	US-10-367-892-657	Sequence 657, Appl

ALIGNMENTS

RESULT 1
US-10-329-465-53/c
; Sequence 53, Application US/10329465
; GENERAL INFORMATION:
; APPLICANT: Kang et al.
; TITLE OF INVENTION: GENES ABNORMALLY EXPRESSED IN MYELOID LEUKEMIA CELLS WITH AN MLL
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-53

Query Match 100.0%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
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Db 7 GCTTCAG 1

RESULT 2
US-10-293-222-131/c
; Sequence 131, Application US/10293222
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: BP 00201698.8
 PRIOR FILING DATE: 2000-05-11
 PRIOR APPLICATION NUMBER: BP 00202284.6
 PRIOR FILING DATE: 2000-06-29
 NUMBER OF SEQ ID NOS: 455
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO 131
 LENGTH: 10
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-293-222-131

Query Match 100.0%; Score 7; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 10 GCTTCAG 4

RESULT 3
 US-10-314-322-34/c
 Sequence 34, Application US/10314322
 GENERAL INFORMATION:
 APPLICANT: Heber-Katz, Ellen
 TITLE OF INVENTION: Compositions and Methods for Wound
 FILE REFERENCE: 000486.00016
 CURRENT APPLICATION NUMBER: US/10/314,322
 PRIOR FILING DATE: 2002-12-09
 PRIOR APPLICATION NUMBER: US 60/074,737
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/097,937
 PRIOR FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: US 60/102,051
 PRIOR FILING DATE: 1998-09-28
 PRIOR APPLICATION NUMBER: US 09/249,155
 PRIOR FILING DATE: 1999-02-12
 NUMBER OF SEQ ID NOS: 346
 SOFTWARE: PatSeQ for Windows Version 4.0
 SEQ ID NO 34
 LENGTH: 11
 TYPE: DNA
 ORGANISM: Mus musculus
 US-10-314-322-34

Query Match 100.0%; Score 7; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 10 GCTTCAG 4

RESULT 4
 US-10-240-580-38
 Sequence 38, Application US/10240580
 GENERAL INFORMATION:
 APPLICANT: Inoue, Takashi
 TITLE OF INVENTION: METHOD AND APPARATUS FOR MICROORGANISM DISCRIMINATION, METHOD OF
 TITLE OF INVENTION: DATABASE FOR MICROORGANISM DISCRIMINATION, AND MICROORGANISM DIS
 TITLE OF INVENTION: PROGRAM AND RECORDING MEDIUM ON WHICH SUCH PROGRAM IS RECORDED
 FILE REFERENCE: 9982-24
 CURRENT APPLICATION NUMBER: US/10/240,580
 PRIOR FILING DATE: 2002-09-30
 PRIOR APPLICATION NUMBER: PCT/JP01/02516
 PRIOR FILING DATE: 2001-03-27
 PRIOR APPLICATION NUMBER: JP 2000-99482
 PRIOR FILING DATE: 2000-03-31
 NUMBER OF SEQ ID NOS: 46
 SOFTWARE: Patentin version 3.1

SEQ ID NO 38
 LENGTH: 12
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Primer
 US-10-240-580-38

Query Match 100.0%; Score 7; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 4 GCTTCAG 10

RESULT 5
 US-10-106-799-13
 Sequence 13, Application US/10106799
 GENERAL INFORMATION:
 APPLICANT: Council of Scientific and Industrial Research
 TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
 TITLE OF INVENTION: Method thereof
 FILE REFERENCE: US 673
 CURRENT APPLICATION NUMBER: US/10/106,799
 PRIOR FILING DATE: 2002-10-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 13
 LENGTH: 13
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Ap34 arbitrary primer for differential display
 US-10-106-799-13

Query Match 100.0%; Score 7; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 3 GCTTCAG 9

RESULT 6
 US-10-106-799-14
 Sequence 14, Application US/10106799
 GENERAL INFORMATION:
 APPLICANT: Council of Scientific and Industrial Research
 TITLE OF INVENTION: Novel DNA sequence in plants Caragana jubata with freeze toleran
 TITLE OF INVENTION: Method thereof
 FILE REFERENCE: US 673
 CURRENT APPLICATION NUMBER: US/10/106,799
 PRIOR FILING DATE: 2002-10-31
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 14
 LENGTH: 13
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Ap35 arbitrary primer for differential display
 US-10-106-799-14

Query Match 100.0%; Score 7; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
 Db 3 GCTTCAG 9

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RESULT 7
US-10-146-505-84/c
; Sequence 84, Application US/10146505
; GENERAL INFORMATION:
; APPLICANT: Sale, Julian E.
; APPLICANT: Neuberger, Michael S.
; APPLICANT: Cumbers, Sarah J.
; TITLE OF INVENTION: Method of Generating Diversity
; FILE REFERENCE: 18396/2005B
; CURRENT APPLICATION NUMBER: US/10/146,505
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/828,717
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 09/879,813
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: FCT/GB99/03358
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: GB 9822104.7
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: GB 9901141.3
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: GB 9913435.5
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8)-(8)
; OTHER INFORMATION: F220
US-10-146-505-84
Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GCTTCAG 7
Db 7 GCTTCAG 1

RESULT 8
US-10-303-778-13859/c
; Sequence 13859, Application US/10303778
; GENERAL INFORMATION:
; APPLICANT: RosettaGenomics
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL VIRAL
; FILE REFERENCE: 47416
; CURRENT APPLICATION NUMBER: US/10/303,778
; CURRENT FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 17608
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13859
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-778-13859

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 8 GCTTCAG 2

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RESULT 9
US-10-294-035-747/c
; Sequence 747, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 747
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 104
US-10-294-035-747

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 12 GCTTCAG 6

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RESULT 10
US-10-294-035-748/c
; Sequence 748, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 748
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Mycobacterium leprae strain TN complete genome.
; FEATURE:
; LOCATION: (1626549)...(1626563)
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectonObjectNumber = 104
US-10-294-035-748

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Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCTTCAG 7
Db 12 GCTTCAG 6

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RESULT 11
US-10-294-035-940/c
; Sequence 940, Application US/10294035
; GENERAL INFORMATION:
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
; TITLE OF INVENTION: Mycobacterium leprae strain TN complete genome.
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333
; CURRENT APPLICATION NUMBER: US/10/294,035
; CURRENT FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: Proprietary
; SEQ ID NO 940
; LENGTH: 15
; TYPE: DNA

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ORGANISM: Mycobacterium leprae strain TN complete genome.
FEATURE:
LOCATION: (2080233)...(2080248)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 1297
US-10-294-035-940

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 7 GCTTCAG 1

RESULT 12
US-10-294-038-1008
Sequence 1008, Application US/10294038
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,038
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 5372
SOFTWARE: Proprietary
SEQ ID NO 1008
LENGTH: 15
TYPE: DNA
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
FEATURE:
LOCATION: (371601)...(371615)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 1249
US-10-294-038-1008

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 8 GCTTCAG 14

RESULT 13
US-10-294-038-2682
Sequence 2682, Application US/10294038
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,038
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 5372
SOFTWARE: Proprietary
SEQ ID NO 2682
LENGTH: 15
TYPE: DNA
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
FEATURE:
LOCATION: (1117875)...(1117888)
OTHER INFORMATION: Chromosome = 1 Strand = positive ConnectorObjectNumber = 3354
US-10-294-038-2682

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 1 GCTTCAG 7

RESULT 14
US-10-294-038-4251
Sequence 4251, Application US/10294038
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Lactococcus lactis subsp. lactis IL1403 complete g
FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/294,038
CURRENT FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 5372
SOFTWARE: Proprietary
SEQ ID NO 4251
LENGTH: 15
TYPE: DNA
ORGANISM: Lactococcus lactis subsp. lactis IL1403 complete g
FEATURE:
LOCATION: (1902455)...(1902469)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 531
US-10-294-038-4251

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 8 GCTTCAG 14

RESULT 15
US-10-287-822-1580/c
Sequence 1580, Application US/10287822
GENERAL INFORMATION:
APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.
TITLE OF INVENTION: Synecocystis PCC6803 complete genome.
FILE REFERENCE: Jim Zegger Law Offices - 703-684-8333
CURRENT APPLICATION NUMBER: US/10/287,822
CURRENT FILING DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 5726
SOFTWARE: Proprietary
SEQ ID NO 1580
LENGTH: 15
TYPE: DNA
ORGANISM: Synecocystis PCC6803 complete genome.
FEATURE:
LOCATION: (959678)...(959693)
OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectorObjectNumber = 208
US-10-287-822-1580

Query Match
Best Local Similarity 100.0%; Score 7; DB 9; Length 15;
Pred. No. 2.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 11 GCTTCAG 5

Search completed: June 26, 2003, 04:15:21
Job time: 168.527 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2003, 22:19:40 ; Search time 593.968 Seconds
(without alignments)
296.308 Million cell updates/sec

Title: US-08-770-564A-12

Perfect score: 7

Sequence: 1 GCTTCAG 7

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 12114646

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18: /cgn2_6/prodata/2/pna/US094_COMB.seq:*

19: /cgn2_6/prodata/2/pna/US095A_COMB.seq:*

20: /cgn2_6/prodata/2/pna/US095B_COMB.seq:*

21: /cgn2_6/prodata/2/pna/US095C_COMB.seq:*

22: /cgn2_6/prodata/2/pna/US095D_COMB.seq:*

23: /cgn2_6/prodata/2/pna/US096A_COMB.seq:*

24: /cgn2_6/prodata/2/pna/US096B_COMB.seq:*

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28: /cgn2_6/prodata/2/pna/US097A_COMB.seq:*

29: /cgn2_6/prodata/2/pna/US097B_COMB.seq:*

30: /cgn2_6/prodata/2/pna/US097C_COMB.seq:*

31: /cgn2_6/prodata/2/pna/US098A_COMB.seq:*

32: /cgn2_6/prodata/2/pna/US098B_COMB.seq:*

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34: /cgn2_6/prodata/2/pna/US099A_COMB.seq:*

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Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	7	11 US-08-770-564A-12	Sequence 12, Appl
2	7	100.0	8	10 US-08-632-782-86	Sequence 86, Appl
3	7	100.0	10	1 PCT-US00-04606-65	Sequence 65, Appl
4	7	100.0	10	1 PCT-US01-10743A-43	Sequence 43, Appl
5	7	100.0	10	1 PCT-US01-10743A-44	Sequence 44, Appl
6	7	100.0	10	1 PCT-US01-18814-44	Sequence 44, Appl
7	7	100.0	10	1 PCT-US01-18814-49	Sequence 49, Appl
8	7	100.0	10	1 PCT-US01-21306-130	Sequence 130, App
9	7	100.0	10	1 PCT-US01-23100-118	Sequence 118, App
10	7	100.0	10	1 PCT-US01-29207-36	Sequence 36, Appl
11	7	100.0	10	1 PCT-US01-42721-58	Sequence 58, Appl
12	7	100.0	10	1 PCT-US02-24250-52	Sequence 52, Appl
13	7	100.0	10	1 PCT-US97-13800-10	Sequence 10, Appl
14	7	100.0	10	1 PCT-US99-13800-226	Sequence 226, App
15	7	100.0	10	1 PCT-US99-13800-1449	Sequence 1449, Ap
16	7	100.0	10	8 US-08-458-785-49	Sequence 49, Appl
17	7	100.0	10	8 US-08-459-444-49	Sequence 49, Appl
18	7	100.0	10	8 US-08-459-448-49	Sequence 49, Appl
19	7	100.0	10	8 US-08-459-504-49	Sequence 49, Appl
20	7	100.0	10	8 US-08-459-504A-49	Sequence 49, Appl
21	7	100.0	10	8 US-08-459-595-49	Sequence 49, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22 7 100.0 10 8 US-08-460-408-49 Sequence 49, Appl
 23 7 100.0 10 17 US-09-335-032-369 Sequence 369, App
 24 7 100.0 10 17 US-09-335-032-2641 Sequence 2641, App
 25 7 100.0 10 17 US-09-335-032-2931 Sequence 2931, App
 26 7 100.0 10 17 US-09-335-032-4373 Sequence 4373, App
 27 7 100.0 10 17 US-09-335-032-8177 Sequence 8177, App
 28 7 100.0 10 17 US-09-335-032-8178 Sequence 8178, App
 29 7 100.0 10 17 US-09-336-376-1613 Sequence 1613, App
 30 7 100.0 10 17 US-09-336-376-1701 Sequence 1701, App
 31 7 100.0 10 17 US-09-336-376-4067 Sequence 4067, App
 32 7 100.0 10 17 US-09-336-376-4990 Sequence 4990, App
 33 7 100.0 10 31 US-09-816-763-61 Sequence 61, Appl
 34 7 100.0 10 37 US-09-988-462-49 Sequence 462, App
 35 7 100.0 10 38 US-10-033-145-226 Sequence 226, Appl
 36 7 100.0 10 38 US-10-033-145-1449 Sequence 1449, App
 37 7 100.0 11 1 PCT-US02-13093A-81 Sequence 81, Appl
 38 7 100.0 11 16 US-09-249-155A-34 Sequence 34, Appl
 39 7 100.0 11 16 US-09-249-155A-34 Sequence 34, Appl
 40 7 100.0 12 16 US-08-864-765A-3 Sequence 3, Appl
 41 7 100.0 12 16 US-09-287-332-20 Sequence 20, Appl
 42 7 100.0 12 18 US-09-424-521-9 Sequence 3, Appl
 43 7 100.0 12 19 US-09-528-209A-2823 Sequence 2823, App
 44 7 100.0 12 19 US-09-528-209A-7616 Sequence 7616, App
 45 7 100.0 12 33 US-09-868-605-25 Sequence 25, Appl

ALIGNMENTS

RESULT 1
 US-08-770-564a-12
 ; Sequence 12, Application US/08770564A
 ; GENERAL INFORMATION:
 ; APPLICANT: Kealey, James T.
 ; APPLICANT: Pruzan, Ron
 ; APPLICANT: Weinrich, Scott L.
 ; TITLE OF INVENTION: Inhibitory Polynucleotides Directed
 ; TITLE OF INVENTION: Against the RNA Component of Telomerase
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/770,564A
 ; FILING DATE: 20-DEC-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Storella, John R.
 ; REGISTRATION NUMBER: 32,944
 ; REFERENCE/DOCKET NUMBER: 015389-002200US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; TELEFAX: 415-576-0300
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-770-564A-12
 Query March 100.0%; Score 7; DB 11; Length 7;
 Best Local Similarity 100.0%; Pred. No. 3.5e+09;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 Db 1 GCTTCAG 7
 RESULT 2
 US-08-632-782-86
 ; Sequence 86, Application US/08632782
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardin, Susan H.
 ; APPLICANT: Homayouni, Ramtin
 ; APPLICANT: Hardin, Paul B.
 ; TITLE OF INVENTION: Design and Optimized Primer Library for
 ; TITLE OF INVENTION: Gene Sequencing and Method Thereof
 ; NUMBER OF SEQUENCES: 566
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski L.L.P.
 ; STREET: 1301 McKinney, Suite 5100
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.A.
 ; ZIP: 77010-3095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/632,782
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paul, Thomas D.
 ; REGISTRATION NUMBER: 32,714
 ; REFERENCE/DOCKET NUMBER: D-5900
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713/651-5525
 ; TELEFAX: 713/651-5246
 ; INFORMATION FOR SEQ ID NO: 86:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "oligonucleotide"
 ; HYPOTHETICAL: YES
 ; ANTI-SENSE: YES
 ; US-08-632-782-86
 Query March 100.0%; Score 7; DB 10; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.1e+09;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCTTCAG 7
 Db 1 GCTTCAG 7
 RESULT 3
 PCT-US00-04606-65/c
 ; Sequence 65, Application PC/TUS0004606
 ; GENERAL INFORMATION:
 ; APPLICANT: Genasense Pharmaceuticals, Inc.
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Schulz, Vincent P.
 ; APPLICANT: Stephens, J. Claiborne
 ; APPLICANT: Chew, Anne
 ; TITLE OF INVENTION: Drug Target Isoforms: Polymorphisms in the Tumor
 ; TITLE OF INVENTION: Necrosis Factor Receptor I Gene
 ; FILE REFERENCE: MMH03030PCT

CURRENT APPLICATION NUMBER: PCT/US00/04606
CURRENT FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: 60/121,314
EARLIER FILING DATE: 1999-02-23
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 10
TYPE: DNA
ORGANISM: HOMO SAPIENS
PCT-US00-04606-65

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 9 GCTTCAG 3

RESULT 4
PCT-US01-10743A-43/C
Sequence 43, Application PC/TUS0110743A
GENERAL INFORMATION:
APPLICANT: Genaisance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
APPLICANT: Choi, Julie Y.
APPLICANT: Koshiy, Beena
TITLE OF INVENTION: Haplotypes of the SCN2B Gene
FILE REFERENCE: MMH-0481PCT SCN2B
CURRENT APPLICATION NUMBER: PCT/US01/10743A
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/196,597
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapien
PCT-US01-10743A-43

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 7 GCTTCAG 1

RESULT 5
PCT-US01-10743A-44
Sequence 44, Application PC/TUS0110743A
GENERAL INFORMATION:
APPLICANT: Genaisance Pharmaceuticals, Inc.
APPLICANT: Chew, Anne
APPLICANT: Choi, Julie Y.
APPLICANT: Koshiy, Beena
TITLE OF INVENTION: Haplotypes of the SCN2B Gene
FILE REFERENCE: MMH-0481PCT SCN2B
CURRENT APPLICATION NUMBER: PCT/US01/10743A
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 60/196,597
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapien
PCT-US01-10743A-44

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 3 GCTTCAG 9

RESULT 6
PCT-US01-18814-44/C
Sequence 44, Application PC/TUS0118814
GENERAL INFORMATION:
APPLICANT: Genaisance Pharmaceuticals, Inc.
APPLICANT: Choi, Julie Y.
APPLICANT: Koshiy, Beena
APPLICANT: Sanchez, Angela
APPLICANT: Saueker, Elizabeth Ann
TITLE OF INVENTION: HAPLOTYPES OF THE PKG2 GENE
FILE REFERENCE: MMH-0770PCT PKG2
CURRENT APPLICATION NUMBER: PCT/US01/18814
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,568
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-18814-44

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 10 GCTTCAG 4

RESULT 7
PCT-US01-18814-49
Sequence 49, Application PC/TUS0118814
GENERAL INFORMATION:
APPLICANT: Genaisance Pharmaceuticals, Inc.
APPLICANT: Choi, Julie Y.
APPLICANT: Koshiy, Beena
APPLICANT: Sanchez, Angela
APPLICANT: Saueker, Elizabeth Ann
TITLE OF INVENTION: HAPLOTYPES OF THE PKG2 GENE
FILE REFERENCE: MMH-0770PCT PKG2
CURRENT APPLICATION NUMBER: PCT/US01/18814
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 60/210,568
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 49
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US01-18814-49

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
|||||
Db 4 GCTTCAG 10

PCT-US01-21306-130
 RESULT 8-21306-130
 Sequence 130. Application PC/RUS0121306
 GENERAL INFORMATION:
 APPLICANT: Genesense Pharmaceuticals, Inc.
 APPLICANT: Gentilevna, Steven C
 APPLICANT: Bieganski, Kathryn M.
 APPLICANT: Kazemli, Amir
 APPLICANT: Koshy, Beena
 TITLE OF INVENTION: Haplotypes of the E7FB Gene
 FILE REFERENCE: MMH-0902PCT E7FB
 CURRENT APPLICATION: PCT/US01/21306
 CURRENT FILING DATE: 2001-07-06
 PRIOR APPLICATION NUMBER: 60/215,984
 PRIOR FILING DATE: 2000-07-05
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 130
 LENGTH: 10
 TYPE: DNA
 ORGANISM: Homo sapiens
 PCT-US01-21306-130

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Query Match      100.0%; Score 7; DB 1; Length 10
Blast Local      100.0%; Pred. No. 7.1e+05;
Matches          7; Conservative 0; Indels
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               3 GCTTACG 9

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PCT-US01-23100-118
PCT-RESULT 9
Sequence 118, Application PC/TUS0123100
GENERAL INFORMATION:
APPLICANT: Genesance Pharmaceuticals
APPLICANT: Duda, Amy
APPLICANT: Koshy, Beena
APPLICANT: Sanchez, Angela
TITLE OF INVENTION: Haplotypes of the CHRNA1
FILE REFERENCE: MMH-071PCT-CHRNA1
CURRENT APPLICATION NUMBER: PCT/US01/23100
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: 60/219,538
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 118
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapien
PCT-US01-23100-118

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```

Query Match      100.0%; Score 7; DB 1; Length 10
Best Local Similarity 100.0%; Pred. No. 7, le+05;
Matches      7; Conservative      0; Mismatches      0; Indels
QY      1 GCTTCAG 7
        |||||
Db       2 GCTTCAG 8

```

RESULT 10
PCT-US01-29207-36
Sequence 36, Application PC/TUS0129207
GENERAL INFORMATION:
APPLICANT: Genalsence Pharmaceuticals
APPLICANT: Koshy, Beena
APPLICANT: Sanchis, Angela
APPLICANT: Tirrell, Charles
-TITLE OF INVENTION: Haplotypes of the GPR7 Gene

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1  LIFE:REFERENCE: MMH-1293PCT
2  CURRENT APPLICATION NUMBER: PCT/US01/29207
3  CURRENT FILING DATE: 2001-09-17
4  PRIOR APPLICATION NUMBER: 60/232,900
5  PRIOR FILING DATE: 2000-09-15
6  NUMBER OF SEQ ID NOS: 46
7  SOFTWARE: PatentIn Ver. 2.1
8  SEQ ID NO 36
9  LENGTH: 10
10 TYPE: DNA
11 ORGANISM: Homo sapien
12
13 CCT-US01-29207-36

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Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; P-rod. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCTTCAG 7
    |||||
Db 1 GCTTCAG 7

```

```

1  RESULT 11
2  PCT-US01-42727-58/c
3  Sequence 58, Application PC/TUS01.42727
4  GENERAL INFORMATION:
5  APPLICANT: Anastasee Pharmaceuticals, Inc.
6  APPLICANT: Anastasio, Alison E.
7  APPLICANT: Chew, Anne
8  APPLICANT: Han, Jin-Hua
9  APPLICANT: Sanchez, Angela
10 TITLE OF INVENTION: HAPLOTYPES OF THE CYP27A1 GENE
11 FILE REFERENCE: CYP27A1 MMH-12/9POT
12 CURRENT APPLICATION NUMBER: PCT/US01/42727
13 CURRENT FILING DATE: 2001-10-15
14 PRIOR APPLICATION NUMBER: 60/239,942
15 PRIOR FILING DATE: 2000-10-13
16 NUMBER OF SEQ ID NOS: 74
17 SOFTWARE: PatentIn version 3.1
18 SEQ ID NO: 58
19 LENGTH: 10
20 TYPE: DNA
21 ORGANISM: Homo sapiens
22 PCT-US01-42727-58

```

```

Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7, 1e+05;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
QY      1 GCTTCAG 7
        |||||
db      7 GCTTCAG 1

```

```

RESULT 12
PCT-US02-24250-52/c
Sequence 52, Application PC/TUS0224250
GENERAL INFORMATION:
APPLICANT: Genesense Pharmaceuticals, Inc.
APPLICANT: Denton, R. Rex
APPLICANT: Drysdale, Connie M.
APPLICANT: Hoffman, Michael
APPLICANT: Judson, Richard S.
APPLICANT: Maerz, Winfried
APPLICANT: Nandabalan, Krishnan
APPLICANT: Stack, Catherine B.
APPLICANT: Stephens, J. Claiborne
APPLICANT: Vanden Eng, Jodi
APPLICANT: Winkelmann, Bernard R.
TITLE OF INVENTION: Association of Low Density Lipoprotein Receptor (LDLR) Gene Haplotypes with Response to Statins
TITLE OF INVENTION: Response to Statins
FILE REFERENCE: MMH-2889PCT LDLR

```


CURRENT APPLICATION NUMBER: PCT/US02/24250
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 60/308,688
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 52
LENGTH: 10
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US02-24250-52

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 10 GCTTCAG 4

RESULT 13
PCT-US97-13001-10/c
Sequence 10, Application PC/TUS9713001
GENERAL INFORMATION:
APPLICANT: Toothman, Penelope
TITLE OF INVENTION: Method of Identifying Aloe Using
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratechun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/13001
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/022,611
FILING DATE: 26-JULY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: UNI_07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE:
PCT-US97-13001-10

Query Match 100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCTTCAG 7
| | | | |
DB 7 GCTTCAG 1

RESULT 14

PCT-US99-13800-226/c
Sequence 226, Application PC/TUS9913800
GENERAL INFORMATION:
APPLICANT: Genzyme Corporation
APPLICANT: Roberts, Bruce L.
TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
FILE REFERENCE: 68126841206940
CURRENT APPLICATION NUMBER: PCT/US99/13800
FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 60/090,039
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,040
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,041
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,853
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,997
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,079
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,035
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,993
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,992
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,072
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,878
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,991
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,000
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,048
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,999
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,043
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,042
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,036
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,044
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,844
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,080
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,833
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/089,994
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,077
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,078
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,047
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,076
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/090,045
FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/111,715
FILING DATE: 1998-12-08
NUMBER OF SEQ ID NOS: 2138
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 226
LENGTH: 10
TYPE: DNA

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Page 6

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; ORGANISM: Homo sapiens
PCT-US99-13800-226

Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
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        9 CCTTCAG 3

RESULT 15
PCT-US99-13800-1449/c
; Sequence 1449, Application PC/TUS9913800
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Roberts, Bruce L.
; APPLICANT: Shankara, Srinivas
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: 68126891206940
; CURRENT APPLICATION NUMBER: PCT/US99/13800
; CURRENT FILING DATE: 1998-06-18
; EARLIER APPLICATION NUMBER: 60/090,039
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,040
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,041
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,853
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,997
; EARLIER FILING DATE: 1998-06-19
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; EARLIER FILING DATE: 1998-06-19
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; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,992
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,072
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,878
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,991
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/090,048
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; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,844
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,080
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,833
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/089,994
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; EARLIER APPLICATION NUMBER: 60/090,077
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,078
; EARLIER FILING DATE: 1998-06-19
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; EARLIER APPLICATION NUMBER: 60/090,047
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,076
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/090,045
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: 60/111,715
; EARLIER FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 2138
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1449
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-13800-1449

Query Match      100.0%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GCTTCAG 7
        |||||
        10 CCTTCAG 4
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Job time : 595.583 secs